

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 21:55:46 ; Search time 817 Seconds  
(without alignments)  
10895.563 Million cell updates/sec

Title: US-09-051-843D-3

Perfect score: 1383  
Sequence: 1 ggcctcaacagcagcagcaag.....tcactgtgacctgtgagaaga 1383

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:.\*  
1: gb env:.\*  
2: gb pat:.\*  
3: gb ph:.\*  
4: gb pl:.\*  
5: gb pr:.\*  
6: gb ro:.\*  
7: gb sts:.\*  
8: gb sy:.\*  
9: gb un:.\*  
10: gb vi:.\*  
11: gb ov:.\*  
12: gb htg:.\*  
13: gb in:.\*  
14: gb om:.\*  
15: gb\_ba:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID       | Description        |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1          | 1383   | 100.0       | 1383   | 2  | AR691934 | AR691934 Sequence  |
| 2          | 1333.8 | 96.4        | 1708   | 5  | HSU81379 | UB1379 Homo sapien |
| 3          | 1333.8 | 96.4        | 2139   | 5  | BC009960 | BC009960 Homo sapi |
| 4          | 1333.8 | 96.4        | 3999   | 5  | HS113RA1 | Y09328 H.sapiens m |
| 5          | 1333.8 | 96.4        | 4009   | 2  | A63257   | A63257 Sequence 3  |
| 6          | 1333.8 | 96.4        | 4038   | 2  | AR541611 | AR541611 Sequence  |
| 7          | 1333.8 | 96.4        | 4039   | 2  | CO894698 | CO894698 Sequence  |
| 8          | 1333.8 | 96.4        | 4039   | 2  | AX335537 | AX335537 Sequence  |
| 9          | 1333.8 | 96.4        | 4039   | 2  | AX411212 | AX411212 Sequence  |
| 10         | 1333.8 | 96.4        | 4039   | 2  | HS113RA  | Y10659 H.sapiens I |
| 11         | 1333.8 | 96.4        | 11927  | 2  | AR282860 | AR282860 Sequence  |
| 12         | 1332.2 | 96.3        | 2153   | 5  | BC015768 | BC015768 Homo sapi |
| 13         | 1330.6 | 96.3        | 1572   | 5  | HSU62858 | U62858 Human inter |
| 14         | 1304.8 | 94.3        | 3960   | 5  | AB209849 | AB209849 Homo sapi |
| 15         | 1262.8 | 89.4        | 3906   | 2  | AY892945 | AY892945 Synthetic |
| 16         | 1236.8 | 85.7        | 3906   | 2  | AX099392 | AX099392 Sequence  |
| 17         | 1185   | 73.2        | 1260   | 5  | AY312267 | AY312267 Macaca fa |
| 18         | 1012   |             | 1547   | 2  | AR483302 | AR483302 Sequence  |

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| C | 19 | 1012   | 73.2 | 1547 | 2  | AR483303 | AR483303 Sequence  |
| C | 20 | 1012   | 73.2 | 1547 | 2  | AX280314 | AX280314 Sequence  |
| C | 21 | 1012   | 73.2 | 1547 | 2  | AX280316 | AX280316 Sequence  |
| C | 22 | 1012   | 73.2 | 1547 | 14 | AF314532 | AF314532 Canis fam |
| C | 23 | 1009.8 | 73.0 | 2382 | 2  | BD231183 | BD231183 Antagonis |
| C | 24 | 1009.8 | 73.0 | 2382 | 2  | CQ796435 | CQ796435 Sequence  |
| C | 25 | 1009.8 | 73.0 | 2382 | 2  | AR242285 | AR242285 Sequence  |
| C | 26 | 1009.8 | 73.0 | 2382 | 2  | AR703553 | AR703553 Sequence  |
| C | 27 | 1009.8 | 73.0 | 2382 | 2  | AX503605 | AX503605 Sequence  |
| C | 28 | 995    | 71.9 | 1272 | 14 | AY266142 | AY266142 Sus scrof |
| C | 29 | 988.4  | 71.5 | 1206 | 14 | AY377582 | AY377582 Ovis arie |
| C | 30 | 983    | 71.1 | 1215 | 2  | AR483304 | AR483304 Sequence  |
| C | 31 | 983    | 71.1 | 1215 | 2  | AR483305 | AR483305 Sequence  |
| C | 32 | 983    | 71.1 | 1215 | 2  | AX280317 | AX280317 Sequence  |
| C | 33 | 983    | 71.1 | 1215 | 2  | AX280318 | AX280318 Sequence  |
| C | 34 | 959.4  | 69.4 | 2355 | 2  | BD231182 | BD231182 Antagonis |
| C | 35 | 959.4  | 69.4 | 2355 | 2  | CQ796433 | CQ796433 Sequence  |
| C | 36 | 959.4  | 69.4 | 2355 | 2  | AR242284 | AR242284 Sequence  |
| C | 37 | 959.4  | 69.4 | 2355 | 2  | AR703552 | AR703552 Sequence  |
| C | 38 | 959.4  | 69.4 | 2355 | 2  | AX503603 | AX503603 Sequence  |
| C | 39 | 956.4  | 69.2 | 966  | 2  | AR577151 | AR577151 Sequence  |
| C | 40 | 956.4  | 69.2 | 966  | 2  | AX280235 | AX280235 Sequence  |
| C | 41 | 946.6  | 68.4 | 2331 | 2  | CS162831 | CS162831 Sequence  |
| C | 42 | 946.6  | 68.4 | 2331 | 2  | CS162833 | CS162833 Sequence  |
| C | 43 | 946.6  | 68.4 | 2331 | 2  | CS162835 | CS162835 Sequence  |
| C | 44 | 946.6  | 68.4 | 2331 | 2  | CS162837 | CS162837 Sequence  |
| C | 45 | 946.6  | 68.4 | 2331 | 2  | CS162839 | CS162839 Sequence  |

#### ALIGNMENTS

RESULT 1  
LOCUS AR691934 1383 bp DNA linear PAT 13-SEP-2005  
DEFINITION Sequence 3 from patent US 6911530.  
ACCESSION AR691934  
VERSION AR691934.1 GI:74480011

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1383)  
AUTHORS Willison,T., Nicola,N.A., Hilton,D.J., Metcalf,D. and Zhang,J.G.  
TITLE Haemopoietin receptor and genetic sequences encoding same  
JOURNAL Patent: US 6911530-A 3 28-JUN-2005;  
Amrad Operations, Pty., Ltd., Richmond;  
AUX;

FEATURES  
source location/Qualifiers  
1..1383 /organism="unknown"  
/mol\_type="genomic DNA"

#### ORIGIN

Query Match 100.0%; Score 1383; DB 2; Length 1383;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGCTTAACACGACCAAGAGTTTAAACATGCGCGCCGCGGTTCCGAGGCGAGAGCTGC 60  
1 GAGCTTAACACGACCAAGAGTTTAAACATGCGCGCGCGGTTCCGAGGCGAGAGCTGC 60  
Db 1 GAGCTTAACACGACCAAGAGTTTAAACATGCGCGCGCGGTTCCGAGGCGAGAGCTGC 60  
QY 61 ATGAGATGCGCGCGCGCGCTCTGCGCGCGCTGCGCGCTGCTGCTGCTGCGCGCGCGCGG 120  
61 ATGAGATGCGCGCGCGCGCTCTGCGCGCGCTGCGCGCTGCTGCTGCTGCGCGCGCGCGG 120  
Db 61 ATGAGATGCGCGCGCGCGCTCTGCGCGCGCTGCGCGCTGCTGCTGCTGCGCGCGCGCGG 120  
QY 121 GCGCGCGCGCGCGCGCGCGCTTACGAAACTCAGACCTGTGCAAAATTTGAGTGTCT 180  
121 GCGCGCGCGCGCGCGCGCGCTTACGAAACTCAGACCTGTGCAAAATTTGAGTGTCT 180  
Db 121 GCGCGCGCGCGCGCGCGCGCTTACGAAACTCAGACCTGTGCAAAATTTGAGTGTCT 180  
QY 181 GTTGAATACTCTGCACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAAT 240  
181 GTTGAATACTCTGCACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAAT 240  
Db 181 GTTGAATACTCTGCACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAAT 240

|    |      |   |      |
|----|------|---|------|
| OY | 241  | TGTAAGCTAATGATATTTTAATGTCATTTTGGCCGAACAAACAAAGATAAGAAAATAGCTCCGAA | 300  |
| Db | 241  | TGTAAGCTAATGATATTTTAATGTCATTTTGGCCGAACAAACAAAGATAAGAAAATAGCTCCGAA | 300  |
| OY | 301  | ACTGTCGTTCAATGAAGATACCCCTGATGAGAGATTTGTCGCAATGGGGGTCGAG           | 360  |
| Db | 301  | ACTGTCGTTCAATGAAGATACCCCTGATGAGAGATTTGTCGCAATGGGGGTCGAG           | 360  |
| OY | 361  | TGTAGCACCAATGAGAGTGAAGAGCTAGACATTTTGTGTAAGAAAATGCAATCCACCCCA      | 420  |
| Db | 361  | TGTAGCACCAATGAGAGTGAAGAGCTAGACATTTTGTGTAAGAAAATGCAATCCACCCCA      | 420  |
| OY | 421  | GAAAGTATTCCTGAGTCTGCTGTGACTGAACCTTGCATGATTTGGCACAACCTGAGCTAC      | 480  |
| Db | 421  | GAAAGTATTCCTGAGTCTGCTGTGAACCTTGCATGATTTGGCACAACCTGAGCTAC          | 480  |
| OY | 481  | ATGAAGTTCCTTGGCTCCCTGGAAAGAAATACCACTCCGACACTAATCTACTCTAC          | 540  |
| Db | 481  | ATGAAGTTCCTTGGCTCCCTGGAAAGAAATACCACTCCGACACTAATCTACTCTAC          | 540  |
| OY | 541  | TATTGGCACAGAGCTTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAA          | 600  |
| Db | 541  | TATTGGCACAGAGCTTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAA          | 600  |
| OY | 601  | TACTTTGGTTCCTTTCATCTGACCAAGAGAGAGTTCCAGTTTGGACAACACAGT            | 660  |
| Db | 601  | TACTTTGGTTCCTTTCATCTGACCAAGAGAGAGTTCCAGTTTGGACAACACAGT            | 660  |
| OY | 661  | GTCCAAATTAATGATCAAGGATTAATGACAGAAAAATTAACATCCTTCAATATAGTGCT       | 720  |
| Db | 661  | GTCCAAATTAATGATCAAGGATTAATGACAGAAAAATTAACATCCTTCAATATAGTGCT       | 720  |
| OY | 721  | TTAATCTCCCGTGTGAAAACCTGATCTCCACATATTAATAAAACCTCTCCTTCCACATGAT     | 780  |
| Db | 721  | TTAATCTCCCGTGTGAAAACCTGATCTCCACATATTAATAAAACCTCTCCTTCCACATGAT     | 780  |
| OY | 781  | GACCTAATATGTCCAATGGGAGAAATCCACAGAAATTTTATAGAGATGTCATTTTATGAA      | 840  |
| Db | 781  | GACCTAATATGTCCAATGGGAGAAATCCACAGAAATTTTATAGAGATGTCATTTTATGAA      | 840  |
| OY | 841  | GTAGAAGTCAAATAACAGCCAAACCTGAGACACATTAATGTTTTCTAGTCCAAGAGGCTAAA    | 900  |
| Db | 841  | GTAGAAGTCAAATAACAGCCAAACCTGAGACACATTAATGTTTTCTAGTCCAAGAGGCTAAA    | 900  |
| OY | 901  | TGTAGGAATCCAGAAATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGATCCCTGCT      | 960  |
| Db | 901  | TGTAGGAATCCAGAAATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGATCCCTGCT      | 960  |
| OY | 961  | GTTCTTCCTGATACTTGTGAACACAGTCAAGAAATAAGTCAAAAACAAATTAAGTTATGCTAT   | 1020 |
| Db | 961  | GTTCTTCCTGATACTTGTGAACACAGTCAAGAAATAAGTCAAAAACAAATTAAGTTATGCTAT   | 1020 |
| OY | 1021 | GAGGATGACAAAATCTGTGAGTAAATTTGGAGCCAAAGAAAGAGTAATGTAAAGAGGCAAT     | 1080 |
| Db | 1021 | GAGGATGACAAAATCTGTGAGTAAATTTGGAGCCAAAGAAAGAGTAATGTAAAGAGGCAAT     | 1080 |
| OY | 1081 | TCACACTCTCATPAACCATGTTACTCATTTGTTCCAGTCATGTCGCAAGGTCAATCYAA       | 1140 |
| Db | 1081 | TCACACTCTCATPAACCATGTTACTCATTTGTTCCAGTCATGTCGCAAGGTCAATCYAA       | 1140 |
| OY | 1141 | GTAATCCTGCTTTAACTTAAAAAGGCTCAAGATTTATTAATTTCCCTCCAAATTCCTGATCT    | 1200 |
| Db | 1141 | GTAATCCTGCTTTAACTTAAAAAGGCTCAAGATTTATTAATTTCCCTCCAAATTCCTGATCT    | 1200 |
| OY | 1201 | GCGCAAGATTTTAAAGAAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAG        | 1260 |
| Db | 1201 | GCGCAAGATTTTAAAGAAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAG        | 1260 |
| OY | 1261 | TACGACATCTATGAGAGCAAAACCAAGAGGAAACCGACTCTGTATGTGCTGATATGAAAAAC    | 1320 |
| Db | 1261 | TACGACATCTATGAGAGCAAAACCAAGAGGAAACCGACTCTGTATGTGCTGATATGAAAAAC    | 1320 |

[illegible]

Db 134 CAGCACCTGTGACAAATTTGAGTGTCTGTTGAAAACTCTGACAGATATATGACACA 193  
 Oy 211 TGGATTCACCCGAGGAGGAGCAGCTCAATTTGTAGTCTATGGTATTTTATGACATTTTGGC 270  
 Db 194 TGGATTCACCCGAGGAGGAGCAGCTCAATTTGTAGTCTATGGTATTTTATGACATTTTGGC 253  
 Oy 271 GACAAACAAATAGATAAATAAGCTCCGAAACTGCTGTTCAATAGATAGATACCCCTGAT 330  
 Db 254 GACAAACAAATAGATAAATAAGCTCCGAAACTGCTGTTCAATAGATAGATACCCCTGAT 313  
 Oy 331 GAGAGATTGTCTGCAAGTGGGCTCCAGTGTAGCAACAAATGAGATGAGAACCTTAGC 390  
 Db 314 GAGAGATTGTCTGCAAGTGGGCTCCAGTGTAGCAACAAATGAGATGAGAACCTTAGC 373  
 Oy 391 ATTTTGGTTAAAAATGATCTCAACCCGAAAGTATCCTGATGCTGCTGTGATCTGAA 450  
 Db 374 ATTTTGGTTAAAAATGATCTCAACCCGAAAGTATCCTGATGCTGCTGTGATCTGAG 433  
 Oy 451 CTTCATATGATTTGGCAACAACCTGAGCTACATGAAAGTCTTGGCTCCCTGAAAGGAT 510  
 Db 434 CTTCATATGATTTGGCAACAACCTGAGCTACATGAAAGTCTTGGCTCCCTGAAAGGAT 493  
 Oy 511 ACCAGTCCGACACTAACTATCTCTCTACTATTGGACAAGAACCTTGAAAAATTTAT 570  
 Db 494 ACCAGTCCGACACTAACTATCTCTCTACTATTGGACAAGAACCTTGAAAAATTTAT 553  
 Oy 571 CAATGTGAAAAACATCTTTTAAAGAAAGCCATATCTTGGTGTCTCTTGTGATCTGACCAA 630  
 Db 554 CAATGTGAAAAACATCTTTTAAAGAAAGCCATATCTTGGTGTCTCTTGTGATCTGACCAA 613  
 Oy 631 GTGAAGATTCAGATTTTGAACAACACAGTGTCCAAATATGTCAGAGATATATGACAGA 690  
 Db 614 GTGAAGATTCAGATTTTGAACAACACAGTGTCCAAATATGTCAGAGATATATGACAGA 673  
 Oy 691 AAAATTAACCATCTTCAATATATAGTCCCTTTAACTTCCGCTGTAACCTGATCTCTCA 750  
 Db 674 AAAATTAACCATCTTCAATATATAGTCCCTTTAACTTCCGCTGTAACCTGATCTCTCA 733  
 Oy 751 CATATTTAAAAACCTCTCTCCCAATGATGACCTATATGTGCAATGGAGAAATCCACAG 810  
 Db 734 CATATTTAAAAACCTCTCTCCCAATGATGACCTATATGTGCAATGGAGAAATCCACAG 793  
 Oy 811 AATTTTATAGAGATGCTATTTTATGAAGTGAAGTCAATTAACAGCAACCTGACACA 870  
 Db 794 AATTTTATAGAGATGCTATTTTATGAAGTGAAGTCAATTAACAGCAACCTGACACA 853  
 Oy 871 CATATGTTTTTCAAGTCCAAAGAGCTAAATGTGAGAAATCCAGAAATTTGAGAAATGTG 930  
 Db 854 CATATGTTTTTCAAGTCCAAAGAGCTAAATGTGAGAAATCCAGAAATTTGAGAAATGTG 913  
 Oy 931 GAGAAATCATCTGTTTCAATGATGCTGCTGTTCTCTGATTAATTTGAAACAGTACAGA 990  
 Db 914 GAGAAATCATCTGTTTCAATGATGCTGCTGTTCTCTGATTAATTTGAAACAGTACAGA 973  
 Oy 991 ATTAAGTCAAAACAAATAGTTATGCTATAGAGATGACAACTCTGAGATTAATTTGAGAC 1050  
 Db 974 ATTAAGTCAAAACAAATAGTTATGCTATAGAGATGACAACTCTGAGATTAATTTGAGAC 1033  
 Oy 1051 CAAGAATAGATATAGTAAAGAACGCAATTTCCACATCTACATTAACATGTTACTATT 1110  
 Db 1034 CAAGAATAGATATAGTAAAGAACGCAATTTCCACATCTACATTAACATGTTACTATT 1093  
 Oy 1111 GTTCAGTCTATGCTCGAGGTGCAATATATGATCTCTGCTTTAACTTAAAGAGCTCAAG 1170  
 Db 1094 GTTCAGTCTATGCTCGAGGTGCAATATATGATCTCTGCTTTAACTTAAAGAGCTCAAG 1153  
 Oy 1171 ATTAATATATTCCTCCCAATTCGATCCGAGCAAGATTTTAAAGAAATGTTTGGAGAC 1230  
 Db 1154 ATTAATATATTCCTCCCAATTCGATCCGAGCAAGATTTTAAAGAAATGTTTGGAGAC 1213  
 Oy 1231 CAGAAATGATATCTCTGCACTGGAAGAAATGACATCTATGAGAAACCAACAGAG 1290

Db 1214 CAGATATGATATCTCTGCACTGGAAGAGTACGACATCTATGAGAAACCAACAGAG 1273  
 Oy 1291 GAAACCGACTCTGATGCTGATGATGAAACCTGAAAGAGCTCTGATGATGAGATTA 1350  
 Db 1274 GAAACCGACTCTGATGCTGATGATGAAACCTGAAAGAGCTCTGATGATGAGATTA 1333  
 Oy 1351 TTTATTTTAACTTCACTGTGACCTTGAGAGA 1383  
 Db 1334 TTTATTTTAACTTCACTGTGACCTTGAGAGA 1366

## REFERENCE

## AUTHORS

Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin M, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Uebli TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loggajano NA, Peters GJ, Abramson RD, Mullany SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SM, Villalón DK, Muzny DM, Sodergren EJ, Lu X, Gibbs RA, Fahey J, Helton E, Kestelman M, Madan A, Rodriguez S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakeley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzyzanski MI, Skalska U, Smalios DE, Schnerch A, Schein JE, Jones SD and Maitra M.

Mammalian Gene Collection Program Team  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932  
 2 (bases 1 to 2139)  
 Director MGC Project.  
 Direct Submission  
 Submitted (02-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 On Dec 9, 2003 this sequence version replaced gi:14602931.  
 Contact: MGC help desk  
 Email: [gcgaps-remail.nih.gov](mailto:gcgaps-remail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Rubin Laboratory  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: [nisc.mgc@hgti.nih.gov](mailto:nisc.mgc@hgti.nih.gov)  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Khong, P., Larric, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeli, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stancirpop, S., Thomas, P.J., Touchman, J.W., Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

## REMARK

COMMENT









|   |      |  |      |
|---|------|--|------|
| D | 136  | CAGCCACCTGGACAAATTTGAGTGTCTCTGTGAAAACCTTGCACAGTAATGACACA       | 195  |
| O | 211  | TGGAATCCACCCGAGGAGCCAGCTCAAAATTGTAGTCTAATGATATTTAGTCATTTTGGC   | 270  |
| D | 196  | TGGAATCCACCCGAGGAGCCAGCTCAAAATTGATGTAATGATATTTAGTCATTTTGGC     | 255  |
| O | 271  | GACAAACAAGATTAAGAAAATAGCTCCGAAAACCTGGTCTCAATGAAATACCCCTGAAT    | 330  |
| D | 256  | GACAAACAAGATTAAGAAAATAGCTCCGAAAACCTGGTCTCAATGAAATACCCCTGAAT    | 315  |
| O | 331  | GAGAGATTTGTCTGCAAGTGGGGGTCCAGATGTACACCAATGAGAGGAGAGGCTCAG      | 390  |
| D | 316  | GAGAGATTTGTCTGCAAGTGGGGGTCCAGATGTACACCAATGAGAGGAGAGGCTCAG      | 375  |
| O | 391  | ATTTTGGTTGAAAAATGCACTCAACCCCAAGAGGTGATCCTGAATCTGCTGTGACTGAA    | 450  |
| D | 376  | ATTTTGGTTGAAAAATGCACTCAACCCCAAGAGGTGATCCTGAATCTGCTGTGACTGAG    | 435  |
| O | 451  | CTTCATATGATTTGGCAACAACCTGAGCTPACATGAAGTGTCTTGAGCTCCCTGGAAGAAAT | 510  |
| D | 436  | CTTCATATGATTTGGCAACAACCTGAGCTPACATGAAGTGTCTTGAGCTCCCTGGAAGAAAT | 495  |
| O | 511  | ACCGATCCCGACACTAATATCTCTACTATTTGGCAACAGAGGCTGGAAAAATTTGAT      | 570  |
| D | 496  | ACCGATCCCGACACTAATATCTCTACTATTTGGCAACAGAGGCTGGAAAAATTTGAT      | 555  |
| O | 571  | CAATGTGAAAAATCTCTTATGAGAAAGCCAAATCTTGGTGTCTTTGATCTGACCAA       | 630  |
| D | 556  | CAATGTGAAAAATCTCTTATGAGAAAGCCAAATCTTGGTGTCTTTGATCTGACCAA       | 615  |
| O | 631  | GTGAAGATTCGAGTTTGAACAACAAGTGTCCAAATATATGTCAGAGATATATGACGA      | 690  |
| D | 616  | GTGAAGATTCGAGTTTGAACAACAAGTGTCCAAATATATGTCAGAGATATATGACGA      | 675  |
| O | 691  | AAATTAACCATCTTCAATATAGTGCCTTAATCTCCGTGTAAACCTGATCTCTCA         | 750  |
| D | 676  | AAATTAACCATCTTCAATATATAGTGCCTTAATCTCCGTGTAAACCTGATCTCTCA       | 735  |
| O | 751  | CATATTTAAAAACCTCTCCCTGCACAATATGACCTAATATATGTCAGAGATATATGACGA   | 810  |
| D | 736  | CATATTTAAAAACCTCTCTCCCTGCACAATATGACCTAATATATGTCAGAGATATATGACGA | 795  |
| O | 811  | AATTTTATATGACAGATGCTATTTTATGAGAGTAAAGTCAATTAACGACCAATCTGACACA  | 870  |
| D | 796  | AATTTTATATGACAGATGCTATTTTATGAGAGTAAAGTCAATTAACGACCAATCTGACACA  | 855  |
| O | 871  | CATAATGTTTCTACGTCAAGAGGCTTAATATGTGGAATCCAGAAATTTGAGAGAAATGTG   | 930  |
| D | 856  | CATAATGTTTCTACGTCAAGAGGCTTAATATGTGGAATCCAGAAATTTGAGAGAAATGTG   | 915  |
| O | 931  | GAGAAATATCTGTTTCAATGATGTCCTCGTGTCTTCTGATATCTTTGAACACAGTCAAG    | 990  |
| D | 916  | GAGAAATATCTGTTTCAATGATGTCCTCGTGTCTTCTGATATCTTTGAACACAGTCAAG    | 975  |
| O | 991  | ATAAGAGTCAAAACAATTAAGTTATGATAGAGTGAACAACCTGTGAGATTAATGAGAGC    | 1050 |
| D | 976  | ATAAGAGTCAAAACAATTAAGTTATGATAGAGTGAACAACCTGTGAGATTAATGAGAGC    | 1035 |
| O | 1051 | CAAGAAATGAGTATAGTAAAGGCGCAATTCACACCTCTACATTAACCATGTTACTCAT     | 1110 |
| D | 1036 | CAAGAAATGAGTATAGTAAAGGCGCAATTCACACCTCTACATTAACCATGTTACTCAT     | 1095 |
| O | 1111 | GTTCCAGTCAATGTCGAGGTGCAATCATATATCTCTGTTTAACTTAACCAAGGCTCAAG    | 1170 |
| D | 1096 | GTTCCAGTCAATGTCGAGGTGCAATCATATATCTCTGTTTAACTTAACCAAGGCTCAAG    | 1155 |
| O | 1171 | ATTATTAATATTCCTTCAATTCCTGATCCTGCGAAGATTTTAAAGAAATGTTTGGAGAC    | 1230 |
| D | 1156 | ATTATTAATATTCCTTCAATTCCTGATCCTGCGAAGATTTTAAAGAAATGTTTGGAGAC    | 1215 |
| O | 1231 | CAGAAATGATATCTCTGCACTGGAAGAGTACGACATCTATGAGAGCAAAACAAGAG       | 1290 |

|     |                            |  |   |                 |
|-----|----------------------------|--|---|-----------------|
| Dd  |                            | 1276   | CAGATGTGTTACTCTGCACCTGGAAAGAAGTACACATCTTAGAAGAACCAACAAGAG   | 1275            |
| Oy  |                            | 1291   | GAAACCGACTCTGTAGTCGTATGAAAACTGAAGAAAGCCTTCAGTGATGAGATAA     | 1350            |
| Dd  |                            | 1276   | GAAACCGACTCTGTAGTCGTATGAAAACTGAAGAAAGCCTTCAGTGATGAGATAA     | 1335            |
| Oy  |                            | 1351   | TTTTATTCTTACCCTCACCTGTGACCTTTGAGAAGA                        | 1383            |
| Dd  |                            | 1336   | TTTTATTCTTACCCTCACCTGTGACCTTTGAGAAGA                        | 1368            |
|     | RESULT 7                   |  |   |                 |
|     | LOCUS                      | CQ894698   | 4039 bp   | DNA             |
|     | DEFINITION                 | Sequence 8 from Patent EP1471075.  |   | linear          |
|     | ACCESSION                  | CQ894698   |   | PAT 05-NOV-2004 |
|     | VERSION                    | CQ894698.1   | GI:55467447   |                 |
|     | KEYWORDS                   |  |   |                 |
|     | SOURCE                     | Homo sapiens (human)   |   |                 |
|     | ORGANISM                   | Homo sapiens<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;<br>Hominiidae; Homo.  |   |                 |
|     | REFERENCE                  |  |   |                 |
|     | AUTHORS                    | Rosenthal,A.D., Pilarsky,C., Dahl,E., Specht,T., Bruemendorf,T.,<br>Lichter,R., Staub,E., Roepcke,S. and Li,X.I.<br>Human nucleic acid sequences expressed in pancreatic carcinomas<br>Patent: EP 1471075-A 8 27-OCT-2004; |   |                 |
|     | TITLE                      | Hinzmann, Bernd (DE); Rosenthal, Andre (DE); Pilarsky, Christian<br>(DE); Dahl, Edgar (DE); Specht, Thomas (DE); Lichtner, Rosemarie<br>(DE).  |   |                 |
|     | JOURNAL                    |  |   |                 |
|     | FEATURES                   |  |   |                 |
|     | source                     | Location/Qualifiers  |   |                 |
|     |                            | 1..4039<br>/organism="Homo sapiens"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:9606"   |   |                 |
|     | ORIGIN                     |  |   |                 |
|     | Query Match                | 96.4%; Score 133.8; DB 2; Length 4039;   |   |                 |
|     | Best Local Similarity      | 99.6%; Pred. No. 0;  |   |                 |
|     | Matches 1348; Conservative | 0; Mismatches 2; Indels 3; Gaps 1;   |   |                 |
| Oy  |                            | 34   | CGGCCGGGTTCCGAGCGAGAGCGTGCATGAGTGCCCGGCGCGCTCTGCGGCTGTGG    | 93              |
| Dd  |                            | 17   | CGGCCGGGCTCCGAGCGAGAGCGTGCATGAGTGCGCGCGCGCTCTGCGGCTGTGG     | 76              |
| Oy  |                            | 94   | GCGCTGCTGCTCTGCGCGCGCGCGCGGCGGCGGCGG--CGCGCTACGGAACCT       | 150             |
| Dd  |                            | 77   | GCGCTGCTGCTCTGCGCGCGCGCGGCGGCGGCGGCGGCGCGCGCTACGGAACCT      | 136             |
| Oy  |                            | 151  | CAGCCACTGTCGAATAATTGAGTGTCTCTGTGAAAACCTCTGCACAAGTAATATGACA  | 210             |
| Dd  |                            | 137  | CAGCCACTGTCGAATAATTGAGTGTCTCTGTGAAAACCTCTGCACAAGTAATATGACA  | 196             |
| Oy  |                            | 211  | TGGAATCCACCCGAGGAGCCAGTCAAATTTGATCTATGATATTTTAACTTTGGC      | 270             |
| Dd  |                            | 197  | TGGAATCCACCCGAGGAGCCAGTCAAATTTGATCTATGATATTTTAACTTTGGC      | 256             |
| Oy  |                            | 271  | GACAAACAAAGTAAGAAATAGCTCCGAAAACCTGTCTCAATAGAAATACCCCTGAAT   | 330             |
| Dd  |                            | 257  | GACAAACAAAGTAAGAAATAGCTCCGAAAACCTGTCTCAATAGAAATACCCCTGAAT   | 316             |
| Oy  |                            | 331  | GAGAGCATTTGTCCTGCAGTGGGGTCCCAGTGTGACCAATGAGAGTGAGAAAGCTTAGC | 390             |
| Dd  |                            | 317  | GAGAGCATTTGTCCTGCAGTGGGGTCCCAGTGTGACCAATGAGAGTGAGAAAGCTTAGC | 376             |
| -Oy |                            | 391  | ATTTTGGTGAANAATSCATCTCACCCCCAGAAGGTATCTGAGTCTGTGACTGAA      | 450             |
| Dd  |                            | 377  | ATTTTGGTGAANAATSCATCTCACCCCCAGAAGGTATCTGAGTCTGTGACTGAG      | 436             |
| Oy  |                            | 451  | CTTAAATGCAATTTGGCCAACCTGAGCTACATGAAGTGTCTTGGCTCCTCGAAGAAAT  | 510             |
| Dd  |                            | 437  | CTTAAATGCAATTTGGCCAACCTGAGCTACATGAAGTGTCTTGGCTCCTCGAAGAAAT  | 496             |

|    |      |  |      |
|----|------|--|------|
| OY | 51   | ACGAGTCCCGACACCTAACCTATCTCTCTATCTATGCGACAGAGAGGCTGGAAAAATTCAT  | 570  |
| Db | 497  | ACGAGTCCCGACACCTAACCTATCTCTCTATCTATGCGACAGAGAGGCTGGAAAAATTCAT  | 556  |
| OY | 571  | CAATGTGAAAACATCTTTAGAGAAAGGCCAATACTTTGGTGTGTTCTCTTGATCTGCACAA  | 630  |
| Db | 557  | CAATGTGAAAACATCTTTAGAGAAAGGCCAATACTTTGGTGTGTTCTCTTGATCTGCACAA  | 616  |
| OY | 631  | GTGAAGGATTCACAGTTTGGAAACAACAAGTGTCCAAATTAAGTGCAAAGATPATGACAGA  | 690  |
| Db | 617  | GTGAAGGATTCACAGTTTGGAAACAACAAGTGTCCAAATTAAGTGCAAAGATPATGACAGA  | 676  |
| OY | 691  | AAAAATTAACCATCTCTCAATATAGTGTGCTTAACTCCCGGTGAAAACCTGATCTGCA     | 750  |
| Db | 677  | AAAAATTAACCATCTCTCAATATAGTGTGCTTAACTCCCGGTGAAAACCTGATCTGCA     | 736  |
| OY | 751  | CATATTTAAAAACCTCTCTCTCCACATGATGACCTATATGTGCAATGGAGATTCACAG     | 810  |
| Db | 737  | CATATTTAAAAACCTCTCTCTCCACATGATGACCTATATGTGCAATGGAGATTCACAG     | 796  |
| OY | 811  | AATTTATTTAGCAGATGCGCTATTTATGAGAGAAAGCAATPAACGCCAACTGACGA       | 870  |
| Db | 797  | AATTTATTTAGCAGATGCGCTATTTATGAGAGAAAGCAATPAACGCCAACTGACGA       | 856  |
| OY | 871  | CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTG | 930  |
| Db | 857  | CATAATGTTTTCTACGTCCAAGAGGCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTG | 916  |
| OY | 931  | GAGAAATACATCTGTGTTTCATGAGTGCCTCGTGTTCTTCTGATACTTTGAACAAGTCAGA  | 990  |
| Db | 917  | GAGAAATACATCTGTGTTTCATGAGTGCCTCGTGTTCTTCTGATACTTTGAACAAGTCAGA  | 976  |
| OY | 991  | ATTAAGAGTCAAAAACAATTAAGTTATGCTATGAGATGGAACAACTCGAGATTAATGGAGC  | 1050 |
| Db | 977  | ATTAAGAGTCAAAAACAATTAAGTTATGCTATGAGATGGAACAACTCGAGATTAATGGAGC  | 1036 |
| OY | 1051 | CAAGAAATGAGTATAGGTAAAGAGCGCAATTCACACTCTACATPAACCATGTTACTCATTT  | 1110 |
| Db | 1037 | CAAGAAATGAGTATAGGTAAAGAGCGCAATTCACACTCTACATPAACCATGTTACTCATTT  | 1098 |
| OY | 1111 | GTTCCAGTCACTGTGCGAGAGTGCATCATATGATACCTCGGCTTTACTTAAAAAGGCTCAAG | 1170 |
| Db | 1097 | GTTCCAGTCACTGTGCGAGAGTGCATCATATGATACCTCGGCTTTACTTAAAAAGGCTCAAG | 1156 |
| OY | 1171 | ATTATTAATATTCCTCCCAATTCCTCGATCCTGCGACAATTTTTAAAGAAATGTTGGAGAC  | 1230 |
| Db | 1157 | ATTATTAATATTCCTCCCAATTCCTCGATCCTGCGACAATTTTTAAAGAAATGTTGGAGAC  | 1216 |
| OY | 1231 | CAGATAGTATGATCCTGCGACCTGGAAGAAAGTACGACATCTATGAGAACCAACCAAGAG   | 1290 |
| Db | 1217 | CAGATAGTATGATCCTGCGACCTGGAAGAAAGTACGACATCTATGAGAACCAACCAAGAG   | 1276 |
| OY | 1291 | GAAGCCGACTCTGTAGTGTGTAAGAAACCTGAAAGAAAGCCTCTCACTGATGAGATTA     | 1350 |
| Db | 1277 | GAAGCCGACTCTGTAGTGTGTAAGAAACCTGAAAGAAAGCCTCTCACTGATGAGATTA     | 1336 |
| OY | 1351 | TTTATTTTACCTTCACTGTGACCTTGGAGAGA                               | 1383 |
| Db | 1337 | TTTATTTTACCTTCACTGTGACCTTGGAGAGA                               | 1369 |

| REFERENCE | AUTHORS  | TITLE   | JOURNAL                                | FEATURES                    | ORIGIN           |
|-----------|--|---|--|-----------------------------|------------------|
| 1         | Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. | Cancer gene determination and therapeutic screening using signature gene sets | Patent: WO 0194629-A 6046 13-DEC-2001; | Avalon Pharmaceuticals (US) | Hominidae; Homo. |
| 2         |  |   |  |                             |                  |
| 3         |  |   |  |                             |                  |
| 4         |  |   |  |                             |                  |
| 5         |  |   |  |                             |                  |
| 6         |  |   |  |                             |                  |
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| 9         |  |   |  |                             |                  |
| 10        |  |   |  |                             |                  |
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| 30        |  |   |  |                             |                  |
| 31        |  |   |  |                             |                  |
| 32        |  |   |  |                             |                  |
| 33        |  |   |  |                             |                  |
| 34        |  |   |  |                             |                  |
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| 36        |  |   |  |                             |                  |
| 37        |  |   |  |                             |                  |
| 38        |  |   |  |                             |                  |
| 39        |  |   |  |                             |                  |
| 40        |  |   |  |                             |                  |
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| 42        |  |   |  |                             |                  |
| 43        |  |   |  |                             |                  |
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| 45        |  |   |  |                             |                  |
| 46        |  |   |  |                             |                  |
| 47        |  |   |  |                             |                  |
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| 50        |  |   |  |                             |                  |
| 51        |  |   |  |                             |                  |
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| 57        |  |   |  |                             |                  |
| 58        |  |   |  |                             |                  |
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| 63        |  |   |  |                             |                  |
| 64        |  |   |  |                             |                  |
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| 66        |  |   |  |                             |                  |
| 67        |  |   |  |                             |                  |
| 68        |  |   |  |                             |                  |
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| 70        |  |   |  |                             |                  |
| 71        |  |   |  |                             |                  |
| 72        |  |   |  |                             |                  |
| 73        |  |   |  |                             |                  |
| 74        |  |   |  |                             |                  |
| 75        |  |   |  |                             |                  |
| 76        |  |   |  |                             |                  |
| 77        |  |   |  |                             |                  |
| 78        |  |   |  |                             |                  |
| 79        |  |   |  |                             |                  |
| 80        |  |   |  |                             |                  |
| 81        |  |   |  |                             |                  |
| 82        |  |   |  |                             |                  |
| 83        |  |   |  |                             |                  |
| 84        |  |   |  |                             |                  |
| 85        |  |   |  |                             |                  |
| 86        |  |   |  |                             |                  |
| 87        |  |   |  |                             |                  |
| 88        |  |   |  |                             |                  |
| 89        |  |   |  |                             |                  |
| 90        |  |   |  |                             |                  |
| 91        |  |   |  |                             |                  |
| 92        |  |   |  |                             |                  |
| 93        |  |   |  |                             |                  |
| 94        |  |   |  |                             |                  |
| 95        |  |   |  |                             |                  |
| 96        |  |   |  |                             |                  |
| 97        |  |   |  |                             |                  |
| 98        |  |   |  |                             |                  |
| 99        |  |   |  |                             |                  |
| 100       |  |   |  |                             |                  |

|   |   |   |                            |
|---|---|---|----------------------------|
| Db  | 797   | AATTTTATTAGCAGATGCCCTATTATTATGAAAGTAAGAATCAATAACAGCCAAATTCAGACA | 856                        |
| Oy  | 871   | CATATATGTTTTCTACGTCCAAGAGGCTAATATGTGAATCCGAATTTTGAGAAATATGG     | 930                        |
| Db  | 857   | CATAATGTTTTCTACGTCCAAGAGGCTAATATGTGAATCCGAATTTTGAGAAATATGG      | 916                        |
| Oy  | 921   | GAGAAATACATCTGTGTTTCATGAGTCCCTGGWGTCTTCTCGATACATTGTAACAACATCGA  | 990                        |
| Db  | 917   | GAGAAATACATCTGTGTTTCATGAGTCCCTGGTGTCTTCTCGATACATTGTAACAACATCGA  | 976                        |
| Oy  | 991   | ATAAGAGTCAAAACCAATTAAGTTATGCTATGAGATGACAACACTCGAGTAATGGAGC      | 1056                       |
| Db  | 977   | ATAAGAGTCAAAACCAATTAAGTTATGCTATGAGATGACAACACTCGAGTAATGGAGC      | 1036                       |
| Oy  | 1051  | CAGAATATGATATATGTTATGTAAGCGCAATTCACACTCTACATACCATGTTACTCAT      | 1110                       |
| Db  | 1037  | CAGAATATGATATATGTTATGTAAGCGCAATTCACACTCTACATACCATGTTACTCAT      | 1098                       |
| Oy  | 1111  | GTTCCAGTCATCGTGGCAGGTCSCATCATATGATACCTCGCTTACCTTAAAAAGGCTCAAG   | 1170                       |
| Db  | 1097  | GTTCCAGTCATCGTGGCAGGTCSCATCATATGATACCTCGCTTACCTTAAAAAGGCTCAAG   | 1156                       |
| Oy  | 1171  | ATTATTATATTTCCCTCCAAATTCCTGATCCTGGCAGATTTTTPAAGAAATGTTTGGAGC    | 1230                       |
| Db  | 1157  | ATTATTATATTTCCCTCCAAATTCCTGATCCTGGCAGATTTTTPAAGAAATGTTTGGAGC    | 1216                       |
| Oy  | 1231  | CAGAAATGATATCTCTGCACCTGGAAGAAAGTACGACATCTATAGAACCAACCAAGAG      | 1290                       |
| Db  | 1217  | CAGAAATGATATCTCTGCACCTGGAAGAAAGTACGACATCTATAGAACCAACCAAGAG      | 1276                       |
| Oy  | 1291  | GAAACCGACTCTGTAGTGTCTGATAGAAAACTGGAAGAAAGCTCTCACTGATGAGATTA     | 1356                       |
| Db  | 1277  | GAAACCGACTCTGTAGTGTCTGATAGAAAACTGGAAGAAAGCTCTCACTGATGAGATTA     | 1336                       |
| Oy  | 1351  | TTTATTTTACCTTCACTGTGTGACCCTTGAGGAAGA                            | 1383                       |
| Db  | 1337  | TTTATTTTACCTTCACTGTGTGACCCTTGAGGAAGA                            | 1369                       |
| RESULT 9  |   |   |                            |
| LOCUS   | AX411212  | 4039 bp   | DNA linear PAT 14-JUN-2002 |
| DEFINITION  | Sequence 3859 from Patent WO0229103.  |   |                            |
| ACCESSION   | AX411212  |   |                            |
| VERSION   | AX411212.1 GI:21443917  |   |                            |
| KEYWORDS  | .   |   |                            |
| SOURCE  | Homo sapiens (human)  |   |                            |
| ORGANISM  | Homo sapiens<br>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;<br>Homnidae; Homo.                   |   |                            |
| REFERENCE   | 1   |   |                            |
| AUTHORS   | Alvarez, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.  |   |                            |
| TITLE   | Gene expression profiles in liver cancer  |   |                            |
| JOURNAL   | Patent: WO 0229103-A 3859 11-APR-2002;  |   |                            |
| FEATURES  | GENE LOGIC INC (US)<br>Location/Qualifiers<br>1..4039<br>/organism="Homo sapiens"<br>/mol_type="unassigned DNA"<br>/db_xref="taxon:9606"<br>/note="EMBL/GenBank Accession No. Y10659" |   |                            |
| ORIGIN  |   |   |                            |
| Query Match   | 96.4%; Score 133.8; DB 2; Length 4039;  |   |                            |
| Best Local Similarity   | 99.6%; Pred. No. 0; Mismatches 2; Indels 3; Gaps 1;   |   |                            |
| Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1; |   |   |                            |
| Oy  | 34  | CGGCCGGGTTCCGAGCGAGAGCGCTGATGAGTGGCCGCGCGGCTCTGCGGGCTGG 93      |                            |
| Db  | 17  | CGGCCGGGCTCCGAGCGAGAGCGCTGATGAGTGGCCGCGCGGCTCTGCGGGCTGG 76      |                            |
| Oy  | 94  | GGCGTCTGCTCTGGCGCGCGCGGGGGCGGGGGCGGGGG--CGCGCTTACGGAACT 150     |                            |

|    |      |   |      |
|----|------|---|------|
| Db | 77   | GCCTGCTGCTCTGCGCCGCGCGGGGGGCGGGGCGCCGCCCTTACGGAACT              | 136  |
| Qy | 151  | CAGCCACCTGTGACAAATTTGAGTGTCTCTGTGAAAACCTCTGCACAGTATATAGCA       | 210  |
| Db | 137  | CAGCCACCTGTGACAAATTTGAGTGTCTCTGTGAAAACCTCTGCACAGTATATAGCA       | 196  |
| Qy | 211  | TGGAATCCACCCGAGGGAGCCAGCTCAATTTGTATGTATGTATTTTATGATTTTGGC       | 270  |
| Db | 197  | TGGAAATCCACCCGAGGGAGCCAGCTCAATTTGTATGTATGTATTTTATGATTTTGGC      | 256  |
| Qy | 271  | GACAAACAAGTAAAGAAATAGCTCCCGGAACTGTGTCTTAATAGAAATGCCCTGAT        | 330  |
| Db | 257  | GACAAACAAGTAAAGAAATAGCTCCCGGAACTGTGTCTTAATAGAAATGCCCTGAT        | 316  |
| Qy | 331  | GAGAGATTTTGTCTGCAAGTGGGGTCCCAAGTGTAGCACAATGTAGAGTGAAGCCTAGC     | 390  |
| Db | 317  | GAGAGATTTTGTCTGCAAGTGGGGTCCCAAGTGTAGCACAATGTAGAGTGAAGCCTAGC     | 376  |
| Qy | 391  | ATTTTGGTTGAAAATGATCTCACCCGAGAAGTGTACTGTAGTCTGTGTGCTGA           | 450  |
| Db | 377  | ATTTTGGTTGAAAATGATCTCACCCGAGAAGTGTACTGTAGTCTGTGTGCTGA           | 436  |
| Qy | 451  | CTTCAATGCAATTTGGCAACCTGAGCTACATGAAGTCTCTTGGCTCCCTGGAAGAT        | 510  |
| Db | 437  | CTTCAATGCAATTTGGCAACCTGAGCTACATGAAGTCTCTTGGCTCCCTGGAAGAT        | 496  |
| Qy | 511  | ACCAAGTCCCGACATACATATACCTCTCATTTTGGGACAAGAAGCTGGAAAAATTCAT      | 570  |
| Db | 497  | ACCAAGTCCCGACATACATATACCTCTCATTTTGGGACAAGAAGCTGGAAAAATTCAT      | 556  |
| Qy | 571  | CAATGTGAAAAATCTTTAGAGAGGCCAATACCTTGGTGTCTCTTGTGATCTGACAA        | 630  |
| Db | 557  | CAATGTGAAAAATCTTTAGAGAGGCCAATACCTTGGTGTCTCTTGTGATCTGACAA        | 616  |
| Qy | 631  | GTGAAGATTCAGATTTTGAACAACAAGTGTCCAAATATATGTGCACAGATATATGACAGA    | 690  |
| Db | 617  | GTGAAGATTCAGATTTTGAACAACAAGTGTCCAAATATATGTGCACAGATATATGACAGA    | 676  |
| Qy | 691  | AAAAATTAACATCCTTCAATATATGAGTGTCTTAATCTCCGCTGGAACCTGATCCTCA      | 750  |
| Db | 677  | AAAAATTAACATCCTTCAATATATGAGTGTCTTAATCTCCGCTGGAACCTGATCCTCA      | 736  |
| Qy | 751  | CATATTAACAACTCTCCTTCCACATAGTAGACCTATATGTGCATGTGGAGATCCACAG      | 810  |
| Db | 737  | CATATTAACAACTCTCCTTCCACATAGTAGACCTATATGTGCATGTGGAGATCCACAG      | 796  |
| Qy | 811  | AATTTTATATGACAGATGCTATTTTATGAGTAGAAGTCAATTAACGCCAAACTGACACA     | 870  |
| Db | 797  | AATTTTATATGACAGATGCTATTTTATGAGTAGAAGTCAATTAACGCCAAACTGACACA     | 866  |
| Qy | 871  | CATATATGTTTCTACGTCGCAAGAGGCTAAATGTGAGAAATCAGAAATTTGAGAGAAATGTG  | 930  |
| Db | 857  | CATATATGTTTCTACGTCGCAAGAGGCTAAATGTGAGAAATCAGAAATTTGAGAGAAATGTG  | 916  |
| Qy | 931  | GAGAAATACATCTGTTCATGTGTCCCTGATGTTTCTCTGTATCTTTGAACACAGTACAGA    | 990  |
| Db | 917  | GAGAAATACATCTGTTCATGTGTCCCTGATGTTTCTCTGTATCTTTGAACACAGTACAGA    | 976  |
| Qy | 991  | ATAAGAGTCAAAACAATTAAGTTATGTCTATGAGATGACAAACTCTGAGTAAATTGAGC     | 1050 |
| Db | 977  | ATAAGAGTCAAAACAATTAAGTTATGTCTATGAGATGACAAACTCTGAGTAAATTGAGC     | 1036 |
| Qy | 1051 | CAGAAGATGTATAGTAAAGAGCGGAATTCACACCTACATACAAACATGTATCTACTT       | 1110 |
| Db | 1037 | CAGAAGATGTATAGTAAAGAGCGGAATTCACACCTACATACAAACATGTATCTACTT       | 1096 |
| Qy | 1111 | GTTTCAAGTCAATGTGCGAGGTGCAATCATATGATCTCTGTGTTTACCTTAAAAAGGCTCAAG | 1170 |
| Db | 1097 | GTTTCAAGTCAATGTGCGAGGTGCAATCATATGATCTCTGTGTTTACCTTAAAAAGGCTCAAG | 1156 |
| Qy | 1171 | ATTATATATTCCTCCAAATTCGTATCTGTGCAAGATTTTAAAAAGAAATGTTTGGAGAC     | 1230 |
| Db |      |   |      |

|                            |   |  |                             |
|----------------------------|---|--|-----------------------------|
| Db                         | 1157  | ATTATATATATTCCTCCCAATTCCTGATCTCTGGCAAGATTTTAAAGAAATGTTGGAGAC | 1216                        |
| Qy                         | 1231  | CAGATGATGATGATCTCTGCACTGGAAGAAATGACATCTATGAGAACCAACCAAGAG    | 1290                        |
| Db                         | 1217  | CAGATGATGATGATCTCTGCACTGGAAGAAATGACATCTATGAGAACCAACCAAGAG    | 1276                        |
| Qy                         | 1251  | GAACCCGCTCGTGTGTCGTATTAATAAACCCTGAAGAAAGCTCTGATGATGAGATTA    | 1350                        |
| Db                         | 1277  | GAACCCGCTCTGATGTCGTATTAATAAACCCTGAAGAAAGCTCTGATGATGAGATTA    | 1336                        |
| Qy                         | 1351  | TTTATTTTACCTTCACCTGTGCTGTGAGAAGA                             | 1383                        |
| Db                         | 1337  | TTTATTTTACCTTCACCTGTGCTGTGAGAAGA                             | 1369                        |
| RESULT 10                  |   |  |                             |
| HSIL13RA                   |   |  |                             |
| LOCUS                      | HSIL13RA  | 4039 bp  | mRNA linear PRI 22-JAN-1997 |
| DEFINITION                 | H.sapiens IL-13RA mRNA.   |  |                             |
| ACCESSION                  | Y10659  |  |                             |
| VERSION                    | Y10659.1  |  | GI:1806035                  |
| KEYWORDS                   | IL13Ra.gene; interleukin-13.  |  |                             |
| SOURCE                     | Homo sapiens (human)  |  |                             |
| ORGANISM                   | Homo sapiens  |  |                             |
| REFERENCE                  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.   |  |                             |
| AUTHORS                    | 1 Gauchat, J.F.M., Schlagenhaut, E., Feng, N.P., Moser, R., Yamage, M., Jeannin, P., Alouani, S., Elson, G., Notarangelo, L.D., Wells, T., Eugster, H.P. and Bonnettoy, J.Y.  |  |                             |
| TITLE                      | A novel 4 kb IL-13RA mRNA expressed in human B, T and endothelial cells, encoding for an alternate type two IL-4/IL-13R   |  |                             |
| JOURNAL                    | 2 (bases 1 to 4039)   |  |                             |
| REFERENCE                  | Gauchat, J.F.M.   |  |                             |
| AUTHORS                    | Direct Submission   |  |                             |
| TITLE                      | Submitted (20-JAN-1997) J.F.M. Gauchat, Geneva Biomedical Research Institute, Immunology, Glaxo Research And Development, 14 Ch Des Aux, Plan-Les-Orates, CH1228, SWITZERLAND   |  |                             |
| JOURNAL                    | Location/Qualifiers   |  |                             |
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| Matches 1348; Conservative | 0;  | Mismatches 2;  | Indels 3; Gaps 1;           |
| 34                         | CGGCCGGATTCCGAGGCGAGAGGCTGCATGAGTGGCCGCGCGGCTTCGCGGGCTGTGG  | 93   |                             |

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| Db | 17   | CGGGCGGGGCTCCGAGGCCGAGAGCTGCAATGAGTGGCCGGGGCGGCGCTCTGGCGGCTGGG | 76   |
| Qy | 94   | GGCGTGTGCTCTGGCGCCGGCGGCCGGGGCGGGGGCGGGG---CGCGCTTACGGAACT     | 150  |
| Db | 77   | GGCGTGTGCTCTGGCGCCGGCGGGGGCGGGGGCGGGGGCGCGCGCCCTACGGAACT       | 136  |
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| Qy | 211  | TGGATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATAGTATTTTATGATTTTGGC       | 270  |
| Db | 197  | TGGATCCACCCGAGGAGCCAGCTCAAAATGTAGTCTATAGTATTTTATGATTTTGGC      | 256  |
| Qy | 271  | GACAAACAAGATTAAGAAATAGCTCCGAAAACCTCGTCAATAGAGTACCCCTGAAT       | 330  |
| Db | 257  | GACAAACAAGATTAAGAAATAGCTCCGAAAACCTCGTCAATAGAGTACCCCTGAAT       | 316  |
| Qy | 331  | GAGAGAAATTTGTCTGCAAGTGGGGGTCCCAAGTGAACAACATGAGAGTGAAGGCTAGC    | 390  |
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| Db | 437  | CTTCAATGCATTTGGCACAACCTGAGCTACATGAAATGTTCTTGGCTCCCTGGAAGGAT    | 496  |
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| Qy | 571  | CAATGTGAAAACATCTTTAGGAAGGCCAATACCTTTGGTGTCTCTTGTGATCTGACAA     | 630  |
| Db | 557  | CAATGTGAAAACATCTTTAGGAAGGCCAATACCTTTGGTGTCTCTTGTGATCTGACAA     | 616  |
| Qy | 631  | GTGAAGGATTCAGTTTGAACAACAACAGTGTCCAAATTAAGTCAAGGATTAAGCAGA      | 690  |
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| Qy | 691  | AAATTAACATCCTTCATATATAGTGCCCTTAACTTCCCGTGAACCTGATCTCTCA        | 750  |
| Db | 677  | AAATTAACATCCTTCATATATAGTGCCCTTAACTTCCCGTGAACCTGATCTCTCA        | 736  |
| Qy | 751  | CATATTAACAACTCTCTCTTCCACATGATGACCTATATGTGCATGGGAGATCCACAG      | 810  |
| Db | 737  | CATATTAACAACTCTCTCTTCCACATGATGACCTATATGTGCATGGGAGATCCACAG      | 796  |
| Qy | 811  | AATTTATTACAGATGGCTATTTTATGAATGAAGCAATTAACGCCAACTGACACA         | 870  |
| Db | 797  | AATTTATTACAGATGGCTATTTTATGAATGAAGCAATTAACGCCAACTGACACA         | 856  |
| Qy | 871  | CATAATGTTTCTACGTCCAGAGGCTTAAATGTGAGAACTCAGAAATTTGAGAGAAATGTG   | 930  |
| Db | 857  | CATAATGTTTCTACGTCCAGAGGCTTAAATGTGAGAACTCAGAAATTTGAGAGAAATGTG   | 916  |
| Qy | 931  | GAGAAATACATCTTGTTCATGAGTCCCTGAGTCTTCTCTGATTAATTTGAACACAGTACA   | 990  |
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| Qy | 991  | ATAAGAGTCAAAACAAATTAAGTATGCTATAGAGATGACAACTCTGAGATTAATTTGAGC   | 1050 |
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| Qy | 1051 | CAAGAAATGAGTATGATTAAGAGGCAATTCACACTATACATTAACATTTACTCATTT      | 1110 |
| Db | 1037 | CAAGAAATGAGTATGATTAAGAGGCAATTTCCACTATACATTAACATTTACTCATTT      | 1096 |
| Qy | 1111 | GTTCAGTCAATGTCGAGGTGCAATATAGTACTCTCTGCTTTAAGCTAAAAAGCTCAAG     | 1170 |



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| Oy                                      | 1171 | ATTATTTATATTCCTCTCAAAATCCGATGCTCGGCAAGATTTTAAAGAAATGTTTGGAGAC    | 1230 |
| Db                                      | 8799 | ATTATTTATATTCCTCTCAAAATTCCTGATTCCTGCGCAAGATTTTAAAGAAATGTTTGGAGAC | 8858 |
| Oy                                      | 1231 | CAGAAATGATGATCACTCTGCACTGGAAGAAGTACGACATCTATGAGAAACAACCAAGAG     | 1290 |
| Db                                      | 8859 | CAGAAATGATGATCACTCTGCACTGGAAGAAGTACGACATCTATGAGAAACAACCAAGAG     | 8918 |
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| LOCUS                                   |      |  |      |
| DEFINITION                              |      |  |      |
| MGC:23204 IMAGE:4868206), complete cds. |      |  |      |
| ACCESSION                               |      |  |      |
| BC015768                                |      |  |      |



| VERSION    | KEYWORDS   |
|------------|--|
| BC015768.1 | GI:16041774  |
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| ORGANISM   | Homo sapiens (human)   |
| SOURCE     | Homo sapiens   |
| ORGANISM   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  |
| REFERENCE  | 1 (bases 1 to 2153)  |
| AUTHORS    | Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Ditchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worcester, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Scherchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A. |
| TITLE      | Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences   |
| JOURNAL    | Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  |
| REFERENCE  | 12477992   |
| AUTHORS    | 2 (bases 1 to 2153)  |
| TITLE      | Straussberg, R.  |
| JOURNAL    | Direct Submission  |
| COMMENT    | Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA   |
| REMARK     | NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>   |
| COMMENT    | Contact: MGC help desk<br>Email: <a href="mailto:cgapbts-remail.nih.gov">cgapbts-remail.nih.gov</a><br>Tissue Procurement: ATCC<br>cDNA Library Preparation: Rubin laboratory<br>DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)<br>BC Cancer Agency, Vancouver, BC, Canada<br><a href="mailto:info@cgsc.bc.ca">info@cgsc.bc.ca</a>  |
| COMMENT    | Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butlerfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Tekla Olson, Diana Palmquist, Ana Petrescu, Anna Liisa Prabh, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska, Duane Smalls, Jeff Stott, Miranda Tsai, George Vang, Jacqui Schein, Asim Siddiqui, Rob Holt, Marco Marra.   |
| FEATURES   | Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a><br>Series: IRAL, Plate: 34 Row: k Column: 19<br>This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.  |
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ACCESSION      AB209849
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KEYWORDS      FLI_CDNA.
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ORGANISM      Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
  1. Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S.,
    Ohara, O., Nagase, T. and F. Kikuno, R.
    None Title
    Published Only in Database (2005)
    2 (bases 1 to 3960)
    Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S.,
    Ohara, O., Nagase, T. and F. Kikuno, R.
    Direct Submission
    Submitted (32-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute,
    Department of Human Gene Research; 2-6-7 Kazusa-Kamatari, Kisarazu,
    Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp,

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COMMENT
  URL: http://protein.gsc.riken.go.jp/, Tel: 81-438-52-3930,
  Fax: 81-438-52-3931
  This work was supported in part by the National Project on Protein
  Structural and Functional Analysis, Ministry of Education, Culture
  Sports, Science and Technology of Japan. Totoki, Y., Toyoda, A.,
  Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S., RIKEN Genomic Sciences
  Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan.
  e-mail: aktanaka@postman.riken.go.jp
  URL: http://protein.gsc.riken.go.jp/.
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      QAKCENPEFERNVNESCFTMPGVLPDLNTRIRVKNKLCTEDDKLSMNSQEMS
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QY 600 ATAATTGTTGTTCTCTTATCTGACCAAAATGAAAGATTCAGTTTGAACAACACAG 659  
Db 541 ATACTTGTGTTGTTCTCTTATCTGACCAAAATGAAAGATTCAGTTTGAACAACACAG 600  
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QY 960 TGTCTTCTCTGATACCTTTGAACACAGTCAGATTAAGAGTCAAAACAATATGTTATGTA 1019  
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QY 1020 TGAGATGACAAACTCTGAGATTAATGGAGCCAAAGAAATGATATAGTAAGAAAGCGAA 1079  
Db 961 TGAGATGACAAACTCTGAGATTAATGGAGCCAAAGAAATGATATAGTAAGAAAGCGAA 1020  
QY 1080 TTCCACACTCTATACATACCATGTTACTCATGTTCCAGTCATGTCGACAGTGCATCAT 1139  
Db 1021 TTCCACACTCTATACATACCATGTTACTCATGTTCCAGTCATGTCGACAGTGCATCAT 1080  
QY 1140 AGTACTCTGCTTACTTACCTTAAAAAGGCTCAAGATTTATATATCCCTCAATCTCTGATCC 1199  
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Db 1201 GTACGACATCTATGAGAGCAAAACCAAGAGAAACCGACTCTGTAGTCTGATAGAA 1260  
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Db 1261 CCGAAGAAAGCCTCTAGTATGAGATTAATTTTAACTTCACTGCTGACCTTGAAG 1320  
QY 1380 AAGA 1383  
Db 1321 AAGA 1324

RESULT 15  
AY892945 1284 bp mRNA linear SYN 29-MAR-2005  
LOCUS AY892945  
DEFINITION Synthetic construct Homo sapiens clone FLH141766.01L Interleukin 13  
ACCESSION AY892945  
VERSION AY892945.1 GI:60654342  
KEYWORDS Human ORF project.  
SOURCE synthetic construct

ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 (bases 1 to 1284)  
AUTHORS  
Hines, L., Rolfe, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,  
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,  
Williamson, J. and LaBaer, J.  
TITLE  
Cloning of human full-length CDS in Creator (TM) recombinational  
vector system  
JOURNAL  
Unpublished  
2 (bases 1 to 1284)  
REFERENCE  
Hines, L., Rolfe, A., Jenson, D., Moreira, D., Raphael, J., Kelley, F.,  
Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E.,  
Williamson, J. and LaBaer, J.  
AUTHORS  
Submitted (05-JAN-2005) Biological Chemistry and Molecular  
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,  
Cambridge, MA 02141, USA  
COMMENT  
This CDS clone is a part of a collection of human full-length  
expression clones generated by Harvard Institute of Proteomics.  
This ORF clone has been cloned without stop-codon (to allow fusion  
with C-terminal tag). The CDS has been directionally cloned using  
BD In-Fusion(TM) cloning system between the SalI and HindIII sites  
of the pDNR-Dual vector. Additional sequences in the clone: 'ACC'  
after SalI site and before 'ATG' to provide Kozak consensus  
sequence; 'GG' after last codon and before HindIII site to maintain  
reading frame. Each clone is clonally isolated and full-length  
sequence-verified.  
FEATURES  
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1..>1284  
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YVHRSLKIHOCENIFREGQYFGCSFDLTKVDSFEQSVQIMVNDNGIKIPSN  
IVPLTSRVPDPENIKLSFHNDDLVOMENPNPFI SRCLFEVEVNVNQSOTETNVEY  
VQAKENBEPERNVENTSCFWPGVLPPTLNTVTRVRYKTKCYEDDKTMSWSDSM  
STGKRNSTLYITMLIVPTVAGAILVILVTKRLKIIIFPPIPDGKIFKMFQDQ  
NDTLHWKYDIYEKQTKETDSVLIENLKASQL"  
ORIGIN  
Query Match 91.3%; Score 1267.8; DB 8; Length 1284;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1277; Conservative 0; Mismatches 2; Indels 3; Gaps 1;  
QY 61 ATGAGATGCGCGCGCGGCTGTCGCGGCTGTGCGGCGCTGCTGCGCGCGCGGCGG 120  
Db 1 ATGAGATGTCGCGCGCGGCTGTCGCGGCTGTGCGGCGCTGCTGCTGCGCGCGCGGCGG 60  
QY 121 GCGCGGGGGGGGGG---CGGCGCTTACGGAATCTGACGACCTGTGACAAATTTGAGTGC 177  
Db 61 GCGCGGGGGGGGGGGCGCGCGCTTACGGAATCTGACGACCTGTGACAAATTTGAGTGC 120  
QY 178 TCTGTGAAAAAAGCTCTGACAGATATATGACATGGAATCCACCGAGAGGAGCGAGCTCA 237  
Db 121 TCTGTGAAAAAAGCTCTGACAGATATATGACATGGAATCCACCGAGAGGAGCGAGCTCA 180  
QY 238 AATTGATGCTATGATATTTAGTCAATTTTGGGACAAACAGATATAGAAATAGTCCG 297  
Db 181 AATTGATGCTATGATATTTAGTCAATTTTGGGACAAACAGATATAGAAATAGTCCG 240

QY 298 GAAACTCGTGTCAATAGAAATACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGCTC 357  
| | | | |  
Db 241 GAAACTCGTGTCAATAGAAATACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGCTC 300  
| | | | |  
QY 358 CAGGTAGAACCAATAGAGTGAAGCCCTGACATTTTGGTTGAAAAATGCATCTCACCC 417  
| | | | |  
Db 301 CAGGTAGAACCAATAGAGTGAAGCCCTGACATTTTGGTTGAAAAATGCATCTCACCC 360  
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| | | | |  
Db 361 CCAGAAAGTGAATCTGAGTCTGCTGACTGAATCAATGCATTTGGCACAACCTGAGC 420  
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QY 478 TACATGAAGTGTCTTGGCTCCCTGGAAGAAATACAGTCCGACACTAACTATCTTC 537  
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Db 601 AGTGTCGAATATATGCTCAAGATTAATGACGAAAAATTAAACCATCTTCAATATATGTG 660  
| | | | |  
QY 718 CCTTTACCTCCCGTGTGAACCTGATCCCTCCACATTTTAAACCTCTCTCCACAAT 777  
| | | | |  
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QY 958 GGTGTTCTTCTGTACTTTGAACACAGTCAGATTAAGATCAAAACAAATAAGTTATGC 1017  
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QY 1078 AATTCACACTCTACACTAACCATGTTACTATGTTCCAGTCATGTCGAGAGTCAATC 1137  
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Db 1021 AATTCACACTCTACACTAACCATGTTACTATGTTCCAGTCATGTCGAGAGTCAATC 1080  
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QY 1138 ATAGTACTCTGCTTACCTTAAAGAGCTCAAGATTAATTATCCCTCAATTCCTGAT 1197  
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Db 1081 ATAGTACTCTGCTTACCTTAAAGAGCTCAAGATTAATTATCCCTCAATTCCTGAT 1140  
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QY 1198 CCTGGCAAGATTTTAAAGAAATGTTGAGACCAAGATGATATCTGCACTGGAAG 1257  
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Db 1141 CCTGGCAAGATTTTAAAGAAATGTTGAGACCAAGATGATATCTGCACTGGAAG 1200  
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QY 1258 AAGTACGACATCTATGAGAAACCAACCAAGAGAGAAACCACTCTGTAGTGTGATAGAA 1317  
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Db 1201 AAGTACGACATCTATGAGAAACCAACCAAGAGAGAAACCACTCTGTAGTGTGATAGAA 1260  
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QY 1318 AACCTGAAGAAAGCTCTCAGT 1339  
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Db 1261 AACCTGAAGAAAGCTCTCAGT 1282  
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Search completed: July 8, 2006, 00:13:42  
Job time : 8122 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 21:42:46 ; Search time 872 Seconds  
(without alignments)  
11058.050 Million cell updates/sec

Title: US-09-051-843D-3  
Perfect score: 1383  
Sequence: 1 gactctaacacagcagcaagg.....tcactgtgaccttgagaaga 1383

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID       | Description        |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1          | 1383   | 100.0       | 1383   | 2  | AAT66165 | AAT66165 Human int |
| 2          | 1333.8 | 96.4        | 3999   | 3  | AAA35213 | AAA35213 Human ade |
| 3          | 1333.8 | 96.4        | 3999   | 3  | AAF21335 | AAF21335 Human low |
| 4          | 1333.8 | 96.4        | 3999   | 10 | ABZ97029 | ABZ97029 Human nuc |
| 5          | 1333.8 | 96.4        | 3999   | 11 | ABD20878 | ABD20878 Human pul |
| 6          | 1333.8 | 96.4        | 4006   | 13 | ACF87407 | ACF87407 Human SIR |
| 7          | 1333.8 | 96.4        | 4006   | 14 | AEC15897 | AEC15897 Human int |
| 8          | 1333.8 | 96.4        | 4009   | 2  | AAT85827 | AAT85827 Human int |
| 9          | 1333.8 | 96.4        | 4038   | 4  | AAA86907 | AAA86907 Human int |
| 10         | 1333.8 | 96.4        | 4038   | 12 | ADL71811 | ADL71811 Human int |
| 11         | 1333.8 | 96.4        | 4038   | 12 | ADN62574 | ADN62574 Human int |
| 12         | 1333.8 | 96.4        | 4039   | 3  | AAA35214 | AAA35214 Human ade |
| 13         | 1333.8 | 96.4        | 4039   | 3  | AAF21336 | AAF21336 Human low |
| 14         | 1333.8 | 96.4        | 4039   | 6  | ABL67709 | ABL67709 Oesophagu |
| 15         | 1333.8 | 96.4        | 4039   | 6  | ABK84753 | ABK84753 Human CDN |
| 16         | 1333.8 | 96.4        | 4039   | 6  | ABN97361 | ABN97361 Gene #385 |
| 17         | 1333.8 | 96.4        | 4039   | 10 | ABZ97030 | ABZ97030 Human nuc |
| 18         | 1333.8 | 96.4        | 4039   | 11 | ABD20879 | ABD20879 Human pul |

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|----|--------|------|-------|----|----------|---------------------|
| 19 | 1333.8 | 96.4 | 4039  | 12 | ADL82842 | ADL82842 Human PRO  |
| 20 | 1333.8 | 96.4 | 4039  | 12 | ADN04503 | ADN04503 Antipsoxi  |
| 21 | 1333.8 | 96.4 | 4039  | 13 | ADR24772 | ADR24772 Breast ca  |
| 22 | 1333.8 | 96.4 | 4039  | 13 | ACN41073 | ACN41073 Tumour-as  |
| 23 | 1333.8 | 96.4 | 4039  | 13 | ADK97460 | ADK97460 Pancreatit |
| 24 | 1333.8 | 96.4 | 4466  | 10 | ADB47358 | ADB47358 Human CDN  |
| 25 | 1333.8 | 96.4 | 11927 | 2  | AAK77356 | AAK77356 Polynucle  |
| 26 | 1333.8 | 96.4 | 11927 | 3  | AAA90388 | AAA90388 Plaemid p  |
| 27 | 1333.8 | 96.4 | 14978 | 3  | AAA35216 | AAA35216 Human ade  |
| 28 | 1333.8 | 96.4 | 14978 | 3  | AAF21338 | AAF21338 Human low  |
| 29 | 1333.8 | 96.4 | 14978 | 10 | ABZ97032 | ABZ97032 Human nuc  |
| 30 | 1333.8 | 96.4 | 14978 | 11 | ABD20881 | ABD20881 Human pul  |
| 31 | 1266.4 | 91.6 | 1284  | 14 | ADV42774 | ADV42774 Human psy  |
| 32 | 1264.8 | 91.5 | 1284  | 10 | ADF17834 | ADF17834 Human IL-  |
| 33 | 1238.4 | 89.5 | 3880  | 6  | ABK35718 | ABK35718 CDNA sequ  |
| 34 | 1236.8 | 89.4 | 3906  | 5  | AAF98394 | AAF98394 Human CDN  |
| 35 | 1181.4 | 85.4 | 1680  | 6  | ABK35719 | ABK35719 CDNA sequ  |
| 36 | 1039.4 | 75.2 | 1389  | 12 | ADO26893 | ADO26893 CDNA enco  |
| 37 | 1012   | 73.2 | 1547  | 4  | AAK59955 | AAK59955 Canine in  |
| 38 | 1012   | 73.2 | 1547  | 4  | AAK59954 | AAK59954 Canine in  |
| 39 | 1009.8 | 73.0 | 2382  | 3  | AAA09050 | AAA09050 IL-13/IL-  |
| 40 | 1009.8 | 73.0 | 2382  | 10 | AAK63744 | AAK63744 Human IL-  |
| 41 | 983    | 71.1 | 1215  | 4  | AAK59957 | AAK59957 Canine in  |
| 42 | 983    | 71.1 | 1215  | 4  | AAK59956 | AAK59956 Canine in  |
| 43 | 959.4  | 69.4 | 2355  | 3  | AAA09049 | AAA09049 IL-13/IL-  |
| 44 | 959.4  | 69.4 | 2355  | 10 | AAK63743 | AAK63743 Human IL-  |
| 45 | 956.4  | 69.2 | 966   | 6  | AAK22979 | AAK22979 Human sol  |

ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| ID       | AAT66165 standard; DNA, 1383 BP.                                      |
| AC       | AAT66165;   |
| DT       | 15-JUL-1997 (first entry)   |
| XX       |   |
| DE       | Human interleukin-12 receptor alpha chain NR4 DNA.                    |
| XX       |   |
| KW       | NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine; |
| KW       | allergy; aschma; therapy; ss.   |
| XX       |   |
| OS       | Homo sapiens.   |
| XX       |   |
| FT       | Key   |
| FT       | CDS   |
| FT       | sig_peptide   |
| FT       | mat_peptide   |
| XX       |   |
| PN       | WO9715663-A1.   |
| XX       |   |
| PD       | 01-MAY-1997.  |
| XX       |   |
| PF       | 23-OCT-1996; 96WO-AU000668.   |
| XX       |   |
| PR       | 23-OCT-1995; 95AU-00006135.   |
| PR       | 22-DEC-1995; 95AU-00007276.   |
| PR       | 09-SEP-1996; 96AU-00002208.   |
| XX       |   |
| PA       | (AMRA-) AMRAD OPERATIONS PTY LTD.                                     |
| XX       |   |
| PI       | Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;                 |
| XX       |   |
| DR       | WPI, 1997-259018/23.  |
| DR       | P-PSDB; AAK09822.   |
| XX       |   |
| PT       | DNA encoding animal haemopoietin receptor which interacts with        |





XX 03-AUG-1998; 98US-0095212P.  
XX (UYEC-) UNIV EAST CAROLINA.  
XX NYCE JW;  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
XX Disclosure; Page 1252-1253; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytoskeletal and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation;  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA3233 to AAA3512 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3233 to  
CC AAA3992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
XX Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;  
SQ  
Query Match 96.4%; Score 1333.8; DB 3; Length 3999;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

Db 367 ATTTGGTTGAAAAATGATCTCAACCCGAAAGGTATCTGATCTGATGATGAG 426  
Qy 451 CTTCAATGCAATTTGGCAACACCTGAGCTACATGAAAGCTTTGGCTCCCTGGAAAGAT 510  
Db 427 CTTCAATGCAATTTGGCAACACCTGAGCTACATGAAAGCTTTGGCTCCCTGGAAAGAT 486  
Qy 511 ACCAGTCCCGACATACTACTCTGATATGAGGACAGAAAGCTGGAAATATTCAT 570  
Db 487 ACCAGTCCCGACATACTACTCTGATATGAGGACAGAAAGCTGGAAATATTCAT 546  
Qy 571 CAATGTAAAAACATCTTTAGAGAAAGGCAATATCTTGGTCTTCTTGTATCTGACCAA 630  
Db 547 CAATGTAAAAACATCTTTAGAGAAAGGCAATATCTTGGTCTTCTTGTATCTGACCAA 606  
Qy 631 GTGAAGATTCAGATTGGAACAAACAGATGCTCAATATATGTCAGAGATATGACAGA 690  
Db 607 GTGAAGATTCAGATTGGAACAAACAGATGCTCAATATATGTCAGAGATATGACAGA 666  
Qy 691 AAATTAACCATCTTCAATATATGATGCTTAACTCCGTTGAAACCTGATCTGCA 750  
Db 667 AAATTAACCATCTTCAATATATGATGCTTAACTCCGTTGAAACCTGATCTGCA 726  
Qy 751 CATATTAACCATCTTCTTCCACATGATGACCTATATGTCAGATGGAGATTCACAG 810  
Db 727 CATATTAACCATCTTCTTCCACATGATGACCTATATGTCAGATGGAGATTCACAG 786  
Qy 811 AATTTTATGACAGATGCTTATTTATGAAAGTGAAGTCAATTAACGCAACCTGACACA 870  
Db 787 AATTTTATGACAGATGCTTATTTATGAAAGTGAAGTCAATTAACGCAACCTGACACA 846  
Qy 871 CATATATTTTATGACAGTCAACGCAAGGCTAAATGAGATCCAGATTTGAGAAATGTG 930  
Db 847 CATATATTTTATGACAGTCAACGCAAGGCTAAATGAGATCCAGATTTGAGAAATGTG 906  
Qy 931 GAGATATCATCTTGTTCATGATGCTCCGATGCTTCTGATTAACCAACAGTGA 990  
Db 907 GAGATATCATCTTGTTCATGATGCTCCGATGCTTCTGATTAACCAACAGTGA 966  
Qy 991 ATTAAGATCAAAACAAATAGTATGCTATGAGATGACAACTGTGAGTAAATGGAGC 1050  
Db 967 ATTAAGATCAAAACAAATAGTATGCTATGAGATGACAACTGTGAGTAAATGGAGC 1026  
Qy 1051 CAAGAATGATATGATGATGAGAGCGCAATTCACATCTACATTAACCATGTTCTCAT 1110  
Db 1027 CAAGAATGATATGATGAGAGCGCAATTCACATCTACATTAACCATGTTCTCAT 1086  
Qy 1111 GTTCAAGTCACTGCTGAGAGTGAATCATATGATCTCTGCTTTAACTTAAGAGCTCAAG 1170  
Db 1087 GTTCAAGTCACTGCTGAGAGTGAATCATATGATCTCTGCTTTAACTTAAGAGCTCAAG 1146  
Qy 1171 ATTATTAATTCCTCCCAATTCCTGATCTGGAAGATTTTAAAGAAATGTTTGAAGC 1230  
Db 1147 ATTATTAATTCCTCCCAATTCCTGATCTGGAAGATTTTAAAGAAATGTTTGAAGC 1206  
Qy 1231 CAGAATGATATGATCTGCACTGGAAGATGATGACATATGAGAGCAACCAAGAG 1290  
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Qy 1291 GAAACGCACTGCTGATGCTGATAGAAACCTGAAAGAAACCTCTGATGAGAGATTA 1350  
Db 1267 GAAACGCACTGCTGATGCTGATAGAAACCTGAAAGAAACCTCTGATGAGAGATTA 1326  
Qy 1351 TTTATTTTATCTTCACTGATGACCTTGAAGA 1383  
Db 1327 TTTATTTTATCTTCACTGATGACCTTGAAGA 1359  
RESULT 3  
AAFP21335  
ID AAFP21335 standard; DNA; 3999 BP.  
XX  
XX AAFP21335;  
AC

|                       |   |               |
|-----------------------|---|---------------|
| XX                    |   |               |
| DT                    | 14-MAR-2001   | (first entry) |
| XX                    |   |               |
| DE                    | Human low adenosine antisense oligonucleotide related sequence #2902.     |               |
| XX                    |   |               |
| KW                    | low adenosine antisense oligonucleotide; phosphorothioate; allergy;       |               |
| KM                    | human, airway disorder; bronchoconstriction; lung inflammation;           |               |
| KM                    | surfactant depletion; respiratory; bronchodilator; antiinflammation;      |               |
| KM                    | immunosuppressive; antisthmatic; analgesic; hypotensive; cytostatic;      |               |
| KM                    | respiratory obstruction; pulmonary obstruction; impeded respiration;      |               |
| KM                    | surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;       |               |
| KM                    | respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  |               |
| KM                    | pulmonary hypertension; emphysema; pulmonary transplantation rejection;   |               |
| KM                    | chronic obstructive pulmonary disease; pulmonary infection; bronchitis;   |               |
| KM                    | cancer; ss.   |               |
| XX                    |   |               |
| OS                    | Homo sapiens.   |               |
| PM                    | WO200062736-A2.   |               |
| PD                    | 26-OCT-2000.  |               |
| PF                    | 24-MAR-2000 ; 2000WO-US008020.  |               |
| PR                    | 06-APR-1999; 99US-0127958P.   |               |
| PA                    | (UYEC-) UNIV EAST CAROLINA.   |               |
| PA                    | (NYCE/) NYCE J W.   |               |
| PI                    | Nyce JW;  |               |
| DR                    | WI; 2000-679539/66.   |               |
| XX                    |   |               |
| PT                    | Low adenosine (A) content antisense oligonucleotides which do not trigger |               |
| PT                    | adenosine receptors during metabolism, useful e.g. for treating cancers   |               |
| PT                    | and respiratory obstructions.   |               |
| XX                    |   |               |
| PS                    | Disclosure; Page 1336-1337; 1592pp; English.                              |               |
| XX                    |   |               |
| CC                    | The present invention describes low adenosine (A) content antisense       |               |
| CC                    | oligonucleotides and compositions (I) comprising them. In the antisense   |               |
| CC                    | oligonucleotides the A is replaced by a 'Universal' or alternative base.  |               |
| CC                    | (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,    |               |
| CC                    | immunosuppressive, antisthmatic, hypotensive and cytostatic activities.   |               |
| CC                    | The antisense oligonucleotides and (I) can be used to down-regulate the   |               |
| CC                    | expression and/or activity of target polypeptides associated with         |               |
| CC                    | lung/respiratory disorders and malignancies, such as stimulating and      |               |
| CC                    | activating peptide factors and transmitters, transcription factors,       |               |
| CC                    | immunoglobulins and antibodies, antibody receptors, cytokines and         |               |
| CC                    | chemokines, endogenously produced specific and non-specific enzymes,      |               |
| CC                    | binding proteins, adhesion molecules and their receptors, cytokine and    |               |
| CC                    | chemokine receptors, adenosine receptors, bradykinin receptors, central   |               |
| CC                    | nervous system (CNS) and peripheral nervous and non-nervous system        |               |
| CC                    | receptors, CNS and peripheral nervous and non-nervous system peptide      |               |
| CC                    | transmitters, defensins, growth factors, vasocactive peptides and         |               |
| CC                    | receptors, binding proteins and malignancy associated proteins. The       |               |
| CC                    | antisense oligonucleotides may be used in this way to treat disorders     |               |
| CC                    | including respiratory obstruction (especially pulmonary obstruction       |               |
| CC                    | and/or bronchoconstriction) and/or lung inflammation, allergies) and/or   |               |
| CC                    | surfactant hypoproduction which are associated with a disease or          |               |
| CC                    | condition selected from pulmonary vasoconstriction, inflammation,         |               |
| CC                    | allergies, asthma, impeded respiration, respiratory distress syndrome     |               |
| CC                    | (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary      |               |
| CC                    | hypertension, emphysema, chronic obstructive pulmonary disease (COPD),    |               |
| CC                    | pulmonary transplantation rejection, pulmonary infections, bronchitis,    |               |
| CC                    | and/or cancer. AA18434 to AA21543 represent human polynucleotide          |               |
| CC                    | fragments and antisense oligonucleotides used in the exemplification of   |               |
| CC                    | the present invention   |               |
| XX                    |   |               |
| SQ                    | Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;             |               |
|                       |   |               |
| Query Match           | 96.4%; Score 1333.8; DB 3; Length 3999;                                   |               |
| Best Local Similarity | 99.6%; Pred No. 0;  |               |

|    | Matches | 1346:         | Conservative   | 0;   | Mismatches | 2; | Indels | 3; | Gaps | 1; |
|----|---------|---------------|--|------|------------|----|--------|----|------|----|
| OY | 34      | CGGCGGGATTC   | CCGAGCGAGAGGCTGCATGAGTGGCGGCGGACTCTCGGGCTGTGG        | 93   |            |    |        |    |      |    |
| Dd | 7       | CGGCGGGGCTC   | CGAGGGGAGGCTGCATGGAAGTGCGGGCGGGCTCTCGGGCTGTGG        | 66   |            |    |        |    |      |    |
| OY | 94      | GGCTGCTGCTCT  | TGCCGCCGGCGGCGGGGGCGGGGGCGGGGG--CGGGCTTAGGAAACT      | 150  |            |    |        |    |      |    |
| Dd | 67      | GGCTGCTGCTCT  | TGCCGCCGGCGGCGGGGGCGGGGGCGGGGGCGGGGGCTTAGGAAACT      | 126  |            |    |        |    |      |    |
| OY | 151     | CAGCCACCTGTGA | CAAAATTGAGTGTCTGTGGAAAACCTCTGCACAGTAATATGTGACA       | 210  |            |    |        |    |      |    |
| Dd | 127     | CAGCCACCTGTGA | CAAAATTGAGTGTCTGTGGAAAACCTCTGCACAGTAATATGTGACA       | 186  |            |    |        |    |      |    |
| OY | 211     | TGGAATCACCCG  | AGGAGGAGCCAGCTCAAATTGATAGTCTATGATATTTTATCATTTTGGC    | 270  |            |    |        |    |      |    |
| Dd | 187     | TGGAATCACCCG  | AGGAGGAGCCAGCTCAAATTGATAGTCTATGATATTTTATCATTTTGGC    | 246  |            |    |        |    |      |    |
| OY | 271     | GACAAACAAGTA  | AGAATAATAGCTCCGGAAACTGTGTTCAATAGAACCTTCTAAT          | 330  |            |    |        |    |      |    |
| Dd | 247     | GACAAACAAGTA  | AGAATAATAGCTCCGGAAAACCTGTGTTCAATAGAACCTTCTAAT        | 306  |            |    |        |    |      |    |
| OY | 331     | GAGGGAATTTGT  | CTCGAAGTGGGGTCCCAAGTATAGCAACAATGAGATGGAAGCCTAGC      | 390  |            |    |        |    |      |    |
| Dd | 307     | GAGGGAATTTGT  | CTCGAAGTGGGGTCCCAAGTATAGCAACAATGAGATGGAAGCCTAGC      | 366  |            |    |        |    |      |    |
| OY | 391     | ATTTTGGTTGAAA | AATGATCTCACCCCCAGAAAGTATCCTGAGTGTGCTGTGACCTGAA       | 450  |            |    |        |    |      |    |
| Dd | 367     | ATTTTGGTTGAAA | AATGATCTCACCCCCAGAAAGTATCCTGAGTGTGCTGTGACCTGAG       | 426  |            |    |        |    |      |    |
| OY | 451     | CTTCAATGCATTT | GGCAACAACCTGAGTACATGAAGTGTCTTGGCTCCCTGGAAAGAT        | 510  |            |    |        |    |      |    |
| Dd | 427     | CTTCAATGCATTT | GGCAACAACCTGAGTACATGAAGTGTCTTGGCTCCCTGGAAAGAT        | 486  |            |    |        |    |      |    |
| OY | 511     | ACGAGTCCCAGCA | CTAATCTACTCTCTACTATTTGGACAGAAAGCCGTGAAAAAATTCAT      | 570  |            |    |        |    |      |    |
| Dd | 487     | ACGAGTCCCAGCA | CTAATCTACTCTCTACTATTTGGACAGAAAGCCGTGAAAAAATTCAT      | 546  |            |    |        |    |      |    |
| OY | 571     | CAATGTAAAAACA | TCTTTTGAAGAAGCCAAATACTTTGGTTCTCTTGTGATCTGCACCAA      | 630  |            |    |        |    |      |    |
| Dd | 547     | CAATGTAAAAACA | TCTTTTGAAGAAGCCAAATACTTTGGTTCTCTTGTGATCTGCACCAA      | 606  |            |    |        |    |      |    |
| OY | 631     | GTGAAGATTCAG  | ATTTTGAACAACAACAGTGTCCAATAATGTCANAGATPATGACAGA       | 690  |            |    |        |    |      |    |
| Dd | 607     | GTGAAGATTCAG  | ATTTTGAACAACAACAGTGTCCAATAATGTCANAGATPATGACAGA       | 666  |            |    |        |    |      |    |
| OY | 691     | AAATTTAAACAT  | CTCTTCAATATATATAGTCCCTTAACTCCCGTGTGAAACCTGATCTCCCA   | 750  |            |    |        |    |      |    |
| Dd | 667     | AAATTTAAACAT  | CTCTTCAATATATATAGTCCCTTAACTCCCGTGTGAAACCTGATCTCCCA   | 726  |            |    |        |    |      |    |
| OY | 751     | CATATTAATAAA  | CCCTCTCTCCACAATGATGACCCTATATGTGCAATGGAGAAATCCACAG    | 810  |            |    |        |    |      |    |
| Dd | 727     | CATATTAATAAA  | CCCTCTCTCCACAATGATGACCCTATATGTGCAATGGAGAAATCCACAG    | 786  |            |    |        |    |      |    |
| OY | 811     | AATTTTATAGCA  | GATSCCTATTTTATGAAGTAGAAGTCAATPACACCAACTGACACA        | 870  |            |    |        |    |      |    |
| Dd | 787     | AATTTTATAGCA  | GATSCCTATTTTATGAAGTAGAAGTCAATPACACCAACTGACACA        | 846  |            |    |        |    |      |    |
| OY | 871     | CATATATGTTTT  | CTATGCTCCAAAGGCTPAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTG | 930  |            |    |        |    |      |    |
| Dd | 847     | CATATATGTTTT  | CTATGCTCCAAAGGCTPAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTG | 906  |            |    |        |    |      |    |
| OY | 931     | GAGAAATCATTGT | TTCATGATCCCGTGGATCTTCTCTATACCTTGGAAACAAGTACAGA       | 990  |            |    |        |    |      |    |
| Dd | 907     | GAGAAATCATTGT | TTCATGATCCCGTGGATCTTCTCTATACCTTGGAAACAAGTACAGA       | 966  |            |    |        |    |      |    |
| OY | 991     | ATAAGAGTCAAAA | CAAAATAAGTTATGCTATGAGGATGACAAACTCTGAGTAATTTGAGC      | 1050 |            |    |        |    |      |    |
| Dd | 967     | ATAAGAGTCAAAA | CAAAATAAGTTATGCTATGAGGATGACAAACTCTGAGTAATTTGAGC      | 1026 |            |    |        |    |      |    |
| OY | 1051    | CAAGAAATGAGTA | TAGGTAAAGAGCGCAATTTCCACACTCTACATPAACCATGTATCTCATTT   | 1110 |            |    |        |    |      |    |
| Dd | 1027    | CAAGAAATGAGTA | TAGGTAAAGAGCGCAATTTCCACACTCTACATPAACCATGTATCTCATTT   | 1086 |            |    |        |    |      |    |



|          |  |   |      |
|----------|--|---|------|
| OY       | 871  | LATATATGTTTCTACGTCCAAAGAGGCTAAATGTGAGATTCAGAAATTTGAGAAATGTG               | 930  |
| Db       | 847  | CATATATGTTTCTACGTCCAAAGAGGCTAAATGTGAGATTCAGAAATTTGAGAAATGTG               | 906  |
| OY       | 921  | GAGAAATACATCTGTGTTTCATGATGCCCTGAGTGTCTTCTGATGATCTTTGAACACAGTCA            | 990  |
| Db       | 907  | GAGAAATACATCTGTGTTTCATGATGCCCTGAGTGTCTTCTGATGATCTTTGAACACAGTCA            | 966  |
| OY       | 991  | ATTAAGAGTCAAAACCAATTAAGTTTATGCTATAGAGATGACAAACTCTGAGATTAATTGAGC           | 1050 |
| Db       | 967  | ATTAAGAGTCAAAACCAATTAAGTTTATGCTATAGAGATGACAAACTCTGAGATTAATTGAGC           | 1026 |
| OY       | 1051   | CAAGAATAGATATATGTTAAGAGCGCAATTCACACTCTATACATTAACCATGTTACTATT              | 1110 |
| Db       | 1027   | CAAGAATAGATATATGTTAAGAGCGCAATTCACACTCTATACATTAACCATGTTACTATT              | 1086 |
| OY       | 1111   | GTTCCAGTCATCGTGGCAGAGTGCAATCATAGTACCTCGTTTACCTTAATAAAGGCTCAAG             | 1170 |
| Db       | 1087   | GTTCCAGTCATCGTGGCAGAGTGCAATCATAGTACCTCGTTTACCTTAATAAAGGCTCAAG             | 1146 |
| OY       | 1171   | ATTATTTATATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGAGAC             | 1230 |
| Db       | 1147   | ATTATTTATATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGAGAC             | 1206 |
| OY       | 1231   | CAGAAATGATGATCTGTGCACCTGGAGAAATGACATCTATAGAGACCAACCAAGAG                  | 1290 |
| Db       | 1207   | CAGAAATGATGATCTGTGCACCTGGAGAAATGACATCTATAGAGACCAACCAAGAG                  | 1266 |
| OY       | 1291   | GAAACCGCATCTGTATAGTGTCTGATTAAGAAACCTGAAAGAAAGCTCTCAATGATGAGATTA           | 1350 |
| Db       | 1267   | GAAACCGCATCTGTATAGTGTCTGATTAAGAAACCTGAAAGAAAGCTCTCAATGATGAGATTA           | 1326 |
| OY       | 1351   | TTTATTTTAACTTCACCTGACGTGACCTTGAGAAAGA                                     | 1383 |
| Db       | 1327   | TTTATTTTAACTTCACCTGACGTGACCTTGAGAAAGA                                     | 1359 |
| RESULT 5 |  |   |      |
| ABD20878 |  |   |      |
| ID       | ABD20878   | standard; DNA; 3999 BP.   |      |
| AC       | ABD20878;  |   |      |
| DT       | 29-JUL-2004  | (first entry)   |      |
| DE       |  | Human pulmonary and inflammatory target DNA #489.                         |      |
| XX       |  | Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;      |      |
| KW       |  | respiratory tract inflammation; adenose sensitivity; lung; cancer;        |      |
| KW       |  | surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;      |      |
| KW       |  | analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;  |      |
| KW       |  | beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; |      |
| KW       |  | respiratory distress syndrome; allergic rhinitis; pulmonary hypertension; |      |
| KW       |  | emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;     |      |
| KW       |  | pulmonary transplantation rejection; ds.                                  |      |
| OS       |  | Homo sapiens.   |      |
| XX       |  |   |      |
| PN       | WO200285309-A2.  |   |      |
| XX       |  |   |      |
| PD       | 31-OCT-2002.   |   |      |
| XX       |  |   |      |
| PF       | 23-APR-2002; 2002WO-US013143.                                |   |      |
| XX       |  |   |      |
| PR       | 24-APR-2001; 2001US-0286036P.                                |   |      |
| XX       |  |   |      |
| PA       | (EPIG-) EPIGENESIS PHARM INC.                                |   |      |
| XX       |  |   |      |
| PI       | Nyge JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D, |   |      |
| PI       | Miller S, Tang L, Shanabuddin S;                             |   |      |
| XX       |  |   |      |
| DR       | WPI; 2003-093058/08.   |   |      |
| XX       |  |   |      |

[illegible]

Db 427 CTTCAAGGCAATTTGGGCAACCTGAGCTACATGAAAGTTCTTGGCTCCCTGGAGGAAT 486  
 QY 511 ACCAGTCCCGACACTAATCTACTCTCTACATTTGGGACGAAAGCTGGAAAAATCAT 570  
 Db 487 ACCAGTCCCGACACTAATCTACTCTCTACATTTGGGACGAAAGCTGGAAAAATCAT 546  
 QY 571 CAATGTGAAAAACATCTTTAGGAGAGGCAATCTTTGGTGTCTCTTGAATCTGACCAA 630  
 Db 547 CAATGTGAAAAACATCTTTAGGAGAGGCAATCTTTGGTGTCTCTTGAATCTGACCAA 606  
 QY 631 GTGAGGATTCGAGTTTGAACACACAGTGTCCAAATTAATGTCAAGATATGACAGA 690  
 Db 607 GTGAGGATTCGAGTTTGAACACACAGTGTCCAAATTAATGTCAAGATATGACAGA 666  
 QY 691 AAAATTAACCATCTTCAATATATAGTCCCTTTAACTCCCGTGGAAACCTGATCCCTCA 750  
 Db 667 AAAATTAACCATCTTCAATATATAGTCCCTTTAACTCCCGTGGAAACCTGATCCCTCA 726  
 QY 751 CATATTTAAAAACCTCTCTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAG 810  
 Db 727 CATATTTAAAAACCTCTCTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAG 786  
 QY 811 AATTTATATGACAGATGCTTATTTATGAAATGAGTCAATTAACAGCCAACTGACACA 870  
 Db 787 AATTTATATGACAGATGCTTATTTATGAAATGAGTCAATTAACAGCCAACTGACACA 846  
 QY 871 CATATCTTTTTCACCTCCCAAGAGGCTTAATGTGAGAAATCCAAATTTGAGAAATGTG 930  
 Db 847 CATATATGTTTTTCACCTCCCAAGAGGCTTAATGTGAGAAATCCAAATTTGAGAAATGTG 906  
 QY 931 GAGAAATCATCTTGTTCATGATGCTCCCTGATGTTCTTCTGATACCTTTGAAACAGTGA 990  
 Db 907 GAGAAATCATCTTGTTCATGATGCTCCCTGATGTTCTTCTGATACCTTTGAAACAGTGA 966  
 QY 991 ATTAAGTCAAAAACAAATTAATGATGCTATGAGAGTGAACAACTCTGAGTAATTTGAGC 1050  
 Db 967 ATTAAGTCAAAAACAAATTAATGATGCTATGAGAGTGAACAACTCTGAGTAATTTGAGC 1026  
 QY 1051 CAGAAATGATATAGTATGAGAAAGCGAATTTCCACATCTACATTAACATGTTACTATT 1110  
 Db 1027 CAGAAATGATATAGTATGAGAAAGCGAATTTCCACATCTACATTAACATGTTACTATT 1086  
 QY 1111 GTTCCAGTATCTGTCGAGGTGCAATCATATGTAATCTCTGCTTAACTTAAAGGCTCAAG 1170  
 Db 1087 GTTCCAGTATCTGTCGAGGTGCAATCATATGTAATCTCTGCTTAACTTAAAGGCTCAAG 1146  
 QY 1171 ATTATTAATTTCCCTCCAAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGAGAC 1230  
 Db 1147 ATTATTAATTTCCCTCCAAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGAGAC 1206  
 QY 1231 CAGAAATGATATCTGTCGAGGTGCAATCATATGTAATCTTATGAGAAAGCAACCAAGAG 1290  
 Db 1207 CAGAAATGATATCTGTCGAGGTGCAATCATATGTAATCTTATGAGAAAGCAACCAAGAG 1266  
 QY 1291 GAAACGCACTCTGATGCTGATAGAAACCTGAAGAAACCTCTGATGATGAGATTA 1350  
 Db 1267 GAAACGCACTCTGATGCTGATAGAAACCTGAAGAAACCTCTGATGATGAGATTA 1326  
 QY 1351 TTTATTTTAACTTCACTGATGACCTTGAGAGA 1383  
 Db 1327 TTTATTTTAACTTCACTGATGACCTTGAGAGA 1359

RESULT 6  
 ACF87407  
 ID ACF87407 standard; DNA; 4006 BP.  
 XX ACF87407;  
 AC ACF87407;  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DE Human SIRS/sepsis diagnostic marker DNA fragment 6267.

XX  
 KW Systemic inflammatory response syndrome; SIRS; antibacterial;  
 KM immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.  
 OS homo sapiens.  
 PN WO2004087949-A2.  
 PD 14-OCT-2004.  
 PF 31-MAR-2004; 2004WO-EP003419.  
 PR 02-APR-2003; 2003DE-01015031.  
 PR 08-AUG-2003; 2003DE-01036511.  
 PR 02-SEP-2003; 2003DE-01040395.  
 PA (SIRS-) SIRS LAB GMBH.  
 PI Russwurm S, Reinhardt K, Saluz H, Straube E, Zipfel PF, Designer H;  
 PI WPI; 2004-748070/73.  
 DR  
 XX  
 PT In vitro detection of systemic inflammatory response syndrome and related  
 PT conditions, for e.g. monitoring progression, comprises detecting abnormal  
 PT expression of disease-related genes.  
 PS Disclosure; Page: 75pp; German.  
 XX  
 CC The invention relates to a novel method for in vitro detection of  
 CC systemic inflammatory response syndrome (SIRS). The method comprises  
 CC detecting abnormal expression of disease-related genes, or their  
 CC associated peptides. The method of the invention demonstrates  
 CC antibacterial, immunosuppressive and antiinflammatory applications and  
 CC may be used for early differential diagnosis, monitoring progression,  
 CC assessing risk, assessing the likely response to treatment and for post  
 CC mortem diagnosis of systemic inflammatory response syndrome, sepsis and  
 CC sepsis-like conditions. The recombinant or synthetic nucleic acid  
 CC sequences of the invention, or derived proteins or peptides, may be  
 CC useful as calibrants in assays for the specified diseases, for evaluating  
 CC activity or toxicity in screening for active agents and/or for  
 CC preparation of agents for treatment or prevention of the specified  
 CC diseases. The current sequence is that of a human SIRS/sepsis diagnostic  
 CC marker DNA fragment of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at ffp.wipo.int/pub/published  
 CC pat\_sequences. Furthermore, a number of arbitrary SEQ ID NO.s are  
 CC disclosed within the specification, however, these have not been taken  
 CC into account during indexing due to inconsistencies in application and  
 CC format  
 CC  
 SQ Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;  
 Query Match 96.4%; Score 1333.8; DB 13; Length 4006;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;  
 QY 34 CGGCCGGGTTCCGAGCGGAGGCTGCATGAGTGCCTCGCGGCTCTGCGGGCTGTGG 93  
 Db 17 CGGCCGGGCTCCGAGCGGAGGCTGCATGAGTGCCTCGCGGCTCTGCGGGCTGTGG 76  
 QY 94 GCGCTGCTGCTGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 150  
 Db 77 GCGCTGCTGCTGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 136  
 QY 151 CAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAACCTCTGACAGATATATGAGACA 210  
 Db 137 CAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAACCTCTGACAGATATATGAGACA 196  
 QY 211 TGGAAATCCACCCGAGGAGCCAGCTCAATTTGATGATGATTTTATCTATTTTGGC 270  
 Db 197 TGGAAATCCACCCGAGGAGCCAGCTCAATTTGATGATGATTTTATCTATTTTGGC 256  
 QY 271 GACAAACAGATTAAGAAATAGCTCGGAAATCTGCTGTTCAATGAGAAATACCCCTGAAT 330

Db 257 GACAAACAGATAGAAAAATAGCTCCGAAACCTGCTTCAATAGAAAGTACCCTGAAT 316  
331 GAGAGATTGTTGTCGAAAGTGGGTCCTCAGTAGACCAATAGAGATGGAAGCCTAGC 390  
317 GAGAGATTGTTGTCGAAAGTGGGTCCTCAGTAGACCAATAGAGATGGAAGCCTAGC 376  
391 ATTTGGTTGAAAAATGCACTTCACCCCGAAGGATCCTGAGTCTGCTGTGACTGAA 450  
377 ATTTGGTTGAAAAATGCACTTCACCCCGAAGGATCCTGAGTCTGCTGTGACTGAG 436  
451 CTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAGTCTTGGCTCCCTGGAAGGAAT 510  
437 CTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAGTCTTGGCTCCCTGGAAGGAAT 496  
511 ACCAGTCCCGACACTACATCTCTCTACTATTGGCAGAGAGCTGAAAAAATTCAT 570  
497 ACCAGTCCCGACACTACATCTCTCTACTATTGGCAGAGAGCTGAAAAAATTCAT 556  
571 CAATGAAAAACATCTTTAGAGAGGCAATACCTTGGTGGTCTTGGATCTGACCCAA 630  
557 CAATGAAAAACATCTTTAGAGAGGCAATACCTTGGTGGTCTTGGATCTGACCCAA 616  
631 GTGAGAGATTCCGATTTTGAACAACACAGTGTCCAAATATGTCGAAGATATGCA 650  
617 GTGAGAGATTCCGATTTTGAACAACACAGTGTCCAAATATGTCGAAGATATGCA 676  
691 AAAATTAACCATCTTCAATATAGTGCTTAACTCCCGTGTGAAACCTGATCCCTCA 750  
677 AAAATTAACCATCTTCAATATAGTGCTTAACTCCCGTGTGAAACCTGATCCCTCA 736  
751 CATATTAACCATCTTCCCTTCCCAATATGATGACCTATATGTGCAATGGAGAAATCCACAG 810  
737 CATATTAACCATCTTCCCTTCCCAATATGATGACCTATATGTGCAATGGAGAAATCCACAG 796  
811 AATTTATATAGAGATGCCATTTTATGAGTGAAGTCAATACAGCCAACTGAGACA 870  
797 AATTTATATAGAGATGCCATTTTATGAGTGAAGTCAATACAGCCAACTGAGACA 856  
871 CATATGTTTTTACGTCCAAGAGGCTAAATGTGAGAAATCAGAAATTTGAGAGAAATGTG 930  
857 CATATGTTTTTACGTCCAAGAGGCTAAATGTGAGAAATCAGAAATTTGAGAGAAATGTG 916  
931 GAGAAATACATCTTGTTCATGTGCTCCCTGATCTTCTCTGATATCTTTGAAACACAGTCAGA 990  
917 GAGAAATACATCTTGTTCATGTGCTCCCTGATCTTCTCTGATATCTTTGAAACACAGTCAGA 976  
991 ATTAAGGTCAAAACAAATAGTTATGTATGAGATGACAAACTCTGAGATTAATGGAGC 1050  
977 ATTAAGGTCAAAACAAATAGTTATGTATGAGATGACAAACTCTGAGATTAATGGAGC 1036  
1051 CAAGAATGAGTATGAGTGAAGAGCGCAATTCACACTCTACATTAACCATGTTACTGAT 1110  
1037 CAAGAATGAGTATGAGTGAAGAGCGCAATTCACACTCTACATTAACCATGTTACTGAT 1096  
1111 GTTCCAGTCATGCTGCGAGGTGCAATCATAGTATCTCTGCTTAACTAAAGGCTCAAG 1170  
1097 GTTCCAGTCATGCTGCGAGGTGCAATCATAGTATCTCTGCTTAACTAAAGGCTCAAG 1156  
1171 ATTAATATATTCCTCCCAATTCCTGATCCGCGCAAGATTTTAAAGAAATGTTTGGAGAC 1230  
1157 ATTAATATATTCCTCCCAATTCCTGATCCGCGCAAGATTTTAAAGAAATGTTTGGAGAC 1216  
1231 CAGAAATGAGTATCTGCACTGGAAGAGTACGACATCTATGAGAAACCAAGAGAG 1290  
1217 CAGAAATGAGTATCTGCACTGGAAGAGTACGACATCTATGAGAAACCAAGAGAG 1276  
1291 GAAACCGACTCTGAGTGTGATAGAAAACCTGAAAGAAACCTCTCAGTATGAGATTA 1350  
1277 GAAACCGACTCTGAGTGTGATAGAAAACCTGAAAGAAACCTCTCAGTATGAGATTA 1336  
1351 TTTATTTTACCTTCACTGAGACTTGAAGA 1383  
|||||

Db 1337 TTTATTTTACCTTCACTGTGACTTGAGAGA 1369  
RESULT 7  
AECL5897  
ID AECL5897 standard; RNA; 4006 BP.  
XX  
AC AECL5897;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Human interleukin-13 receptor alpha 1 (IL-13RA1) cDNA.  
XX  
KW RNA interference; gene silencing; cancer; hyperproliferation; neoplasm;  
KW cytosolic; viral infection; infection; virocyte; inflammation;  
KW antiinflammatory; autoimmune disease; immune disorder; immunosuppressive;  
KW pulmonary disease; respiratory disease; respiratory-gen;  
KW cardiovascular disease; cardiovascular-gen; neurological disease;  
KW neuroprotective; renal disease; endocrine disease; gastrointestinal disease;  
KW nephrotropic; endocrine-gen.; liver disease; gastrointestinal disease;  
KW hepatotropic; ocular disease; ophthalmological; reproductive disorder;  
KW infertility; antiinfertility; gynecology and obstetrics; andrology;  
KW mitochondrial disease; prion disease; degeneration;  
KW interleukin-13 receptor alpha 1; IL-13 receptor alpha 1; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 44..1327  
FT /tag a  
FT /product= "interleukin-13 receptor alpha 1 (IL-13RA1)"  
XX  
PD US2005182007-A1.  
XX  
18-AUG-2005.  
XX  
PF 20-AUG-2004; 2004US-00922675.  
XX  
18-MAY-2001; 2001US-0292217P.  
PR 20-JUL-2001; 2001US-030683P.  
PR 13-AUG-2001; 2001US-0311865P.  
PR 20-FEB-2002; 2002US-0358580P.  
PR 06-MAR-2002; 2002US-0362016P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 17-MAY-2002; 2002WO-US015876.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
PR 14-FEB-2003; 2003WO-US004566.  
PR 20-FEB-2003; 2003WO-US005028.  
PR 20-FEB-2003; 2003WO-US005346.  
PR 30-APR-2003; 2003US-00427160.  
PR 23-MAY-2003; 2003US-00444853.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826966.  
PR 30-APR-2004; 2004WO-US013456.  
PR 24-MAY-2004; 2004WO-US016390.  
PR 09-JUN-2004; 2004US-00863973.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Mcswiggen J, Beigelman L;  
XX  
DR WPI: 2005-581759/59.  
XX  
DR REFSO; NM\_001560.  
XX



PT New chemically synthesized double stranded siRNA molecule that directs  
PT cleavage of an interleukin-13 receptor (IL-13R) RNA via RNA interference,  
PT useful in preparing a composition for treating e.g., inflammatory  
PT disorders.

PS Claim 32; Page; 127/p; English.

XX The invention relates to chemically synthesized short interfering nucleic  
CC acids (siRNAs) which downregulate expression of receptors for interleukin-  
CC 13 (e.g., IL-13 receptor (IL-13R), IL-4 receptor (IL-4R) and IL-2  
CC receptor gamma (IL-2RG)) by RNA interference. The invention also relates  
CC to siRNAs which interfere with the expression of the ligands for  
CC these receptors, namely IL-13 and IL-4. The siRNAs of the invention may or  
CC may not comprise ribonucleotides, can contain deoxyribonucleotides, can  
CC be chemically modified and may be double or single stranded. They further  
CC comprise sense and antisense regions, or alternatively are assembled from  
CC a sense oligonucleotide and an antisense oligonucleotide. Specifically,  
CC the siRNAs include short interfering RNA (siRNA), double-stranded RNA,  
CC micro-RNA (miRNA) and short hairpin RNA (shRNA). The invention also  
CC relates to pharmaceutical compositions comprising an siRNA targeted to  
CC human IL-13R (e.g., IL-13R alpha 1 (IL13RA1), see RefSeq accession number  
CC NM\_001560), IL-4R, IL-2RG, IL-4 or IL-13, especially the siRNAs shown in  
CC AEC14082-AEC15892. The invention further discloses expression vectors and  
CC host cells comprising an siRNA of the invention. The siRNAs exhibit  
CC increased resistance to nuclease degradation compared to the prior art.  
CC The siRNAs of the invention can be used to modulate expression of their  
CC target genes in cells, tissue explants or organisms (e.g., by ex vivo  
CC gene therapy), or in grafts and transplants for the treatment of a  
CC variety of interleukin-related conditions. They may be used in the  
CC treatment of cancers and other proliferative conditions, viral infection,  
CC inflammatory conditions, autoimmune diseases, respiratory and pulmonary  
CC diseases (e.g., asthma, chronic obstructive pulmonary disease (COPD),  
CC allergies), cardiovascular diseases, neurological diseases, renal  
CC diseases, ocular diseases, liver diseases, mitochondrial diseases,  
CC endocrine diseases, prion diseases and reproduction-related conditions.  
CC The siRNAs may also be used in drug screening, diagnosis, therapeutic  
CC target identification and validation, genetic engineering,  
CC pharmacogenomics, studying gene function, and gene mapping (e.g., of  
CC single nucleotide polymorphisms). The present sequence represents a cDNA  
CC corresponding to human IL-13RA1 mRNA, which is specifically claimed as a  
CC target for siRNAs of the invention. Note: The present sequence is not  
CC shown in the specification, but was obtained from RefSeq accession number  
CC NM\_001560. Other sequence data for this patent is also available in  
CC electronic format directly from the US patent office at  
CC seqdata.uspto.gov/sequence.html?docid=20050182007.

XX Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;

Query Match 96.4%; Score 133.8; DB 14; Length 4006;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 34 CGGCGGGGTTCCGAGCGGAGGCTGATGAGTGCCTGGCGGCTCTGCGGGCTGTGG 93  
DB 17 CGGCGGGGCTCCGAGCGGAGGCTGATGAGTGCCTGGCGGCTCTGCGGGCTGTGG 76  
QY 94 GCGCTGCTGCTCGCGCGCGCGCGGGGGCGGGGGCGGGGG--CGGCGCTACGGAAACT 150  
DB 77 GCGCTGCTGCTCGCGCGCGCGCGGGGGCGGGGGCGGGGGCGCGCGCTACGGAAACT 136  
QY 151 CAGCCACCTGTGACCAATTGAGTGTCTGTTGAAAACTCTGCACAGTAATATGAGCA 210  
DB 137 CAGCCACCTGTGACCAATTGAGTGTCTGTTGAAAACTCTGCACAGTAATATGAGCA 196  
QY 211 TGGATTCACCCGAGGAGCCAGCTCAATTTGATGTTATTTTAACTTTTGGC 270  
DB 197 TGGATTCACCCGAGGAGCCAGCTCAATTTGATGTTATTTTAACTTTTGGC 256  
QY 271 GACAAACAAGATTAAGAAATAGCTCCGAAACTGCTGTTCAATAGAAAGTACCTGAAAT 330  
DB 257 GACAAACAAGATTAAGAAATAGCTCCGAAACTGCTGTTCAATAGAAAGTACCTGAAAT 316  
QY 331 GAGAGATTTTGTGCAAGTGGGGTCCAGTGTAGCACAATGAGAGTGAAGCTTAGC 390

DB 317 GAGAGATTTTGTGCAAGTGGGGTCCAGTGTAGCAACATGAGAGTGAAGAGCTTAGC 376  
QY 391 ATTTTGGTTGAAAAATGATCTACACCCCGAAGAGTATCTGAGTCTGCTGTGACGAA 450  
DB 377 ATTTTGGTTGAAAAATGATCTACACCCCGAAGAGTATCTGAGTCTGCTGTGACGAA 436  
QY 451 CTTCAATGATTTTGGCAACCTAGCTGATGAGTGTCTGAGCTCCCTGGAAGAAAT 510  
DB 437 CTTCAATGATTTTGGCAACCTAGCTGATGAGTGTCTGAGCTCCCTGGAAGAAAT 496  
QY 511 ACCAGTCCCGACACTAATCTATCTCTACTATTGGCAAGAGCTGGAAGAAATTCAT 570  
DB 497 ACCAGTCCCGACACTAATCTATCTCTACTATTGGCAAGAGCTGGAAGAAATTCAT 556  
QY 571 CAATGTAAAAATCTTTAGAGAAAGCCAAATCTTTGTTGTTCTTGTGATCTGACCAA 630  
DB 557 CAATGTAAAAATCTTTAGAGAAAGCCAAATCTTTGTTGTTCTTGTGATCTGACCAA 616  
QY 631 GTGAAGATTCAGTTTGAACAACAGTGTCCAAATATATGTCAGATTAATGACAGA 690  
DB 617 GTGAAGATTCAGTTTGAACAACAGTGTCCAAATATATGTCAGATTAATGACAGA 676  
QY 691 AAAATTAACCATCTTCAATATATATGTCCTTTAACTTCCGTTGAAACCTGATCTCCA 750  
DB 677 AAAATTAACCATCTTCAATATATATGTCCTTTAACTTCCGTTGAAACCTGATCTCCA 736  
QY 751 CATATTAAAACTCTCTCCACATGATGACCTATATGTGCAATGAGAGAAATTCACAG 810  
DB 737 CATATTAAAACTCTCTCCACATGATGACCTATATGTGCAATGAGAGAAATTCACAG 796  
QY 811 AATTTTATGAGAGATCCATTTATGAGTGAAGTAACTCAATACAGCAATGACAGA 870  
DB 797 AATTTTATGAGAGATCCATTTATGAGTGAAGTAACTCAATACAGCAATGACAGA 856  
QY 871 CATATGTTTCTACGTCCAAAGAGCTAAATGTGAGATCCAGATTTGAGAGAAATGTG 930  
DB 857 CATATGTTTCTACGTCCAAAGAGCTAAATGTGAGATCCAGATTTGAGAGAAATGTG 916  
QY 931 GAGATATCATCTGTTTCAATGATGTCCTGTTGTTCTTCTGATTACTTTGAACACAGTCA 990  
DB 917 GAGATATCATCTGTTTCAATGATGTCCTGTTGTTCTTCTGATTACTTTGAACACAGTCA 976  
QY 991 ATTAAGATCAAAACAAATTAATGATGATGATGAGATGACAACTCTGAGTAATTTGAGC 1050  
DB 977 ATTAAGATCAAAACAAATTAATGATGATGATGAGATGACAACTCTGAGTAATTTGAGC 1036  
QY 1051 CAAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1110  
DB 1037 CAAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1096  
QY 1111 GTTCACTGATCGTGGAGGTGCAATATGATGATGATGATGATGATGATGATGATGATG 1170  
DB 1097 GTTCACTGATCGTGGAGGTGCAATATGATGATGATGATGATGATGATGATGATGATG 1156  
QY 1171 ATTAATTAATTCCTCAATTCCTGATCCTGAGAAATTTTAAAGAAATCTTTGGAGC 1230  
DB 1157 ATTAATTAATTCCTCAATTCCTGATCCTGAGAAATTTTAAAGAAATCTTTGGAGC 1216  
QY 1231 CAGATATGATATCTGCACTGGAAGAGTACGATCTATGAGAGCAAAACCAAGAG 1290  
DB 1217 CAGATATGATATCTGCACTGGAAGAGTACGATCTATGAGAGCAAAACCAAGAG 1276  
QY 1291 GAAACGAGCTGTGATGCTGATGAGAAACCTGAGAAAGCTCTCAATGATGAGATTA 1350  
DB 1277 GAAACGAGCTGTGATGCTGATGAGAAACCTGAGAAAGCTCTCAATGATGAGATTA 1336  
QY 1351 TTTATTTTACCTTCACTGATGAGCTTGAAGA 1383  
DB 1337 TTTATTTTACCTTCACTGATGAGCTTGAAGA 1369

RESULT 8



AA85827  
ID AA85827 standard; DNA; 4009 BP.  
XX  
AC AA85827;  
XX  
DT 22-JUN-1998 (first entry)  
XX  
DE Human interleukin-13 alpha receptor DNA.  
XX  
KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 34..1317  
FT FT /\*tag= a  
FT FT /product= "IL-13\_alpha\_receptor"  
XX  
PN MO9720926-A1.  
XX  
PD 12-JUN-1997.  
XX  
PF 07-NOV-1996; 96MO-FR001756.  
XX  
PR 06-DEC-1995; 95FR-00014424.  
XX  
PA (SNP1) SANOFI SA.  
XX  
PI Caput D, Petrara P, Laurent P, Vltá N;  
XX  
DR WPI; 1997-319773/29.  
DR P-PSDB; AAMW4973.  
XX  
PT New purified human interleukin-13 receptors - and related nucleic acids,  
PT useful for diagnosis and treatment of inflammation, allergy, etc.  
XX  
PS Claim 12; Page 44-45; 83pp; French.  
XX  
XX This sequence encodes human interleukin-13 (IL-13) alpha receptor. The  
CC invention relates to new purified peptides comprising 380 or 427 amino  
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
CC affinity, but acquires high affinity when associated with the IL-4  
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as  
CC diagnostic probes to identify aberrant synthesis or genetic anomalies  
CC such as loss of heterozygosity and rearrangements, or chromosomal  
CC anomalies. They are also used for production of recombinant IL-13R beta  
CC and alpha which can be used as IL-13 antagonists, specifically to  
CC regulate IL-13-induced responses for treatment of inflammation and  
CC allergy. IL-13 receptors are also useful as antisense molecules for gene  
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard  
CC immunoassays) to diagnose diseases associated with abnormal expression of  
CC IL-13 receptors; when coupled to a toxin also for treatment of  
CC overproduction of IL-13R. Cells that express IL-13R at the surface are  
CC used to identify ligands and modulators of IL-13R  
XX  
SQ Sequence 4009 BP; 1137 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;  
Query Match 96.4%; Score 1333.8; DB 2; Length 4009;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;  
QY 34 CGGCGGGGTTCCAGGCGAGAGCTGATGAGTGGCGGGCGGGCTCTGCGGGCTGTG 93  
DB 7 CGGCGGGGCTCCAGAGCGAGAGGCTGATGAGTGGCGGGCGGGCTCTGCGGGCTGTG 66  
QY 94 GCGCTCTGCTCTGCGCGCGCGCGGGGCGGGGCGCGGGG---CGGCGCTTACGGAAT 150  
DB 67 GCGCTCTGCTCTGCGCGCGCGGGGCGGGGCGGGGCGCGGGGCGGCTTACGGAAT 126  
QY 151 CAGCCACCTGTGACAAATTTGAGTGTCTGTGAAACCTTGCACAGTAATATGGACA 210  
|||||

DB 127 CAGCCACCTGTGACAAATTTGAGTGTCTGTGAAACCTTGCACAGTAATATGGACA 186  
QY 211 TGGAAATCCACCCGAGGAGCCAGCTCAATTTGAGTCTATGTAATTTTATGCTATTTGGC 270  
DB 187 TGGAAATCCACCCGAGGAGCCAGCTCAATTTGAGTCTATGTAATTTTATGCTATTTGGC 246  
QY 271 GACAAACAAAGATTAAGAAATAGCTCCGAAACTCGTCGTTCAATAGAAAGTACCCCTGAAT 330  
DB 247 GACAAACAAAGATTAAGAAATAGCTCCGAAACTCGTCGTTCAATAGAAAGTACCCCTGAAT 306  
QY 331 GAGAGATTGTGTGCAAGTGGGGTCCAGTGTAGCACCATAGAGTGAAGGCTTAGC 390  
DB 307 GAGAGATTGTGTGCAAGTGGGGTCCAGTGTAGCACCATAGAGTGAAGGCTTAGC 366  
QY 391 ATTTTGTTGAAAAATGCAATCTCCAGGAGGATGATCTGAGTCTGCTGACTGA 450  
DB 367 ATTTTGTTGAAAAATGCAATCTCCAGGAGGATGATCTGAGTCTGCTGACTGA 426  
QY 451 CTTCGAATGCAATTTGGACAACCTGAGCTACATGAAGTGTCTTGCTCCCTGGAAGGAAT 510  
DB 427 CTTCGAATGCAATTTGGACAACCTGAGCTACATGAAGTGTCTTGCTCCCTGGAAGGAAT 486  
QY 511 ACCAGTCCCGACACTAATTAATCTCTAATTTGGACAAGAGCCGTGAAAAATTCAT 570  
DB 487 ACCAGTCCCGACACTAATTAATCTCTAATTTGGACAAGAGCCGTGAAAAATTCAT 546  
QY 571 CATGTGAAAAACATCTTTAGAGAGGCCAATATCTTGTTGTTCTTGAATCTGACCAA 630  
DB 547 CATGTGAAAAACATCTTTAGAGAGGCCAATATCTTGTTGTTCTTGAATCTGACCAA 606  
QY 631 GTGAAGATTTCCAGTTTGAACAACACAGTGTCCAAATATAGTCAAGATATGACAGA 690  
DB 607 GTGAAGATTTCCAGTTTGAACAACACAGTGTCCAAATATAGTCAAGATATGACAGA 666  
QY 691 AAAATTAACCAATCTTCAATATAGTGTCCCTTAATCTCCGNTGAAACCTGATCTCCA 750  
DB 667 AAAATTAACCAATCTTCAATATAGTGTCCCTTAATCTCCGNTGAAACCTGATCTCCA 726  
QY 751 CATATTAACCAATCTTCTCTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAG 810  
DB 727 CATATTAACCAATCTTCTCTCCACAAATGATGACCTATATGTGCAATGGAGAAATCCACAG 786  
QY 811 AATTTTATTAAGCATGATGCTATTTTATGAATGAAGTCAATTAACGCCAACTGAGACA 870  
DB 787 AATTTTATTAAGCATGATGCTATTTTATGAATGAAGTCAATTAACGCCAACTGAGACA 846  
QY 871 CATATGTTTTTACGTCACAGAGGCTAATATGGAATCCAGAAATTTGAGAAATGTG 930  
DB 847 CATATGTTTTTACGTCACAGAGGCTAATATGGAATCCAGAAATTTGAGAAATGTG 906  
QY 931 GAGAAATACATCTTGTTCATGTGCTCCGTGTTCTTCTGATATCTTGAACACAGTCAGA 990  
DB 907 GAGAAATACATCTTGTTCATGTGCTCCGTGTTCTTCTGATATCTTGAACACAGTCAGA 966  
QY 991 ATTAAGTCAAAAACAATAATGTTATGCTATGAGATGACAAATCTGAGTAATTGGAGC 1050  
DB 967 ATTAAGTCAAAAACAATAATGTTATGAGATGACAAATCTGAGTAATTGGAGC 1026  
QY 1051 CAAGAATAGTATAGTAAGAAAGGCAATTCACACTGACATAACATGTTACTATT 1110  
DB 1027 CAAGAATAGTATAGTAAGAAAGGCAATTCACACTGACATAACATGTTACTATT 1086  
QY 1111 GTTCCAGTCACTGTCCAGGTGCAATCATAGTACTCTGCTTACTTAAAGGCTCAAG 1170  
DB 1087 GTTCCAGTCACTGTCCAGGTGCAATCATAGTACTCTGCTTACTTAAAGGCTCAAG 1146  
QY 1171 ATTATTAATTTCCCTCAATTTCTGATCTCTGCAAGATTTTAAAGAAATGTTTGGAGAC 1230  
DB 1147 ATTATTAATTTCCCTCAATTTCTGATCTCTGCAAGATTTTAAAGAAATGTTTGGAGAC 1206  
QY 1231 CAGAAATGATGATCTGTGCACTGGAAGAGTGAAGATCTATATGAGAAAGCAACAGGAG 1290  
DB 1207 CAGAAATGATGATCTGTGCACTGGAAGAGTGAAGATCTATATGAGAAAGCAACAGGAG 1266  
|||||

|          |   |   |           |  |  |
|----------|---|---|-----------|--|--|
| Oy       | 1291  | GAACACCGACTCGTGTGCTGATAGAAAACCTGAAGAACGCTTCAGTGAATGAGAGTAA    | 1359      |  |  |
| Db       | 1267  | GAACCCGACTCTGTGTGCTGCTGATGAAAACCTGAGAAAAGCCTCTCACTGATGAGATPAA | 1326      |  |  |
| Oy       | 1351  | TTTATTTTACCTTCAGCTGTGACCTTGAGAGA                              | 1383      |  |  |
| Db       | 1327  | TTTATTTTACCTTCAGCTGTGACCTTGAGAGA                              | 1359      |  |  |
| RESULT 9 |   |   |           |  |  |
| xx       | AAA88907  | AAA88907 standard; cDNA; 4038 BP.                             |           |  |  |
| xx       | AAA88907;   |   |           |  |  |
| xx       | 05-MAR-2001   | (first entry)   |           |  |  |
| xx       | Human interleukin-13 receptor alpha-1 cDNA.                               |   |           |  |  |
| xx       | Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;             |   |           |  |  |
| xx       | atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;               |   |           |  |  |
| xx       | dermatological; antiallergic; antiallergic therapy; diagnosis; ss.        |   |           |  |  |
| xx       | Homo sapiens.   |   |           |  |  |
| xx       | Key   | Location/Qualifiers   |           |  |  |
| xx       | CDS   | 43..1326  |           |  |  |
| xx       | FT  | /*tag= a  |           |  |  |
| xx       | FT  | sig_peptide   | 43..120   |  |  |
| xx       | FT  | /*tag= b  |           |  |  |
| xx       | FT  | mat_peptide   | 121..1323 |  |  |
| xx       | FT  | /*tag= c  |           |  |  |
| xx       | US6143871-A.  |   |           |  |  |
| xx       | 07-NOV-2000.  |   |           |  |  |
| xx       | 12-NOV-1997;  | 97US-00969125.  |           |  |  |
| xx       | 13-DEC-1996;  | 96GB-00025899.  |           |  |  |
| xx       | (GAUC/) GAUCHAT J.  |   |           |  |  |
| xx       | (BONN/) BONNEFOY J.   |   |           |  |  |
| xx       | Gauchat J, Bonnefoy J;  |   |           |  |  |
| xx       | WPI; 2001-006445/01.  |   |           |  |  |
| xx       | P-PSDB; AAB19807.   |   |           |  |  |
| xx       | Novel polypeptide capable of binding interleukin-13 or interleukin-4      |   |           |  |  |
| xx       | useful for treating atopy, atopic dermatitis, allergies, rhinitis,        |   |           |  |  |
| xx       | eczema, asthma or AIDS.   |   |           |  |  |
| xx       | Example 1; Fig 1A-B; 26pp; English.                                       |   |           |  |  |
| xx       | The present sequence is that of cDNA encoding a protein (see AAB19807)    |   |           |  |  |
| xx       | capable of binding human interleukin-13 (IL-13) and/or human interleukin- |   |           |  |  |
| xx       | 4 (IL-4) in the presence of IL-4 receptor alpha. To isolate the cDNA, PCR |   |           |  |  |
| xx       | primers (see AAB88908-10) were designed from expressed sequence tags      |   |           |  |  |
| xx       | isolated from a database using mouse IL-13 receptor alpha. The primers    |   |           |  |  |
| xx       | were used to amplify human IL-13 receptor cDNA from activated tonsillar B |   |           |  |  |
| xx       | cell cDNA. The resulting cDNA fragment was used to screen a lambda gt10   |   |           |  |  |
| xx       | library of activated tonsillar B cell cDNA and sequencing of the largest  |   |           |  |  |
| xx       | cDNA insert provided the present sequence. This IL-13 receptor alpha-1    |   |           |  |  |
| xx       | can be used to inhibit IL-13 or IL-4 induced IgE synthesis in B cells,    |   |           |  |  |
| xx       | useful in the treatment of diseases where IgE or Th2 differentiation      |   |           |  |  |
| xx       | plays a role, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema,   |   |           |  |  |
| xx       | asthma or AIDS. Antibodies raised against the polypeptide are useful for  |   |           |  |  |
| xx       | detecting IL-13 and IL-4 receptor or parts of them which have been shed   |   |           |  |  |
| xx       | from cells as a result of disease, e.g. cancer, leukemia, atopy, atopic   |   |           |  |  |
| xx       | dermatitis, allergies, rhinitis, eczema, asthma, AIDS, lupus              |   |           |  |  |
| xx       | erythematous, thyroiditis, diabetes, uveitis, dermatitis, psoriasis,      |   |           |  |  |

[illegible]

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QY 991 ATTAGAGTCAAAACAAATTAATTATGCTATGAGATGACAACTCTGGAGTAATTGGAGC 1050
  |||
  |||
  |||
Db 976 ATTAGAGTCAAAACAAATTAATTATGCTATGAGATGACAACTCTGGAGTAATTGGAGC 1035
  |||
  |||
  |||
QY 1051 CAAAGAAATAGATAGATAGAAAGGCAATTCACACTCTACATTAACCATGTTACATCATT 1110
  |||
  |||
  |||
Db 1036 CAAAGAAATAGATAGATAGAAAGGCAATTCACACTCTACATTAACCATGTTACATCATT 1095
  |||
  |||
  |||
QY 1111 GTTCCAGTATGCTGCTCCAGGTCGAATCATAGTACTCTGCTTACCTTAAAGGCTCAAG 1170
  |||
  |||
  |||
Db 1096 GTTCCAGTATGCTGCTCCAGGTCGAATCATAGTACTCTGCTTACCTTAAAGGCTCAAG 1155
  |||
  |||
  |||
QY 1171 ATTATTAATATTCCTCCCAATTCCTGATTCCTGCGCAAGATTTTAAAGAAATGTTTGAAGAC 1230
  |||
  |||
  |||
Db 1156 ATTATTAATATTCCTCCCAATTCCTGATTCCTGCGCAAGATTTTAAAGAAATGTTTGAAGAC 1215
  |||
  |||
  |||
QY 1231 CAGAAATGATGATCTCTGCACTGCGAAGAAAGTACGACATCTATGAGAAAGCAACCAAGAG 1290
  |||
  |||
  |||
Db 1216 CAGAAATGATGATCTCTGCACTGCGAAGAAAGTACGACATCTATGAGAAAGCAACCAAGAG 1275
  |||
  |||
  |||
QY 1291 GAAACCGACTCTGTATGCTGATAGAAAACTGAAAGAAAGCTCTCAGTATGAGATTA 1350
  |||
  |||
  |||
Db 1276 GAAACCGACTCTGTATGCTGATAGAAAACTGAAAGAAAGCTCTCAGTATGAGATTA 1335
  |||
  |||
  |||
QY 1351 TTTATTTTACCTTCACTGTGACCTTGAAGA 1383
  |||
  |||
  |||
Db 1336 TTTATTTTACCTTCACTGTGACCTTGAAGA 1368
  |||
  |||
  |||

RESULT 10
ADL71811
ID ADL71811 standard; cDNA; 4038 BP.
AC ADL71811;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human interleukin-13 receptor alpha (IL-13 Ralpha) cDNA.
DE Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
XX Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KM eczema; asthma; AIDS; gene therapy; gene; ss; interleukin.
XX
XX Homo sapiens.
OS
XX
XX Location/Qualifiers
FH CDS 43..1326
FT /tag= b
FT /product= "Human IL-13 protein"
FT sig_peptide 43..120
FT /tag= a
FT CDS 121..1323
FT /tag= c
FT /product= "Human mature IL-13 protein"
FT misc_feature 1321..1380
FT /tag= d
FT /note= "GC rich region"
FT
FT US2004043921-A1.
FT
FT 04-MAR-2004.
PD
XX
XX 29-SEP-2003; 2003US-00671697.
PF
XX
XX 13-DEC-1996; 96GB-00025899.
PR 12-NOV-1997; 97US-00969125.
PR 06-APR-2000; 2000US-00545002.
XX
XX (BONN/) BONNEFOY J.
PA (GAUC/) GAUCHAT J.
XX
XX Bonnefoy J, Gauchat J;
XX
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DR WFI; 2004-225726/21.
DR P-PSDB; ADL71812.
XX
XX PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
XX Example 1; SEQ ID NO 8; 27bp; English.
XX
XX The invention relates to polypeptides capable of binding human
CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
CC invention also relates to a method of treatment of a disease in which
CC IL13 and IL4 cause adverse effects. The method is useful for treating a
CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
CC of the invention are useful in raising antibodies. It is also useful in
CC gene therapy. The present sequence is human interleukin-13 receptor alpha
CC (IL-13 Ralpha) cDNA.
XX
XX Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;
SQ
XX
XX Query Match 96.4%; Score 1333.8; DB 12; Length 4038;
XX Best Local Similarity 99.6%; Pred. No. 0;
XX Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
XX
QY 34 CGGCGGGGTTCCGAGCGAGAGGCTGCATGAGTGGCGGGCGGCTTGGCGGGCTGTGG 93
  |||
  |||
  |||
Db 16 CGGCGGGGTTCCGAGCGAGAGGCTGCATGAGTGGCGGGCGGCTTGGCGGGCTGTGG 75
  |||
  |||
  |||
QY 94 GCGCTGCTCTCTGCGCGCGCGCGCGGGGGCGGGGGGGGGG---CGCGGCTACGAGAACT 150
  |||
  |||
  |||
Db 76 GCGCTGCTCTCTGCGCGCGCGCGGGGGGGGGGGGGGGGGGGCGCGGCTACGAGAACT 135
  |||
  |||
  |||
QY 151 CAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCGACAGATTAATAGACA 210
  |||
  |||
  |||
Db 136 CAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCGACAGATTAATAGACA 195
  |||
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  |||
QY 211 TGGATCCACCCGAGGAGCCAGCTCAATTTGATGCTATGTTATTTAGTCATTTTGGC 270
  |||
  |||
  |||
Db 196 TGGATCCACCCGAGGAGCCAGCTCAATTTGATGCTATGTTATTTAGTCATTTTGGC 255
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  |||
QY 271 GACAAACAGATTAAGAAATAGCTCCGGAACCTCGCTTCAATTAAGATCCCGTGAAT 330
  |||
  |||
  |||
Db 256 GACAAACAGATTAAGAAATAGCTCCGGAACCTCGCTTCAATTAAGATCCCGTGAAT 315
  |||
  |||
  |||
QY 331 GAGAGATTTGTCTGCAAGTGGGGGTCCAGTGNAGCACAATAGAGTGAAGCCTAGC 390
  |||
  |||
  |||
Db 316 GAGAGATTTGTCTGCAAGTGGGGGTCCAGTGNAGCACAATAGAGTGAAGCCTAGC 375
  |||
  |||
  |||
QY 391 ATTTGGTTGAAAAATGATCTCACCCCCAGAAAGTGATCTGAGTCTGCTGACTGAA 450
  |||
  |||
  |||
Db 376 ATTTGGTTGAAAAATGATCTCACCCCCAGAAAGTGATCTGAGTCTGCTGACTGAG 435
  |||
  |||
  |||
QY 451 CTTCAATGATTTGGGACAACTGAGCTACAGAAATGTTTGGCTCCCTGGAAGGAAT 510
  |||
  |||
  |||
Db 436 CTTCAATGATTTGGGACAACTGAGCTACAGAAATGTTTGGCTCCCTGGAAGGAAT 495
  |||
  |||
  |||
QY 511 ACCAGTCCGACACTACTACTCTCTACTATTGGCAGAGAAAGCTGGAAAAAATTCAAT 570
  |||
  |||
  |||
Db 496 ACCAGTCCGACACTACTACTCTCTACTATTGGCAGAGAAAGCTGGAAAAAATTCAAT 555
  |||
  |||
  |||
QY 571 CAATGTGAAAAACATCTTTAGAGAGGCAATACCTTTGGTTGCTTTGATCTGACCAA 630
  |||
  |||
  |||
Db 556 CAATGTGAAAAACATCTTTAGAGAGGCAATACCTTTGGTTGCTTTGATCTGACCAA 615
  |||
  |||
  |||
QY 631 GTGAAGGATTCAGATTTGAACAACACAGTGTCCAAATATAGTCAAGATATAGAGAA 650
  |||
  |||
  |||
Db 616 GTGAAGGATTCAGATTTGAACAACACAGTGTCCAAATATAGTCAAGATATAGAGAA 635
  |||
  |||
  |||
QY 691 AAAATTAAACATCTTCAATATAGTGGCTTTAACTTCCCGTGTGAACCTGATCTCTCA 750
  |||
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  |||
Db 676 AAAATTAAACATCTTCAATATAGTGGCTTTAACTTCCCGTGTGAACCTGATCTCTCA 735
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Db 316 GAGAGATTGTTCTGCAAGTGGGGTCCAGTGTAGCACCAATGAGAGTGAAGACCTAGC 375  
QY 391 ATTTTGGTGAATAATGCACTCTCACCCCGAAGAGTATCTGATCTGCTGTGACTGAA 450  
Db 376 ATTTTGGTGAATAATGCACTCTCACCCCGAAGAGTATCTGATCTGCTGTGACTGAG 435  
QY 451 CTTCAATGCAATTTGGGCAAACTGAGCTACATGAAAGTGTCTTGGGCTCCCTGGAAGGAAT 510  
Db 436 CTTCAATGCAATTTGGGCAAACTGAGCTACATGAAAGTGTCTTGGGCTCCCTGGAAGGAAT 495  
QY 511 ACCAGTCCGAGCACTACTACTCTCTACTATTTGGAGAGAGCCCTGGAAAAATTCAT 570  
Db 496 ACCAGTCCGAGCACTACTACTCTCTACTATTTGGAGAGAGCCCTGGAAAAATTCAT 555  
QY 571 CAATGGAATAACATCTTGTAGAGAGAGGCAATACCTTGGTGTCTTGTGATCTGACCAA 630  
Db 556 CAATGGAATAACATCTTGTAGAGAGAGGCAATACCTTGGTGTCTTGTGATCTGACCAA 615  
QY 631 GTGAGAGATTCCAGTTTGTGAACAACACAGTGTCCAAATAATGTCAGATTAATGACAGA 690  
Db 616 GTGAGAGATTCCAGTTTGTGAACAACACAGTGTCCAAATAATGTCAGATTAATGACAGA 675  
QY 691 AAAATTAACCACTCTTCAATATATAGTCCCTTAACTCCGCTGGAAACCTGATCCTCCA 750  
Db 676 AAAATTAACCACTCTTCAATATATAGTCCCTTAACTCCGCTGGAAACCTGATCCTCCA 735  
QY 751 CATATTAATAAACCTCTCTTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG 810  
Db 736 CATATTAATAAACCTCTCTTCCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG 795  
QY 811 AATTTTATTAGCAGATGCTTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGACAGA 870  
Db 796 AATTTTATTAGCAGATGCTTATTTTATGAAGTAGAAGTCAATAACAGCCAAACTGACAGA 855  
QY 871 CATTAAGTTTTCACGTCCAGAGAGGCTAAATGTGAAATCCCAATTTGGAGAAATGTCG 930  
Db 856 CATTAAGTTTTCACGTCCAGAGAGGCTAAATGTGAGAAATCCCAATTTGGAGAAATGTCG 915  
QY 931 GAGAAATACATCTTGTTCATGTGTCCCTGAGTGTCTTCTCTGATATCTTTGAACACAGTCA 990  
Db 916 GAGAAATACATCTTGTTCATGTGTCCCTGAGTGTCTTCTCTGATATCTTTGAACACAGTCA 975  
QY 991 ATTAGAGTCAAAAACAATAAGTATGTCTATGAGAGTACAAACTCTGGAGTAAATTTGAGC 1050  
Db 976 ATTAGAGTCAAAAACAATAAGTATGTCTATGAGAGTACAAACTCTGGAGTAAATTTGAGC 1035  
QY 1051 CAGAATAAGTATAGGTAAAGAGCGCAATTCACACTCTACATTAACCAATGTTACTCAT 1110  
Db 1036 CAGAATAAGTATAGGTAAAGAGCGCAATTCACACTCTACATTAACCAATGTTACTCAT 1095  
QY 1111 GTTCCAGTATCGTCCAGGTGCAATCATATGTACTCCTGCTTAACTTAAAGAGGCTCAAG 1170  
Db 1096 GTTCCAGTATCGTCCAGGTGCAATCATATGTACTCCTGCTTAACTTAAAGAGGCTCAAG 1155  
QY 1171 ATTATATATATCCCTCCCAATTCCTGATCTCTGAGCAAGATTTTAAAGAAATGTTTGGAGAC 1230  
Db 1156 ATTATATATATCCCTCCCAATTCCTGATCTCTGAGCAAGATTTTAAAGAAATGTTTGGAGAC 1215  
QY 1231 CAGAAATGATATCTCTGCACTGGAAGAGTACATCTATAGAAAGCAAAACCAAGAGAG 1290  
Db 1216 CAGAAATGATATCTCTGCACTGGAAGAGTACATCTATAGAAAGCAAAACCAAGAGAG 1275  
QY 1291 GAAACCGAATCTGTAGTGTGATAGAAAACCTGAAAGAAAGCCTCTGATGAGAGATTA 1350  
Db 1276 GAAACCGAATCTGTAGTGTGATAGAAAACCTGAAAGAAAGCCTCTGATGAGAGATTA 1335  
QY 1351 TTTATTTTAACTTCACTGTGACCTTGAGAGA 1383  
Db 1336 TTTATTTTAACTTCACTGTGACCTTGAGAGA 1368

RESULT 12  
AAA35214

ID AAA35214 standard; DNA; 4039 BP.  
XX  
AC AAA35214;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:88.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KM phosphorothioate; impaired respiration; inflammation; allergy;  
KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KM antiinergic; antiaesthetic; cyrostatic; analgesic; impaired airway;  
KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KM respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Disclosure; Page 1253-1254; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antisthmatic, cyrostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
XX listing  
XX  
SQ Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;  
QY  
Query Match 96.4%; Score 1333.8; DB 3; Length 4039;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;  
34 CGCGCGGGTTCCGAGCGGAGAGGCTGCATGAGTGGCGGCGGCTTGCGGGCTGTGG 93

|    |      |   |      |
|----|------|---|------|
| Db | 17   | CGGCGGGGCTCCGAGCGAGAGGCTGACATGAGTGGCCGGCGCGGCTGTCGGGGCTGTG    | 76   |
| OY | 94   | GGGCTGCTGCTCTTCGGCGCGCGCGGGGGCGGGGGCGGGGG--CGCGCTTACGAAAT     | 150  |
| Db | 77   | GGCTGCTGCTCTGCGCGCGCGGGGGCGGGGGCGGGGGCGCGCGCGCTACGGAAAT       | 136  |
| OY | 151  | CAGCCACCCTGATCAAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAAATGAGCA  | 210  |
| Db | 137  | CAGCCACCCTGATCAAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAAATGAGCA  | 196  |
| OY | 211  | TGGAATCCACCCGAGGAGCCAGCTCAAAATGTAGCTATGGTATTTTATGATTTTGGC     | 270  |
| Db | 197  | TGGAATCCACCCGAGGAGCCAGCTCAAAATTTGATCTTATGATTTTATGATTTTGGC     | 256  |
| OY | 271  | GACAAACAAGATTAAGAAAATAGCTCCGAAACTCGTCTTCAATAGAAATACCCCTGAAT   | 330  |
| Db | 257  | GACAAACAAGATTAAGAAAATAGCTCCGAAACTCGTCTTCAATAGAAATACCCCTGAAT   | 316  |
| OY | 331  | GAGAGGATTTTGTCTGCAAGTGGGGTCCCACTGTAGCACCAATGAGATGAGAGCTTACG   | 390  |
| Db | 317  | GAGAGGATTTTGTCTGCAAGTGGGGTCCCACTGTAGCACCAATGAGATGAGAGCTTACG   | 376  |
| OY | 391  | ATTTGGTTGAAAAATNGATCTCACCCCGAAGGTGATCCGATCGCTGTGCTGAC         | 450  |
| Db | 377  | ATTTGGTTGAAAAATNGATCTCACCCCGAAGGTGATCCGATCTGTGCTGTGAC         | 436  |
| OY | 451  | CTTCATGATTTTGGCACACACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAAGAT     | 510  |
| Db | 437  | CTTCATGATTTTGGCACACACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAAGAT     | 496  |
| OY | 511  | ACCACTCCCGACATPACTATATCTCTATATTGGCA CAGAAGCTGGAAAAATTTAT      | 570  |
| Db | 497  | ACCACTCCCGACATPACTATATCTCTATATTGGCA CAGAAGCTGGAAAAATTTAT      | 556  |
| OY | 571  | CAATGTGAAAACATCTTTAGAGAAAGCCAAATCTTGGTGTCTTGTGATCTGCMAA       | 630  |
| Db | 557  | CAATGTGAAAACATCTTTAGAGAAAGCCAAATCTTGGTGTCTTGTGATCTGCMAA       | 616  |
| OY | 631  | GTGAAGATTCAGTTTTGAAACAACAAGTGCMAAATATGGTCAAGATTAATGACAGA      | 690  |
| Db | 617  | GTGAAGATTCAGTTTTGAAACAACAAGTGCMAAATATGGTCAAGATTAATGACAGA      | 676  |
| OY | 691  | AAAAATTAACCATCTTCATATATAGTGCCCTTAATCTCCCGTGTGAAAACCTGATCTTCA  | 750  |
| Db | 677  | AAAAATTAACCATCTTCATATATAGTGCCCTTAATCTCCCGTGTGAAAACCTGATCTTCA  | 736  |
| OY | 751  | CATATTA AAAACCTCTCCTTCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG  | 810  |
| Db | 737  | CATATTA AAAACCTCTCCTTCACAATGATGACCTATATGTGCAATGGAGAAATCCACAG  | 796  |
| OY | 811  | AATTTATTAACAAGTGCCTATTTTATTAAGATGAAGCAATTAACGCCAACTGACACA     | 870  |
| Db | 797  | AATTTATTAACAAGTGCCTATTTTATTAAGATGAAGCAATTAACGCCAACTGACACA     | 856  |
| OY | 871  | CATAATGTTTCTACGTCACAAGAGCTAAATGTGGAATCCAGAATTTGAGAGAAATGTG    | 930  |
| Db | 857  | CATAATGTTTCTACGTCACAAGAGCTAAATGTGGAATCCAGAATTTGAGAGAAATGTG    | 916  |
| OY | 931  | GAGAAATCATTTGTTTATGATGTCCTGCTGTGTTCTTCTGATTAATTTGAAACACAGTACA | 990  |
| Db | 917  | GAGAAATCATTTGTTTATGATGTCCTGCTGTGTTCTTCTGATTAATTTGAAACACAGTACA | 976  |
| OY | 991  | ATAAGAGTCAAAACAATAATGATATGCTATAGATGACAAATCTGAGATTAATTTGAGC    | 1050 |
| Db | 977  | ATAAGAGTCAAAACAATAATGATATGCTATAGATGACAAATCTGAGATTAATTTGAGC    | 1036 |
| OY | 1051 | CAAGAAATGATATGATTAAGAGGCAATTCACACTCTACATPAACATGTTACTAT        | 1110 |
| Db | 1037 | CAAGAAATGATATGATTAAGAGGCAATTCACACTCTACATPAACATGTTACTAT        | 1096 |
| OY | 1111 | GTTCCAGTCAATGTCGACAGTGTGCAATATAGTACTCTGCTTTTACTTAAAAAGCTCAAG  | 1170 |

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|----|------|--|-----------------------------|------|
| Db | 1097 | CTTCGAGTCATCGTGGAGGGCAATCATATGTA             | CTCTCGCTTTACTTAAAAAGGCTCAAG | 1156 |
| OY | 1171 | ATTATTTATTTCCCTCCCAATTCCTGATCTCGGCAAGATTTT   | TTTAAAGAAATGTTTGGAGAC       | 1230 |
| Db | 1157 | ATTATTTATTTATTCCTCCAAATTCCTGATCTCGGCAAGATTTT | TTTAAAGAAATGTTTGGAGAC       | 1216 |
| OY | 1231 | CAGATATGATGTACTCTGCACCTGGAGAGAAGTACAGATCTAT  | GTGAGAGCAAACTCAAGAG         | 1290 |
| Db | 1217 | CAGATATGATGTACTCTGCACCTGGAGAGAAGTACAGATCTAT  | GTGAGAGCAAACTCAAGAG         | 1276 |
| OY | 1291 | GAAACCGACTCTGTAGTCTGATAGAAAACTGTGAAGAGCCTCT  | CATGATGAGATGATAA            | 1350 |
| Db | 1277 | GAAACCGACTCTGTAGTCTGATAGAAAACTGTGAAGAGCCTCT  | CATGATGAGATGATAA            | 1336 |
| OY | 1351 | TTTTTTTTTTCCTTCATCTGTGACCTTGAGAGA            | 1383                        |      |
| Db | 1337 | TTTTTTTTTTCCTTCATCTGTGACCTTGAGAGA            | 1369                        |      |

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| RESULT 13  |
| AAF21336   |
| ID AAF21336 standard; DNA; 4039 BP.  |
| XX   |
| XX   |
| AC   |
| AAF21336;  |
| XX   |
| DT 14-MAR-2001 (first entry)   |
| XX   |
| DE Human low adenosine antisense oligonucleotide related sequence #2903.     |
| XX   |
| XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;       |
| KW human; airway disorder; bronchoconstriction; lung inflammation;           |
| KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;      |
| KW immunosuppressive; antialasthmatic; analgesic; hypotensive; cyostatic;    |
| KW respiratory obstruction; pulmonary obstruction; impeded respiration;      |
| KW surfactant hypoproduction; pulmonary vasocostriction; asthma; RDS;        |
| KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  |
| KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;   |
| KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;   |
| KW cancer; ss.   |
| XX   |
| OS Homo sapiens.   |
| XX   |
| XX WO200062736-A2.   |
| XX   |
| XX 26-OCT-2000.  |
| XX   |
| PF 24-MAR-2000; 2000WO-US008020.   |
| XX   |
| XX 06-APR-1999; 99US-0127958P.   |
| XX   |
| PA (UEC-) UNIV EAST CAROLINA.  |
| PA (NYCE/) NYCE J W.   |
| XX   |
| XX NYce JW;  |
| XX   |
| XX WPI; 2000-679539/66.  |
| XX   |
| PT Low adenosine (A) content antisense oligonucleotides which do not trigger |
| PT adenosine receptors during metabolism, useful e.g. for treating cancers   |
| PT and respiratory obstructions.   |
| XX   |
| PS Disclosure; Page 1337-1338; 1592pp; English.                              |
| XX   |
| XX The present invention describes low adenosine (A) content antisense       |
| CC oligonucleotides and compositions (I) comprising them. In the antisense   |
| CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  |
| CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,    |
| CC immunosuppressive, antiaschmatic, hypotensive and cyostatic activities.   |
| CC The antisense oligonucleotides and (I) can be used to down-regulate the   |
| CC expression and or activity of target polypeptides associated with         |
| CC lung/respiratory disorders and malignancies, such as stimulating and      |
| CC activating peptide factors and transmitters, transcription factors,       |
| CC immunoglobulins and antibodies, antibody receptors, cytokines and         |
| CC   |



chemokine, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasocactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasocstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

SQ Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;

Query Match 96.4%; Score 1333.8; DB 3; Length 4039;

Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| OY | 34  | TGGCGGGGTTCCGAGGCCAAGAAGGCTGCATGGAATGGCTGGCGCGGGCTTCGGGGCTGTGG   | 93  |
| Db | 17  | CGGGCGGGGCTCCGAGGCCAAGGGCTGCATGGAATGGCCGGCGGGCTTCGGGGGCTGTGG     | 76  |
| OY | 94  | GCGCTGCTGCTGTGGCGCGGGGGGGGGGGGGGGGGGG---GGGGCTTAAGGAACCT         | 150 |
| Db | 77  | GCGCTGCTGCTGTGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGCTTAAGGAACCT  | 136 |
| OY | 151 | CAGCCACTGTGACAATAATTGAGTGTCTGTGTGA AAAACCTCTGCACAGTAATATGACAA    | 210 |
| Db | 137 | CAGCACTCTGTGACA AATTTAGTGTC TCTGTGTGA AAACCTCTGCACAGTAATATGACAA  | 196 |
| OY | 211 | TGGAATCACC CGGAGGAGCCAGCTCAAATGTAGTCTAATGGATTTTTAGTCATTTTGGC     | 270 |
| Db | 197 | TGGAATCACCCGAGGAGCCAGCTCAAATGTAGTCTATGGATATTTTAGTCATTTTGGC       | 256 |
| OY | 271 | GACAAA CAAGTAAGAAAAATAGCTCCGGAAA CTGGTGTTCATTTGAAGTACCCCTGAAT    | 330 |
| Db | 257 | GACAAA CAAGATTAAGAAAAATAGCTCCGGAAA CTCGTGTTCAATTTGAAGTACCCCTGAAT | 316 |
| OY | 331 | GAGAGGATTTTGTCTCAAGTGGGGGTCCCAGTGTACACAATAGAGTGAGAAAGCTTAC       | 390 |
| Db | 317 | GAGAGGATTTTGTCTCAAGTGGGGGTCCCAGTGTACACAATAGAGTGAGAAAGCTTAC       | 376 |
| OY | 391 | AATTTGGTTGAAAAATGCACTTCA CCCCCAGAAAGGTGATCTGAGTCTGCTGTGACTGAA    | 450 |
| Db | 377 | AATTTGGTTGAAAAATGCACTTCA CCCCCAGAAAGGTGATCTGAGTCTGCTGTGACTGAG    | 436 |
| OY | 451 | CTTCAATGCAATTTGGCACACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAAAGAAAT     | 510 |
| Db | 437 | CTTCAATGCAATTTGGCACACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAAAGAAAT     | 496 |
| OY | 511 | ACCAAGTCCCGACACTAACCTATACCTCTACATTTGGCACAGAAAGCTGGAAAAAATTCAT    | 570 |
| Db | 497 | ACCAAGTCCCGACACTAACCTATACCTCTACATTTGGCACAGAAAGCTGGAAAAAATTCAT    | 556 |
| OY | 571 | CAATGTGAAAAATCTTTAGAGAGAGCCAAATACCTTGGTGTCTCTTGATCTGACCAA        | 630 |
| Db | 557 | CAATGTGAAAAATCTTTAGAGAGAGCCAAATACCTTGGTGTCTCTTGATCTGACCAA        | 616 |
| OY | 631 | GTGAAGATTC GAGTTTGAACACACAGTGTCCAATTAATGTCAAGATTAATGACAGA        | 690 |
| Db | 617 | GTGAAGATTC GAGTTTGAACACACAGTGTCCAATTAATGTCAAGATTAATGACAGA        | 676 |
| OY | 691 | AAAAATTAACCATCTTCAATTAATAGTGGCTTTAATCTCCCGTGTGA AACCTGATCTTCCA   | 750 |
| Db | 677 | AAAAATTAACCATCTTCAATTAATAGTGGCTTTAATCTCCCGTGTGA AACCTGATCTTCCA   | 736 |

|    |      |   |      |
|----|------|---|------|
| QY | 751  | AATATTTAAAAACCTCTCTCTTCCAAATGATGACCTTAATGTGCATATGGAGAAATCCACAG      | 810  |
| Db | 737  | CATATTTAAAAACCTCTCTCTTCCAAATGATGACCTTAATGTGTGCATATGGAGAAATCCACAG    | 796  |
| QY | 811  | AATTTTATTTAGCAGATGACCTTATTTTATGAAAGTAGAATCAATTAACAGCCAAACCTGAGACA   | 870  |
| Db | 797  | AATTTTATTTAGCAGATGACCTTATTTTATGAAAGTAGAATCAATTAACAGCCAAACCTGAGACA   | 856  |
| QY | 871  | CATAATGTTTTCTATGCTCCAAAGAGCTAAATGTGAGATCCAGATTTTGAGAGAAATGTG        | 930  |
| Db | 857  | CATATATGTTTTCTATGCTCCAAAGAGCTAAATGTGAGATCCAGATTTTGAGAGAAATGTG       | 916  |
| QY | 931  | GAGAAATCATTTGTTCATGAGTCCCTGGATGTTCTTCTGTATCTTTGAACACAGCTGAGA        | 990  |
| Db | 917  | GAGAAATCATTTGTTCATGAGTCCCTGGATGTTCTTCTGTATCTTTGAACACAGCTGAGA        | 976  |
| QY | 991  | ATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACCTGTGAGTAAATTTGAGC      | 1050 |
| Db | 977  | ATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACCTGTGAGTAAATTTGAGC      | 1036 |
| QY | 1051 | CAAGAAATGAGTAAAGGTAAGAAAGCGCAATTTCCACATCTTACATTAACCAATGTTACTATT     | 1110 |
| Db | 1037 | CAAGAAATGAGTAAAGGTAAGAAAGCGCAATTTCCACATCTTACATTAACCAATGTTACTATT     | 1096 |
| QY | 1111 | GTTCCAGATCATGCTGCGAGGAGTGCAATCATATGTACTCTCTGCTTTTAACTPAAAAAGGCTCAAG | 1170 |
| Db | 1097 | GTTCCAGATCATGCTGCGAGGAGTGCAATCATATGTACTCTCTGCTTTTAACTPAAAAAGGCTCAAG | 1156 |
| QY | 1171 | ATTATTTATTTCCCTCCCAATTCCTGATCTGTGCGACAGATTTTAAAAAGAAATGTTTGGAGAC    | 1230 |
| Db | 1157 | ATTATTTATTTCCCTCCCAATTCCTGATCTGTGCGACAGATTTTAAAAAGAAATGTTTGGAGAC    | 1216 |
| QY | 1231 | CAGAAATGATGTAATCTGTGCACTGGAAGAAACTGACATCTATAGAGAAACCAAGAGAG         | 1290 |
| Db | 1217 | CAGAAATGATGTAATCTGTGCACTGGAAGAAAGTACACATCTATAGAGAAACCAAGAGAG        | 1276 |
| QY | 1291 | GAACCCGACCTGTAGTGTGTGATGTGAAGAAACCTGGAAGAAACCTCTCAGTATGAGATTA       | 1350 |
| Db | 1277 | GAACCCGACCTGTAGTGTGTGATGTGAAGAAACCTGGAAGAAACCTCTCAGTATGAGATTA       | 1336 |
| QY | 1351 | TTTATTTTATTCCTTCACTGTGACTGTGAGAGA                                   | 1383 |
| Db | 1337 | TTTATTTTATTCCTTCACTGTGACTGTGAGAGA                                   | 1369 |

## RESULT 14

ID ABL67709 standard; DNA; 4039 BP.

AC ABL67709;

DT 15-MAY-2002 (first entry)

DE Oesophagus cancer related gene sequence SEQ ID NO:6046.

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

XX

XX 7

XX

XX

XX

PR 05-JUN-2000; 2000US-0209531P.

PR 18-SEP-2000; 2000US-0233617P.







```
QY 631 GTGAAGATTCAGTTTGGAAACACAGTGTCCAAATATAGTCAAGATPATGACGA 690
    |||||
Db 617 GTGAAGATTCAGTTTGGAAACACAGTGTCCAAATATAGTCAAGATPATGACGA 676
QY 691 AAAATTAACCATCTTCAATATAGTGCCTTAATCTCCGTTGAAACCTGATCTCCA 750
    |||||
Db 677 AAAATTAACCATCTTCAATATAGTGCCTTAATCTCCGTTGAAACCTGATCTCCA 736
QY 751 CATATTAACCACTCTCTCTTCCACAAATGATGACCTATATGCAATGGAGAAATCCACAG 810
    |||||
Db 737 CATATTAACCACTCTCTCTTCCACAAATGATGACCTATATGCAATGGAGAAATCCACAG 796
QY 811 AATTTTATAGCAGATGCTATTTTATGAGTAGAAGTCAATTAACGCCAAACTGAGACA 870
    |||||
Db 797 AATTTTATAGCAGATGCTATTTTATGAGTAGAAGTCAATTAACGCCAAACTGAGACA 856
QY 871 CATATGTTTTTCTACGTCCAGAGAGCTTAATGTGAAATCCAGAAATTTGAGAAATGTG 930
    |||||
Db 857 CATATGTTTTTCTACGTCCAGAGAGCTTAATGTGAAATCCAGAAATTTGAGAAATGTG 916
QY 931 GAGAAATACATCTTGTTCATGATGCTCCGTGATGCTCTCTGATACCTTGAACACAGTCAGA 990
    |||||
Db 917 GAGAAATACATCTTGTTCATGATGCTCCGTGATGCTCTCTGATACCTTGAACACAGTCAGA 976
QY 991 ATAAAGATCAAAACAAATAAGTTATGCTATGAGATGACAAACTCTGAGTAAATTTGAGAC 1050
    |||||
Db 977 ATAAAGATCAAAACAAATAAGTTATGCTATGAGATGACAAACTCTGAGTAAATTTGAGAC 1036
QY 1051 CAAGAAATGAGTATAGTAAAGAGCGCAATTCACACTTACATTAACCATGTTACTCATTT 1110
    |||||
Db 1037 CAAGAAATGAGTATAGTAAAGAGCGCAATTCACACTTACATTAACCATGTTACTCATTT 1096
QY 1111 GTTCAGTCAATCGTCGAGGTGCAATCATAGTACTCCGTGCTTACCTTAAAGGCTCAAG 1170
    |||||
Db 1097 GTTCAGTCAATCGTCGAGGTGCAATCATAGTACTCCGTGCTTACCTTAAAGGCTCAAG 1156
QY 1171 ATTATTTATTTCCCTCCAAATTCCTGATCTGCAAGATTTTAAAGAAATGTTTGAGAC 1230
    |||||
Db 1157 ATTATTTATTTCCCTCCAAATTCCTGATCTGCAAGATTTTAAAGAAATGTTTGAGAC 1216
QY 1231 CAGAAATGATGATCTCTGCACTGGAAGAGTAGACATCTATGGAAGCAAAACCAAGAG 1290
    |||||
Db 1217 CAGAAATGATGATCTCTGCACTGGAAGAGTAGACATCTATGGAAGCAAAACCAAGAG 1276
QY 1291 GAAACGACTCTGATGCTGATGAAAAACCTGAAAGAAAGCTCTCAGTATGAGATTA 1350
    |||||
Db 1277 GAAACGACTCTGATGCTGATGAAAAACCTGAAAGAAAGCTCTCAGTATGAGATTA 1336
QY 1351 TTTATTTTACCTTCACTGATGACCTTGAGAGA 1383
    |||||
Db 1337 TTTATTTTACCTTCACTGATGACCTTGAGAGA 1369
    |||||
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Search completed: July 7, 2006, 22:02:28  
Job time : 881 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:02:42 ; Search time 6243 Seconds  
(without alignments)  
12387.704 Million cell updates/sec

Title: US-09-051-843D-3

Perfect score: 1383

Sequence: 1 gagctcaacgacgacgaag.....tcactgtaccttgagaaga 1383

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est3: \*  
3: gb\_est4: \*  
4: gb\_est5: \*  
5: gb\_est6: \*  
6: gb\_est7: \*  
7: gb\_est8: \*  
8: gb\_est9: \*  
9: gb\_est10: \*  
10: gb\_est11: \*  
11: gb\_gss1: \*  
12: gb\_gss2: \*  
13: gb\_gss3: \*  
14: gb\_gss4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 1174  | 84.9        | 1756   | 6  | CR603161 full-length |
| 2          | 978.2 | 70.7        | 1016   | 1  | AL543336 AL543336    |
| 3          | 911.6 | 65.9        | 1865   | 6  | AK0898984 Mus muscu  |
| 4          | 908.4 | 65.7        | 1817   | 6  | AK082889 Mus muscu   |
| 5          | 902.2 | 65.2        | 1677   | 6  | AK080147 Mus muscu   |
| 6          | 899   | 64.5        | 3718   | 6  | AK154675 Mus muscu   |
| 7          | 891.6 | 64.5        | 3662   | 6  | AK143292 Mus muscu   |
| 8          | 863.8 | 62.5        | 951    | 3  | BM905033 AGENCOURT   |
| 9          | 785   | 56.8        | 978    | 3  | BO678245 AGENCOURT   |
| 10         | 766.2 | 55.4        | 799    | 4  | CB956372 AGENCOURT   |
| 11         | 739.4 | 53.5        | 866    | 14 | DQ034842 Homo sapi   |
| 12         | 720.8 | 52.1        | 729    | 14 | DQ034843 Homo sapi   |
| 13         | 710   | 51.3        | 764    | 2  | BG699187 602678850   |
| 14         | 655   | 47.4        | 842    | 5  | CK000442 AGENCOURT   |
| 15         | 631.4 | 45.7        | 633    | 4  | CA391344 cs14a05.y   |
| 16         | 631   | 45.6        | 724    | 2  | BP969803 602272251   |
| 17         | 601.8 | 43.5        | 621    | 8  | CN265110 170005321   |
| 18         | 601   | 43.5        | 902    | 4  | CA488843 AGENCOURT   |
| 19         | 593.8 | 42.9        | 1009   | 2  | BI464939 603207417   |

|    |       |      |     |   |          |
|----|-------|------|-----|---|----------|
| 20 | 577   | 41.7 | 580 | 9 | DA102323 |
| 21 | 573   | 41.4 | 573 | 9 | DB150552 |
| 22 | 567   | 41.0 | 567 | 9 | DA757245 |
| 23 | 565.8 | 40.9 | 673 | 1 | AL036221 |
| 24 | 560.4 | 40.5 | 632 | 1 | AI768613 |
| 25 | 560.2 | 40.5 | 633 | 2 | BG565689 |
| 26 | 555   | 40.1 | 570 | 9 | DA707381 |
| 27 | 554.4 | 40.1 | 556 | 9 | DB148485 |
| 28 | 553.8 | 40.0 | 578 | 3 | BP267255 |
| 29 | 552   | 39.9 | 552 | 9 | DA992396 |
| 30 | 549.2 | 39.7 | 634 | 7 | BE971462 |
| 31 | 548.8 | 39.7 | 581 | 9 | DA549879 |
| 32 | 545.4 | 39.4 | 547 | 9 | DA340823 |
| 33 | 544.8 | 39.4 | 580 | 3 | BP268026 |
| 34 | 543.6 | 39.3 | 719 | 9 | DN105857 |
| 35 | 543.6 | 39.3 | 719 | 9 | DN114427 |
| 36 | 543   | 39.3 | 543 | 9 | DA990183 |
| 37 | 542.8 | 39.2 | 887 | 3 | BQ938919 |
| 38 | 541   | 39.1 | 541 | 4 | CB161269 |
| 39 | 538.8 | 39.0 | 599 | 3 | BM788541 |
| 40 | 538.4 | 38.9 | 552 | 9 | DA294933 |
| 41 | 538.4 | 38.9 | 619 | 7 | BE971324 |
| 42 | 537.2 | 38.8 | 595 | 3 | BM763177 |
| 43 | 533.4 | 38.6 | 551 | 9 | DB061920 |
| 44 | 532.2 | 38.5 | 560 | 9 | DA325930 |
| 45 | 530.6 | 38.4 | 706 | 9 | DN114783 |

## ALIGNMENTS

RESULT 1  
LOCUS CR603161 1756 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CSOD1001YN10 of Placenta Cot 25-normalized  
of Homo sapiens (human).  
ACCESSION CR603161 GI:50483968  
VERSION CR603161.1  
KEYWORDS HTC; CNSIT\_CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 1756)  
AUTHORS Li, W.B., Gruber, C., Jesses, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact: Feng Liang Email: fliang@life.technet.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
Redwood City, CA 94063  
REFERENCE 2 (bases 1 to 1756)  
AUTHORS Faraday Avenue  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqret@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
Location/Qualifiers  
1..1756  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSOD1001YN10"  
/issue="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 84.9%; Score 1174; DB 6; Length 1756;

|    |      | Best Local Similarity 98.5%; Pred. No. 2.8e-309;           |      | Matches 1196; Conservative 0; Mismatches 15; Indels 3; Gaps 1; |  |
|----|------|--|------|--|--|
| QY | 61   | ATGAGTGGCGCGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGCGGCGGG     | 120  |  |  |
| Db | 1    | ATGGAATGGCGCGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGCGGCGGG    | 60   |  |  |
| QY | 121  | GGCGGGGGCGGGG---CGCGCTACGGAACTCAGCCACCTGTGACAAATTTGAGTGC   | 177  |  |  |
| Db | 61   | GGCGGGGGCGGGGCGCGCGCTACGGAACTCAGCCACCTGTGACAAATTTGAGTGC    | 120  |  |  |
| QY | 178  | TCTGTGAAAACTCTGCAAGTAATATGACATGGAATCCACCCGAGGAGCCAGTCA     | 237  |  |  |
| Db | 121  | TCTGTGAAAACTCTGCAAGTAATATGACATGGAATCCACCCGAGGAGCCAGTCA     | 180  |  |  |
| QY | 238  | AATTAGTCTATGATTTTATGATTTTGGCGACAAACAGATAAGAAATAGCTCG       | 297  |  |  |
| Db | 181  | AATTAGTCTATGATTTTATGATTTTGGCGACAAACAGATAAGAAATAGCTCG       | 240  |  |  |
| QY | 298  | GAAGTCTGCTCAATAGAAAGTACCCTGATGAGAGATTTGTCTGCAAGTGGGCTCC    | 357  |  |  |
| Db | 241  | GAAGTCTGCTCAATAGAAAGTACCCTGATGAGAGATTTGTCTGCAAGTGGGCTCC    | 300  |  |  |
| QY | 358  | CAGTGTAGACCAATAGAGTGAAGCCCTAGCATTTTGGTGAATAATGCACTCACCC    | 417  |  |  |
| Db | 301  | CAGTGTAGACCAATAGAGTGAAGCCCTAGCATTTTGGTGAATAATGCACTCACCC    | 360  |  |  |
| QY | 418  | CCAGAAGTGAATCTGAGTCTGCTGAGCACTTCAATGCAATTTGGCACAACCTGAGC   | 477  |  |  |
| Db | 361  | CCAGAAGTGAATCTGAGTCTGCTGAGCACTTCAATGCAATTTGGCACAACCTGAGC   | 420  |  |  |
| QY | 478  | TACATGAAGTCTTCTGGCTCCCTGGAAGGAATACAGTCCGACACTAACTACTCTC    | 537  |  |  |
| Db | 421  | TACATGAAGTCTTCTGGCTCCCTGGAAGGAATACAGTCCGACACTAACTACTCTC    | 480  |  |  |
| QY | 538  | TACTATTTGGACAGAACCTTGAAAAATTCATATGTGAATAACCTTTAGAGAGCC     | 597  |  |  |
| Db | 481  | TACTATTTGGACAGAACCTTGAAAAATTCATATGTGAATAACCTTTAGAGAGCC     | 540  |  |  |
| QY | 598  | CAATACCTTTGGTGTCTCTTGTGATCTGACCAAGTGAAGGATTCAGTTTGAACAAC   | 657  |  |  |
| Db | 541  | CAATACCTTTGGTGTCTCTTGTGATCTGACCAAGTGAAGGATTCAGTTTGAACAAC   | 600  |  |  |
| QY | 658  | AGTGTCCAATAATGTGTCAAGATTAATGACAGAAAAATTAACCATCTTCAATATAGT  | 717  |  |  |
| Db | 601  | AGTGTCCAATAATGTGTCAAGATTAATGACAGAAAAATTAACCATCTTCAATATAGT  | 660  |  |  |
| QY | 718  | CCTTTACTTCCCGTGTGAAACCTGATCCCTCCACATATTAATAACCTCTCTCCACAT  | 777  |  |  |
| Db | 661  | CCTTTACTTCCCGTGTGAAACCTGATCCCTCCACATATTAATAACCTCTCTCCACAT  | 720  |  |  |
| QY | 778  | GATGACCTATATGTGCAATGGAGAAATCCACAGAAATTTATAGAGATGCTATTATTAT | 837  |  |  |
| Db | 721  | GATGACCTATATGTGCAATGGAGAAATCCACAGAAATTTATAGAGATGCTATTATTAT | 780  |  |  |
| QY | 838  | GAAGTGAAGTCAATAACAGCCAACTGAGACACATATATGTTTTCATCGTCCAAGAGCT | 897  |  |  |
| Db | 781  | GAAGTGAAGTCAATAACAGCCAACTGAGACACATATATGTTTTCATCGTCCAAGAGCT | 840  |  |  |
| QY | 898  | AAATGTGAATTCAGAAATTTTGAGAGAAATGTGAGAAATCATCTTGTTCATAGTCCCT | 957  |  |  |
| Db | 841  | AAATGTGAATTCAGAAATTTTGAGAGAAATGTGAGAAATCATCTTGTTCATAGTCCCT | 900  |  |  |
| QY | 958  | GGTGTCTTCTGATATCTTGAACACAGTCAATATAGATCAAAACAAATTAAGTATGC   | 1017 |  |  |
| Db | 901  | GGTGTCTTCTGATATCTTGAACACAGTCAATATAGATCAAAACAAATTAAGTATGC   | 960  |  |  |
| QY | 1018 | TATGAGATGACAAACTCTGAGATAATGGAGCCAAAGAAATGAGTATAGGTAAAGAGCG | 1077 |  |  |
| Db | 961  | TATGAGATGACAAACTCTGAGATAATGGAGCCAAAGAAATGAGTATAGGTAAAGAGCG | 1020 |  |  |
| QY | 1078 | AATTCAACTCTACATTAACATGTTACTATGTTTCACTCATCGTCCGAGGTGCATC    | 1137 |  |  |

|  |  |   |           |              |                 |
|--|--|---|-----------|--------------|-----------------|
| Db   | 1021   | AATTCCACTCTACATTAACCATGTTATCTCATTTGTTCCAGTATCGTCCGAGGTGCATC   | 1080      |              |                 |
| QY   | 1138   | ATAGTACTCTCTGCTTACCTTAATAAAGGCTCAAGATATTATATTCCTCCATTCCTGAT   | 1197      |              |                 |
| Db   | 1081   | ATAGTACTCTCTGCTTACCTTAATAAAGGCTCAAGATATTATATATTCCTCCATTCCTGAT | 1140      |              |                 |
| QY   | 1198   | CCTGCAAGATTTTAAAGAAATGTTTGGAGACCAGAAATGATATCTCTGCACTGGAG      | 1257      |              |                 |
| Db   | 1141   | CCTGCAAGATTTTAAAGAAATGTTTGGAGACCAGAAATGATATCTCTGCAACAAAC      | 1200      |              |                 |
| QY   | 1258   | AGTAGACATCTA 1271   |           |              |                 |
| Db   | 1201   | CATCAGGCTTCCCA 1214   |           |              |                 |
| RESULT 2   |  |   |           |              |                 |
| LOCUS  | AL543336   | 1016 bp   | mRNA      | linear       | EST 24-MAR-2004 |
| DEFINITION   | AL543336 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA                       |   |           |              |                 |
| ACCESSION  | AL543336   |   |           |              |                 |
| VERSION  | AL543336.3   | GI:45718896   |           |              |                 |
| KEYWORDS   | EST.   |   |           |              |                 |
| SOURCE   | Homo sapiens (human)   |   |           |              |                 |
| ORGANISM   | Homo sapiens   |   |           |              |                 |
| REFERENCE  | Li, W.B., Gruber, C., Jessee, J. and Polyes, D.  |   |           |              |                 |
| AUTHORS  | Full-length cDNA libraries and normalization   |   |           |              |                 |
| TITLE  | Unpublished (2001)   |   |           |              |                 |
| JOURNAL  | On Feb 15, 2001 this sequence version replaced gi:31265183.                              |   |           |              |                 |
| COMMENT  | Genoscope  |   |           |              |                 |
|  | Genoscope - Centre National de Sequenage   |   |           |              |                 |
|  | 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE                               |   |           |              |                 |
|  | Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr                               |   |           |              |                 |
|  | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime                      |   |           |              |                 |
|  | end enriched, double-strand cDNA was digested with Not I and cloned                      |   |           |              |                 |
|  | into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library                       |   |           |              |                 |
|  | was normalized. Library was constructed by Life Technologies, a                          |   |           |              |                 |
|  | division of Invitrogen. This sequence belongs to sequence cluster                        |   |           |              |                 |
|  | 11048.f  |   |           |              |                 |
| For more information about this cluster, see                 |  |   |           |              |                 |
| http://www.genoscope.cns.fr/cdna?s=CSODI001D605QPlc=11048.f. |  |   |           |              |                 |
| Location/Qualifiers  |  |   |           |              |                 |
| FEATURES   | 1..1016  |   |           |              |                 |
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|  | /db_xref="taxon:9606"  |   |           |              |                 |
|  | /clone="CSODI001YN10"  |   |           |              |                 |
|  | /rissue_type="PLACENTA COT 25-NORMALIZED"  |   |           |              |                 |
|  | /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"                                     |   |           |              |                 |
|  | /notes="1st strand cDNA was primed with a NotI-oligo(dT)                                 |   |           |              |                 |
|  | primer. Five prime end enriched, double-strand cDNA was                                  |   |           |              |                 |
|  | digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." |   |           |              |                 |
| ORIGIN   |  |   |           |              |                 |
| Query Match  | 70.7%;   | Score 978.2;  | DB 1;     | Length 1016; |                 |
| Best Local Similarity  | 98.1%;   | Pred. No. 8.5e-256;   |           |              |                 |
| Matches 997;   | Conservative   | 3; Mismatches 12;   | Indels 4; | Gaps 1;      |                 |
| QY   | 61   | ATGAGTGGCGCGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGGCGGG          | 120       |              |                 |
| Db   | 1  | ATGGAATGGCGCGCGGCTCTGCGGGCTGTGGGCGCTGTGCTCTGCGCGGCGGG         | 60        |              |                 |
| QY   | 121  | GGCGGGGGCGGGG---CGCGCTACGGAACTCAGCACTGTGACAAATTTGAGTGT        | 176       |              |                 |
| Db   | 61   | GGCGGGGGCGGGGCGCGCGCTACGGAACTCAGCACTGTGACAAATTTGAGTGT         | 120       |              |                 |
| QY   | 177  | CTCTGTTGAAACCTCTGCAAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTC      | 236       |              |                 |



|    |      |  |                              |      |
|----|------|--|------------------------------|------|
| Db | 121  | CTCTGTGAAAACTTCGACAGTAAATATGSA                                 | CATGGAAATCCACCCGAGGAGCCAGCTC | 180  |
| OY | 237  | AAATTGTAGTCTATGTGATATTTTAGTCATTTTGGCCGACAAACAAATPAAGAAATAGCTCC |                              | 296  |
| Db | 181  | AAATTGTAGTCTATGTGATATTTTAGTCATTTTGGCCGACAAACAAATPAAGAAATAGCTCC |                              | 240  |
| OY | 297  | GGAAACTCGTCGTTCAATZGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTC     |                              | 356  |
| Db | 241  | GGAAACTCGTCGTTCAATZGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTC     |                              | 300  |
| OY | 357  | CCAGTGTAGCACCAATGAGAGTGAAGAGCCTGACATTTTGGTGA AAAATGCACTCACC    |                              | 416  |
| Db | 301  | CCAGTGTAGCACCAATGAGAGTGAAGAGCCTGACATTTTGGTGA AAAATGCACTCACC    |                              | 360  |
| OY | 417  | CCCAAGGTGATCCGTGAGTCTGCTGTGACCTGAATCTGAATGCACTTTGGCCACACCTGAG  |                              | 476  |
| Db | 361  | CCCAAGGTGATCCGTGAGTCTGCTGTGACCTGAATCTGAATGCACTTTGGCCACACCTGAG  |                              | 420  |
| OY | 477  | CTACATGAAGTGTCTTGGCTCCCTGGAAGAAATACAGATCCCGACACATACTATCTCT     |                              | 536  |
| Db | 421  | CTACATGAAGTGTCTTGGCTCCCTGGAAGAAATACAGATCCCGACACATACTATCTCT     |                              | 480  |
| OY | 537  | CTACTATTGGCAGAGAAAGCTTGAAAAAATTCATCAATGTGAAAAATCTTTTGAAGAGG    |                              | 596  |
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[illegible]

**REFERENCE**  
**AUTHORS** Carninci, P. and Hayashizaki, Y.  
**TITLE** High-efficiency full-length cDNA cloning  
**JOURNAL** Meth. Enzymol. 303, 19-44 (1999)  
**PUBMED** 10349636  
**REFERENCE**

**AUTHORS** 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
**TITLE** Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
**JOURNAL** Genome Res. 10 (10), 1617-1630 (2000)  
**PUBMED** 11042159  
**REFERENCE**

**AUTHORS** 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Kitasuna, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashitani, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ichikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawaji, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.  
**TITLE** RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multichannel sequencer  
**JOURNAL** Genome Res. 10 (11), 1757-1771 (2000)  
**PUBMED** 11076661  
**REFERENCE**

**AUTHORS** 4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.  
**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409, 685-690 (2001)  
**PUBMED** 11076661  
**REFERENCE**

**AUTHORS** 5 The PANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.  
**TITLE** Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
**JOURNAL** Nature 420, 563-573 (2002)  
**PUBMED** 11076661  
**REFERENCE**

**AUTHORS** 6 RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the PANTOM Consortium.  
**TITLE** Antisense Transcription in the Mammalian Transcriptome  
**JOURNAL** Science 309, 1564-1566 (2005)  
**PUBMED** 11076661  
**REFERENCE**

**AUTHORS** 7 The PANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).  
**TITLE** The Transcriptional Landscape of the Mammalian Genome  
**JOURNAL** Science 309, 1559-1563 (2005)  
**PUBMED** 11076661  
**REFERENCE**

**AUTHORS** 8 (bases 1 to 1865)  
Adechi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hizumoto, K., Hirooka, T., Hirozane, T., Hoti, F., Imomari, K., Ichii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komoto, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, Y., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sobab, Y., Tagami, M., Tadaga, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

**TITLE** Direct Submission  
**JOURNAL** Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, Fax: 81-45-503-9216)  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/

FEATURES  
URL:http://fantom.gsc.riken.jp/  
Location/Qualifiers

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1..1865

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ORIGIN

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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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HTC; CAP trapper.  
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Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1  
Carninci, P. and Hayashizaki, Y.

- TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636  
REFERENCE
- 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
PUBMED 11042159  
REFERENCE
- 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, Y., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
PUBMED 11076861  
REFERENCE
- 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11701001  
REFERENCE
- 5 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
PUBMED 12001001  
REFERENCE
- 6 RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium. Antisense transcription in the mammalian transcriptome  
JOURNAL Science 309, 1564-1566 (2005)  
PUBMED 15641566  
REFERENCE
- 7 The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group). The transcriptional landscape of the mammalian genome  
JOURNAL Science 309, 1559-1563 (2005)  
PUBMED 15591563  
REFERENCE
- 8 (bases 1 to 1817)  
ADACHI, S., AIZAWA, K., AKIMURA, T., ARAKAWA, T., BONO, H., CARNINCI, P., FUKUDA, S., FURUKAWA, M., HANAGAKI, T., HARA, A., HASHIZUME, W., HAYASHIDA, K., HAYATSU, N., HIRAMOTO, K., HIRAOKA, T., HIROZANE, T., HORI, F., IMOTOH, K., ISHII, Y., ITOH, M., KAGAWA, I., KASUKAWA, T., KATO, H., KAWAI, J., KOJIMA, Y., KONDO, S., KONO, H., KOUDE, M., KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., MURATA, M., NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHATO, N., OKAZAKI, Y., SAITO, R., SAITOH, H., SAKAI, C., SAKAI, K., SAKAZUME, N., SANO, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y. Direct Submission
- TITLE Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
- COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ Location/Qualifiers
- FEATURES

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| Db         |  | 896  | GTACAAAGTGTTCCTCCACTCCCTGATGTCTTTCGAGCGATGTCTTACACAGTCAGAGATA    | 955  |
| Oy         |  | 995  | GAGTCAAAACAAATATAGTTATGCTATGAGATGACCAATCTCGAGATTAATGGAGCCAG      | 1054 |
| Db         |  | 956  | GAGTCCAACCAACAAGATTATGCTTATATGACACCAACTGTGGAGTATTTGGAGTAGAG      | 1015 |
| Oy         |  | 1055 | AAATGATATATAGTAAAGAGCGCAATTCACACTGTACATTAACCATGTACTCTTGTTC       | 1114 |
| Db         |  | 1016 | CACAGAGATATAGTAAAGAGCCAACTCCACTCTTACACCACCATGTTACTCACCATTC       | 1075 |
| Oy         |  | 1115 | CAGTCATGCTGGCAGGTGCATCATATGATCTCTGCTTTACTTAAAAAGGCTCAAGATTA      | 1174 |
| Db         |  | 1076 | CAGCTTTGTGCGACATGGCAGTCATATCTTCCTTTTACCTGGAAAGGCTTAAAGATCA       | 1135 |
| Oy         |  | 1175 | TTATATTCCTCCCAATATTCCTGATCCTGGCAAGATTTTAAAAAATGTTTGGAGCCAGA      | 1234 |
| Db         |  | 1136 | TTATATTTCTCTCCAAATCTCTGATCTCGCAAGATTTTAAAAAATGTTTGGAGCCAGA       | 1195 |
| Oy         |  | 1235 | ATGATGATATCTGTCGACTGGAAGAGTAGACGACATCTATGAGAAGCAAAACCAAGAGNAA    | 1294 |
| Db         |  | 1196 | ATGATGATATCCCTGCACTGGAAGAGTAGATCATCTATGAGAAACAATCCAAAAGAGAA      | 1255 |
| Oy         |  | 1295 | CCGACTCTGTATGTGCTGATATGAAAACTGGAAGAAAAGCCTCTCAGTATGATGAGATPATTTA | 1354 |
| Db         |  | 1256 | CGGATTCGTATGTGCTGATATGAAAACTGGAAGAAAAGCAAGCTCCTTGATGGGAGAGATGA   | 1315 |
| Oy         |  | 1355 | TTT-----TTACCTTCACCTGACGACCTTGAGAGA                              | 1383 |
| Db         |  | 1316 | TTTCTTTCTTGCTTCATATGATGATGACCTCTGTAGAGA                          | 1349 |
| RESULT 5   |  |      |  |      |
| AKO80147   |  |      |  |      |
| LOCUS      |  |      |  |      |
| DEFINITION |  |      |  |      |
| Accession  |  |      |  |      |
| KEYWORDS   |  |      |  |      |
| SOURCE     |  |      |  |      |
| ORGANISM   |  |      |  |      |
| REFERENCE  |  |      |  |      |
| AUTHORS    |  |      |  |      |
| TITLE      |  |      |  |      |

JOURNAL. Mech. Enzymol. 303, 19-44 (1999)

POBMED 10349636

REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL. Genome Res. 10 (10), 1617-1630 (2000)

POBMED 11042159

REFERENCE 3

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitanishi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sekiguchi, S., Ikegami, T., Katsuwagi, K., Fujimake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL. Genome Res. 10 (11), 1757-1771 (2000)

POBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL. Nature 409, 685-690 (2001)

POBMED 11571511

REFERENCE 5

AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL. Nature 420, 563-573 (2002)

POBMED 12002151

REFERENCE 6

AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.

TITLE Antisense Transcription in the Mammalian Transcriptome

JOURNAL. Science 309, 1564-1566 (2005)

POBMED 15841511

REFERENCE 7

AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

TITLE The Transcriptional Landscape of the Mammalian Genome

JOURNAL. Science 309, 1559-1563 (2005)

POBMED 16171511

REFERENCE 8 (bases 1 to 1677)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsumura, T., Miyazaki, A., Murata, M., Nakamura, Y., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohata, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Saeki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL. Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

PLEASE VISIT OUR WEB SITE FOR FURTHER DETAILS.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

LOCATION/Qualifiers 1..1677

FEATURES source

```

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/clone="A530070009"
/sex="male"
/tissue_type="aorta and vein"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1..1677
/note="interleukin 13 receptor, alpha 1 (MGI:105052
GB|S80963, evidence: BLASTN, 98%, match=1630)
putative"
misc_feature

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## ORIGIN

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Matches 1100; Conservative 0; Mismatches 243; Indels 12; Gaps 4;

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DB 7 GGCACGCTCCGAGGGGAGGGGCTGATGGCGCGCCAGCGCTGCTGGCGAGCTGTGG 66
QY 95 CGCTGCTCTGCGCGCGCGGGGGCGGGGGCGGGCGCGCTTACGGAATCTGAGC 154
DB 67 TGCTGCTACTGTGGAGCCGCGCCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCG 123
QY 155 CACCTGTGCAATTTGAGTGTCTCTGTTGAAAACCTCTGCAAGTAAATATGACATGA 214
DB 124 CACCTGTGAGAAATTTGAGGCTCTGTGCAAAAATCTGCAAGTAAATATGACATGA 183
QY 215 ATCCACCCGAGGAGCGACGCTCAAAATGTAGTCTATGATTTTATGATTTTGGCGCA 274
DB 184 GTCTCTGTGAGAGGAGCGAGCTCAAAATGTAGTCTATGATTTTATGATTTTGGCGCA 243
QY 275 AACAGATTAAGAAATATGCTCCGGAATCTGCTGTTCAATGAGTAAATCCCTGAGTGA 334
DB 244 AACAGATTAAGAAATATGCTCCGGAATCTGCTGTTCAATGAGTAAATCCCTGAGTGA 303
QY 335 GGAATTTGTCTGCAAGTGGGCTCCAGTGTGACACCAATGAGTGAAGTGAAGCTTGA 394
DB 304 AAATCTGTCTGCAAGTGGGCTCCAGTGTGACACCAATGAGTGAAGTGAAGCTTGA 363
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DB 721 TTTAAACATCTTCTTCAAAATATGAGCTTTTAACTTGAATGAGGAATCCACAGATT 780
QY 815 TTTATGACAGATGCTTATTTTATGAAAGTGAAGTCAATTAACGCCAAATGAGACATA 874

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DB 781 TTAGAGCAGATGCTTAACTTATAGAGTGAAGTCAATTAATCAACCAACGACATTA 840
QY 875 ATGTTTCTCGTCCAGAGAGGCTTAAATGTAGATTCAGAAATTTGAGGAATGTGAGA 934
DB 841 ATATTTTAGAGGTGAAAGAGGCAAAATGCCAAATTCGAAATCTGATGAAACAATGAGG 900
QY 935 ATACATCTTGTTCATGATGCTCCGTGTTCTTCTTCTGTAATCTTGAACACATCGAATA 994
DB 901 GTACAAATGTTTTCACACTCCCTGTTCTTCTGCGAGCGCTGTACACATCGACAGATTA 960
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QY 1115 CAGTCATCTGTGCGAGGAGCAATCATGATCTCTGCTTACCTTAAAGGCTCAAGATTA 1174
DB 1081 CAGTCATCTGTGCGAGGAGCAATCATGATCTCTGCTTACCTTAAAGGCTTAAAGTCA 1140
QY 1175 TTTATTTCCCTCCAAATTCCTGATCTTGGCAAGATTTTAAAGAAATGTTGAGACCA 1234
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DB 1201 ATGATGATTAACCTTGTGCACTGGAAGAGTATAGACATCTATGAGAAACCAACAGAA 1260
QY 1294 ACCGATCTGTAGTGTGATAGAAACCTGAGAAAGCTCTCTGATGAGTGAATATT 1353
DB 1261 ACCGATCTGTAGTGTGATAGAAACCTGAGAAAGCTCTCTGATGAGTGAATATT 1320
QY 1354 ATTT-----TTACCTTCACTGTGACCTTGAGAAAG 1383
DB 1321 ATTTCTTTCTTGCCTTCAATGTGACCTGTGAAAG 1355

RESULT 6
AK154675
LOCUS
DEFINITION
Mus musculus NOD-derived Cd11c +ve dendritic cells cDNA, RIKEN
full-length enriched library, clone: F630103B18 product: interleukin
13 receptor, alpha 1, full insert sequence.
ACCESSION
AK154675
VERSION
AK154675.1 GI:74185756
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2
REFERENCE
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
3
JOURNAL
PUBMED
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,

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|  |   |
|--|---|
| TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS | Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.<br>RIKEN integrated sequence analysis (RISA) system -384-format<br>sequencing pipeline with 384 multicapillary sequencer<br>Genome Res. 10 (11), 1757-1771 (2000)<br>11076861   |
|  | 4<br>Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,<br>Arakawa, T., Hara, A., Fukunishi, Y., Komno, H., Adachi, J., Fukuda, S.,<br>Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,<br>Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,<br>Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,<br>Fleischmann, W., Gaasterland, T., Giesi, C., King, B., Kochiwa, H.,<br>Kuehl, P., Lewis, S., Matsuo, Y., Nakado, I., Pesole, G.,<br>Quackenbush, J., Schriml, L.M., Staudli, F., Suzuki, R., Tomita, M.,<br>Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,<br>Baldarini, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,<br>Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,<br>Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,<br>Hotamian, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,<br>Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,<br>Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,<br>Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,<br>Tovo-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,<br>Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.<br>and Hayashizaki, Y.   |
|  | CONSTRM<br>RIKEN Genome Exploration Research Group Phase II Team and the<br>FANTOM Consortium   |
|  | TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS<br>Functional annotation of a full-length mouse cDNA collection<br>Nature 409 (6821), 685-690 (2001)<br>11217851   |
| TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS | Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,<br>Nikaido, I., Oseato, N., Saito, R., Suzuki, H., Yamana, I.,<br>Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,<br>Schonbach, C., Gojobori, T., Baldarini, R., Hill, D.P., Bult, C.,<br>Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,<br>Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V.,<br>Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dargatz, T.A.,<br>Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T.,<br>Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,<br>Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,<br>Kawaji, H., Kawasawa, Y., Kedzietski, R.M., King, B.L., Konagaya, A.,<br>Kurochkin, I.V., Lee, Y., Lennard, B., Lyons, P.A., Maglott, D.R.,<br>Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,<br>Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,<br>Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,<br>Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,<br>Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,<br>Sulana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,<br>Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,<br>Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,<br>Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,<br>Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M.,<br>Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,<br>Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,<br>Itoh, M., Kaga, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,<br>Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,<br>Rogers, J., Birney, E. and Hayashizaki, Y.  |
|  | CONSTRM<br>FANTOM Consortium  |
|  | TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS<br>Analysis of the mouse transcriptome based on functional annotation<br>of 60,770 full-length cDNAs<br>Nature 420 (6915), 563-573 (2002)<br>12466851  |
|  | 6<br>Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Fritsch, M.C.,<br>Maeda, N., Oyama, R., Ravasi, T., Lennard, B., Wells, C., Kodzuts, R.,<br>Shimokawa, K., Bajic, V.B., Bremner, S.E., Batalov, S., Forrest, A.R.,<br>Zavolan, M., Davis, M.J., Wilming, L.G., Aldanis, V., Allen, J.E.,<br>Ambesi-Impombato, A., Apweiler, R., Atturali, R.N., Bailey, T.L.,<br>Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M.,<br>Chiu, K.P., Choudhary, V., Chisoffels, A., Clutterbuck, D.R.,<br>Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G.,<br>di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G.,  |
| TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS | Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M.,<br>Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E.,<br>Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N.,<br>Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwana, A., Ishikawa, T.,<br>Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H.,<br>Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K.,<br>Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, U.,<br>Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L.,<br>Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,<br>Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakauchi, H.,<br>Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O.,<br>Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G.,<br>Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J., Ring, B.Z.,<br>Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A.,<br>Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Sengo, S.,<br>Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D.,<br>Sinclair, B., Sperling, S., Stupka, E., Sugura, K., Sultana, R.,<br>Takenaka, Y., Takai, K., Tamoya, K., Tan, S.L., Tang, S., Taylor, M.S.,<br>Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R.,<br>Wei, C.L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A.,<br>Hide, M., Bult, C., Grimmond, S.M., Teasdale, R.D., Liu, E.T.,<br>Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A.,<br>Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, Katayama, M.,<br>Suzuki, M., Aoki, U., Arakawa, T., Iida, J., Imamura, K., Itoh, M.,<br>Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M.,<br>Kondo, S., Komno, H., Nakano, K., Nimomiyama, N., Nishio, T., Okada, M.,<br>Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,<br>Watanabe, A., Okamura-Ohno, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y. |
|  | CONSTRM<br>FANTOM Consortium  |
|  | TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS<br>The transcriptional landscape of the mammalian genome<br>Science 309 (5740), 1559-1563 (2005)<br>16141072   |
|  | 7<br>Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakashima, M.,<br>Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H.,<br>Carninci, P., Hayashizaki, Y., Wells, C., Fritsch, M., Ravasi, T.,<br>Pang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L.,<br>Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A.,<br>Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lennard, B. and<br>Wahlestedt, C.   |
| TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS | CONSTRM<br>RIKEN Genome Exploration Research Group  |
|  | TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS<br>Antisense transcription in the mammalian transcriptome<br>Science 309 (5740), 1564-1566 (2005)<br>16141073  |
|  | 8 (bases 1 to 3718)<br>Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,<br>Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S.,<br>Kawai, J., Kojima, M., Komno, H., Murata, M., Nakamura, M., Nimomiyama, N.,<br>Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D.,<br>Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A.,<br>Muramatsu, M. and Hayashizaki, Y.   |
|  | Submitted<br>Direct Submission  |
| TITLE<br>JOURNAL<br>PUBMED<br>REFERENCE<br>AUTHORS | Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of<br>Physical and Chemical Research (RIKEN), Laboratory for Genome<br>Exploration Research Group, RIKEN Genomic Sciences Center (GSC),<br>RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama,<br>Kanagawa, 230-0045, Japan (E-mail: genome-resgsc.riken.jp,<br>URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,<br>Fax: 81-45-503-9216)  |
|  | COMMENT<br>cDNA library was prepared and sequenced in Mouse Genome<br>Encyclopedia Project of Genome Exploration Research Group in Riken<br>Genomic Sciences Center and Genome Science Laboratory in RIKEN.<br>Division of Experimental Animal Research in Riken contributed to<br>prepare mouse tissues.<br>Tissues were provided by Dr. John Todd (Dept. of Medical Genetics<br>Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome<br>Trust/MRC building Addenbrookes Hospital Cambridge) whose<br>assistance we gratefully acknowledge.<br>Please visit our web site for further details.<br>URL: http://genome.gsc.riken.jp/<br>URL: http://fantom.gsc.riken.jp/<br>Location/Qualifiers<br>1. 3718  |
|  | FEATURES<br>source  |





sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,  
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, K.,  
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,  
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Cavaletto, T.,  
Pletschmann, W., Gaasterland, T., Gissi, C., Kling, B., Kochiwa, H.,  
Kuehl, P., Lewis, S., Matsuo, Y., Niki, I., Pesole, G.,  
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Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,  
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,  
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,  
Pletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,  
Hofman, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,  
Marchionni, L., Mashima, U., Mazzarelli, J., Mombauts, P., Nordone, P.,  
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,  
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,  
Toyo-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L.,  
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and Hayashizaki, Y.

CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)

11217851

5

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Oshio, N., Saito, R., Suzuki, H., Yamana, K.,  
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V.,  
Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
Flecher, C.P., Forrest, A., Frazer, K.S., Gaasterland, T.,  
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Jarvis, E.D., Kana, A.,  
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kana, A.,  
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B., Lyons, P.A.,  
Kurachin, I.V., Lee, Y., Lemhard, B., Lyons, P.A., Maglott, D.R.,  
Malais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
Nunata, K., Okido, T., Pavan, W.J., Petrea, G., Pesole, G.,  
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,  
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
Santella, A., Schneider, C., Sempole, C.A., Setton, M., Shimada, K.,  
Sulana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
Sakazume, N., Saito, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.

CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

Analysis of the mouse transcriptome based on functional annotation  
of 60 770 full-length cDNAs  
Nature 420 (6915), 563-573 (2002)

12466851

6

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C.,  
Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzumi, R.,  
Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R.,  
Zavolan, M., Davis, M.O., Wilming, L.G., Aidinis, V., Allen, J.E.,  
Ambesi-Impomato, A., Apweiler, R., Attalaya, R.N., Bailey, J.L.,  
Banerai, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M.,  
Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R.,  
Croke, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G.,  
di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G.,  
Flecher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M.,  
Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E.,

CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

The transcriptional landscape of the mammalian genome  
Science 309 (5740), 1559-1563 (2005)

16141072

7

Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M.,  
Nakamura, M., Nishida, H., Yagi, C., Suzuki, M., Kawai, J., Suzuki, H.,  
Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T.,  
Pang, K.C., Hallinan, J., Matlick, J., Hume, D.A., Lipovich, L.,  
Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Santella, A.,  
Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and  
Wahlestedt, C.

CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

RIKEN Genome Exploration Research Group  
Antisense transcription in the mammalian transcriptome  
Science 309 (5740), 1564-1566 (2005)

16141073

8

CONSRM  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS

(bases 1 to 3662)  
Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,  
Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S.,  
Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Nimomiya, N.,  
Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D.,  
Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanabe, A.,  
Muramatsu, M. and Hayashizaki, Y.

COMMENT  
FEATURES  
source

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa, 230-0045, Japan (E-mail: genome-resgsc.riken.jp,  
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
Location: Qualifiers  
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VERSION BM905033.1 GI:1935424
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 951)
NIH-MGC http://mgi.nci.nih.gov/
REFERENCE 1
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC/DCMP/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
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FEATURES High quality sequence stop: 719.

Location/Qualifiers 1..951

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ORIGIN

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RESULT 9

BO678245

BO678245 978 bp mRNA linear EST 15-JUL-2002

DEFINITION

AGENCOURT 8419682 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:5274012

VERSION

BO678245 5', mRNA sequence.

KEYWORDS

BO678245.1 GI:21790924

SOURCE

EST.

ORGANISM

Homo sapiens (human)

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE

Homidae; Homo.

JOURNAL

NIH-MGC <http://mgs.nci.nih.gov/>.

COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph. D.

1 (bases 1 to 978)

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

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High quality sequence stop: 627.

Location/Qualifiers

1..978

source

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/note="Organ: skin; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: ggcacgagc(g). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 56.8%; Score 785; DB 3; Length 978;  
Best Local Similarity 94.8%; Pred. No. 6e-203;  
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Db 136 TCACCCACCTGTGCAAAATTTGAGTCTCTGTGAAAACTCTGCACAGTAATATGAC 195  
Qy 210 ATGGAATCCACCCGAGGAGGAGCAGCTCAATTTAGTATGATATTTTAACTTTGG 269  
Db 196 ATGGAATCCACCCGAGGAGGAGCAGCTCAATTTAGTATGATATTTTAACTTTGG 255  
Qy 270 CGACAAACAGATAGAAAATAGCTCCGAAAACCTCGTTCAATAGAAAGTACCCTGAA 329  
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Qy 330 TGAAGAGATTTGTCTGCAAGTGGGTCCCACTGTAAGCAATGAGTGAAGCTTAG 389  
Db 316 TGAAGAGATTTGTCTGCAAGTGGGTCCCACTGTAAGCAATGAGTGAAGCTTAG 375  
Qy 390 CATTTGGTTGAAAATATGCTACACCCCGAGAGGTATCTGTGCTGTGACCTGA 449  
Db 376 CATTTGGTTGAAAATATGCTACACCCCGAGAGGTATCTGTGCTGTGACCTGA 435  
Qy 450 ACTTCAATGCAATTTGGGCAACCTGAGCTACATGAAAGTGTCTTGCTCCCTGGAAGAA 509  
Db 436 GCTTCAATGCAATTTGGGCAACCTGAGCTACATGAAAGTGTCTTGCTCCCTGGAAGAA 495  
Qy 510 TACCAATCCGACACTAACTACTCTCTACTATTGGGCAAGAAAGCTGGAAAAATTC 569  
Db 496 TACCAATCCGACACTAACTACTCTCTACTATTGGGCAAGAAAGCTGGAAAAATTC 555  
Qy 570 TCAATGTAAGAAACATCTTTAGAGAGGCAATCTTTGGTGTCTTTGATCTGA -CCA 628  
Db 556 TCAATGTAAGAAACATCTTTAGAGAGGCAATCTTTGGTGTCTTTGATCTGA -CCA 615  
Qy 629 AAGTGAAGATTCAGTTTGGAAACAAGTGTCCAAATATAGTCAAGATATATGAG 688  
Db 616 AAGTGAAGATTCAGTTTGGAAACAAGTGTCCAAATATAGTCAAGATATATGAG 675  
Qy 689 GAAAAATTTAAACATCTCTCAATATAGTGTCTTAACTT -CCGTTGGAACCTGATCTT 747  
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Qy 748 CCAATATTTAAACCTCTCTCTCAAT -GATGACCTATATGCAATGG -AGATC 805  
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Qy 806 CACAGATTTTATAGCAGATGCTATTTTATGAAGTAGAAGTCAATTAAGCCAACTG 865  
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Qy 866 AGACACATTAATGTTTCTACGTCAGAGGCTTAATGTG -AGAAATCCAGATTTGAGAGA 924  
Db 855 AAACATTAATGTTTCTACGTCAGAGGCTTAATGTGAGAAATTTCCCAATTTGAGAGA 914  
Qy 925 AATGTGAGAAATCATCTTGTTCATAGTCCCTGCTG 961  
Db 915 AATGTGAGAAATCATCTTGTTCATAGTCCCTGCTG 951

RESULT 10  
CB956372  
LOCUS CB956372 799 bp mRNA linear EST 29-Apr-2003  
DEFINITION ABENCOUR\_1366655 NIH MGC 184 Homo sapiens cDNA clone  
IMAGE:3053391 5', mRNA sequence.  
CB956372  
VERSION CB956372.1 GI:30212489  
KEYWORDS EST  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 799)  
REFERENCE  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.lnl.gov>  
Plate: NDCM154 row: a column: 16  
High quality sequence stop: 651.  
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/note="Organ: Pooled-Glandular; Vector: pDR-LIB; Site\_1:  
SfiI (ggccatagcgc); Site\_2: SfiI (ggcgccgcgc);  
Library is oligo-dT primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTAAGGC-3' and 3' adaptor  
sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 55.4%; Score 766.2; DB 4; Length 799;  
Best Local Similarity 99.2%; Pred. No. 7.8e-198;  
Matches 790; Conservative 0; Mismatches 4; Indels 2; Gaps 2;  
Qy 258 TAGCATTTTGGGCAACAAGATAGAAATAGTCTCCGAACTGCTCTCAATAGA 317  
Db 3 TAGCATTTTGGGCAACAAGATAGAAATAGTCTCCGAACTGCTCTCAATAGA 62  
Qy 318 AGTACCCCTGAATAGAGATTTGTCTGCAAGTGGGTCCTGAGTACCAATAGAG 377  
Db 63 AGTACCCCTGAATAGAGATTTGTCTGCAAGTGGGTCCTGAGTACCAATAGAG 122  
Qy 378 TGAGAACCTTAGCATTTTGGTTGAAAATGATCTCACCCGAGAGGTATCTGAGTC 437  
Db 123 TGAGAACCTTAGCATTTTGGTTGAAAATGATCTCACCCGAGAGGTATCTGAGTC 182  
Qy 438 TGCTGTACCTGAATTTAAATGCAATTTGGGCAACCTGAGTACATGAAGTCTTGGCT 497  
Db 183 TGCTGTACCTGAATTTAAATGCAATTTGGGCAACCTGAGTACATGAAGTCTTGGCT 242  
Qy 498 CCTGGAAGAAATTCAGTCCCGACACTAATCTACTCTGACATTTGGGCAAGAGGCT 557  
Db 243 CCTGGAAGAAATTCAGTCCCGACACTAATCTACTCTGACATTTGGGCAAGAGGCT 302  
Qy 558 GAAAAAATTCATCAATGTAGAAAACATCTTTAGAGAGGCCAATATCTTTGTTCTCTT 617  
Db 303 GAAAAAATTCATCAATGTAGAAAACATCTTTAGAGAGGCCAATATCTTTGTTCTCTT 362  
Qy 618 TGATCTGACCAAGTGAAGATTTCCAGTTTGAACAACAGTGTCCAAATATAGTTC 677  
Db 363 TGATCTGACCAAGTGAAGATTTCCAGTTTGAACAACAGTGTCCAAATATAGTTC 422  
Qy 678 GGAATATGACGAAAAATTTAAACCATCTTCAATATAGTCTTTAATCTCCGCTGAA 737  
Db 423 GGAATATGACGAAAAATTTAAACCATCTTCAATATAGTCTTTAATCTCCGCTGAA 482  
Qy 738 ACCTGATCTTCCATATTTAAAACTCTCTTCCACATGATGAGCTATATGTGCATG 797  
Db 483 ACCTGATCTTCCATATTTAAAACTCTCTTCCACATGATGAGCTATATGTGCATG 542

QY 798 GGAGAAATCCACAGAAATTTATTTAGCAGATGCTTATTTTATGAAGTACATAACAG 857  
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Db 543 GGAGATCCACAGAAATTTTATTTAGCAGATGCTTATTTTATGAAGTACATAACAG 602  
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QY 858 CCAAAATGAGACACATTAATCTTTTACGCTCAAGAGGCTAATATGTAAGATCCAGAAAT 917  
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Db 663 TGAGAAATATGAGAAATATCATCTTGTTCATGATGCTCGATGTCTTCTGATACTT 722  
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QY 977 TGAACACAGTCAAGATTAAGATCAAAACAAATAAGTTATGATGATGACAAATC- 1035  
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Db 723 TGAACACAGTCAAGAAATAGAGTCAAAACAAATAAGTTATGATGATGACAAATC 782  
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QY 1036 TGGAGTAATTTGAGCC 1051  
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RESULT 11  
DQ034842 866 bp DNA linear GSS 02-JUN-2005  
LOCUS Homo sapiens IL13RA1 gene, VIRUTAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION DQ034842  
VERSION DQ034842.1 GI:66886051  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 866)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,  
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
JOURNAL (er) Plos Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
REFERENCE 2 (bases 1 to 866)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,  
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
Submitted (05-May-2005) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment. Translation starts at the beginning of  
alignment.  
FEATURES  
source Location/Qualifiers  
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/chromosome="X"  
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/locus\_tag="HC4262"  
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Query Match 53.5%; Score 739.4; DB 14; Length 866;  
Best Local Similarity 88.6%; Pred. No.1.7e-190;  
Matches 740; Conservative 0; Mismatches 95; Indels 0; Gaps 0;  
QY 146 AAATCTGACGACCTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTGCACAGTAAAT 205  
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Db 1 AAATCTGACGACCTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTGCACAGTAAAT 60  
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QY 206 GGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTTGATGCTATGGTATTTTATGTCATT 265  
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Db 61 GGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTTGATGCTATGGTATTTTATGTCATT 120  
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QY 266 TTGGCCGCAAAACAAGATTAAGAAATATGCTCCGAAACTGCTGTTCAATGAATGACCC 325  
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Db 121 TTGGCCGCAAAACAAGATTAAGAAATATGCTCCGAAACTGCTGTTCAATGAATGACCC 180  
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QY 326 TGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCACCAATGAGAGTGAGAGC 385  
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Db 181 TGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCACCAATGAGAGTGAGAGC 240  
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QY 386 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGAGTATCTTGAATCTGCTGTGA 445  
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Db 241 CTAGCATTTTGGTTGAAAAATGATCTCACCCCAAGAGTATCTTGAATCTGCTGTGA 300  
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QY 446 CTGAATCTCAATGATTTGGGCAACCTGAGTACATGAAAGTTCCTTGGCTCCCTGGAA 505  
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Db 301 CTGAGCTTCAATGATTTGGGCAACCTGAGTACATGAAAGTTCCTTGGCTCCCTGGAA 360  
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QY 506 GGAATACAGTCCCGACACTAACTATCTCTACTATTGGCACAGAAAGCTGGAAAAA 565  
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Db 361 GGAATACAGTCCCGACACTAACTATCTCTACTATTGGCACAGAAAGCTGGAAAAA 420  
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Db 541 CAGAAAAATTAAACCATCTTCATATATAGTGCCTTAACTTCCGCTGAAAACTGATC 600  
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Db 601 CTCACATATTAATAAACCTCTCTTCCACAATGATATACCTATATGTCATGGGAATC 660  
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QY 806 CACAGATTTTATTTACAGATGCGCTATTTATATAGTAGAAGCAATTAACAGCCAAACTG 865  
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Db 661 CACAGATTTTATTTACAGATGCGCTATTTATATAGTAGAAGCAATTAACAGCCAAACTG 720  
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Db 781 NNN 835  
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RESULT 12  
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LOCUS Pan troglodytes IL13RA1 gene, VIRUTAL TRANSCRIPT, partial sequence,  
DEFINITION genomic survey sequence.  
ACCESSION DQ034843  
VERSION DQ034843.1 GI:66886052  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Pan.  
REFERENCE 1 (bases 1 to 729)  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civejlo,D.,  
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
JOURNAL (er) Plos Biol. 3 (6), E170 (2005)  
PUBMED 15869325



REFERENCE 2 (bases 1 to 729)  
 AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeillio,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

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 source location/Qualifiers  
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 /gene="IL13RA1"  
 /locus\_tag="HC4262"

ORIGIN  
 Query Match 52.1%; Score 720.8; DB 14; Length 729;  
 Best Local Similarity 99.0%; Pred. No. 2e-185;  
 Matches 722; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 157 CTTGTGACAAATTGAGTGTCTCTGTTGAAAACCTTGACAGTAATATGACATGAAAT 216  
 DB 1 CTTGTGACAAATTGAGTGTCTCTGTTGAAAACCTTGACAGTAATATGACATGAAAT 60  
 QY 217 CCACCCGAGGAGGACCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 276  
 DB 61 CCACCCGAGGAGGACCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
 QY 277 CAAGATAGAAATAGCTCCGAAACCTGCTGTTCAATAGAGTACCCCTGAATAGAGG 336  
 DB 121 CAAGATAGAAATAGCTCCGAAACCTGCTGTTCAATAGAGTACCCCTGAATAGAGG 180  
 QY 337 ATTGTGTGCAAGTGGGGTCCCACTGTAGACCAATGAGTGAAGCCCTGACATTTG 396  
 DB 181 ATTGTGTGCAAGTGGGGTCCCACTGTAGACCAATGAGTGAAGCCCTGACATTTG 240  
 QY 397 GTTGAAAAATGATCTCTACCCCGAAGGATGATCTGATGCTGCTGATGAACTTCAA 456  
 DB 241 GTTGAAAAATGATCTCTACCCCGAAGGATGATCTGATGCTGCTGATGAACTTCAA 300  
 QY 457 TGCATTGGACACACCTGAGCTACATGAGTGTCTTGCGTCCCTGGAAGGAATACAGT 516  
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 DB 361 CCGGACACTAATACTCTCTATTTGGACAGAGCTGGAAAAAATTCATCAATGT 420  
 QY 577 GAAAAATCTTTAGAGAGGCCAATCTTGTGTTCTTTGATCTGACCAAGTGAAG 636  
 DB 421 GAAAAATCTTTAGAGAGGCCAATCTTGTGTTCTTTGATCTGACCAAGTGAAG 480  
 QY 637 GATTTCAGTTTGAACAACAGATGTCACAAATAATGTCAGGAATATGAGAAAAAT 696  
 DB 481 GATTTCAGTTTGAACAACAGATGTCACAAATAATGTCAGGAATATGAGAAAAAT 540  
 QY 697 AAACCATCTCTCAATATAGTGCCTTTAACTCCCGTGTGAACCTGATCTCCACATTT 756  
 DB 541 AAACCATCTCTCAATATAGTGCCTTTAACTCCCGTGTGAACCTGATCTCCACATTT 600  
 QY 757 AAAAACTCTCTCCCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 816  
 DB 601 AAAAACTCTCTCCCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 817 ATTAGCAGATGCTATTTTATGAGTGAAGTCAATTAAGCCAAATGAGACACATAT 876  
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 QY 877 GTTTCTAC 885

Db 721 GTTTCTAC 729

RESULT 13  
 EG699187  
 LOCUS  
 DEFINITION 602678850F1 NIH\_MGC\_95 Homo sapiens CDNA clone IMAGE:4811485 5', mRNA sequence.  
 ACCESSION EG699187  
 VERSION EG699187.1 GI:13967231  
 KEYWORDS EST.  
 ORGANISM Homo sapiens (human)  
 SOURCE Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 764)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Miklos Palcovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.lnl.gov  
 plate: LLM10702 row: d column: 14  
 High quality sequence stop: 755.

FEATURES  
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 /clone="IMAGE:4811485"  
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 /notes="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-xhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTCTTTT-3', size-selected for average insert size 2.5 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/NHRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 51.3%; Score 710; DB 2; Length 764;  
 Best Local Similarity 98.2%; Pred. No. 1.8e-182;  
 Matches 729; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 34 CGGCGGGGTCGAGGCGAGAGGCTGCATGAGTGGCCGCGGCTCTCGGCGTGTG 93  
 DB 8 CGGCGGGGTCGAGGCGAGAGGCTGCATGAGTGGCCGCGGCTCTCGGCGTGTG 67  
 QY 94 GCGCTGTGTCTGCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 150  
 DB 68 GCGCTGTGTCTGCGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 127  
 QY 151 CAGCCACCTGTGCAAAATTTGAGTGTCTGTTGAAAACCTTGACAGTAATATGAGACA 210  
 DB 128 CAGCCACCTGTGCAAAATTTGAGTGTCTGTTGAAAACCTTGACAGTAATATGAGACA 187  
 QY 211 TGGAAATCCACCGAGGAGCGACCTCAATTTGATGATGATGATGATGATGATGATGAT 270  
 DB 188 TGGAAATCCACCGAGGAGCGACCTCAATTTGATGATGATGATGATGATGATGATGAT 247

QY 271 GACAAACAGATAGAAAATAGCTCGGAAACCTGTCGTTCAATAGAGTACCCCTGAAT 330  
 DB 248 GACAAACAGATAGAAAATAGCTCGGAAACCTGTCGTTCAATAGAGTACCCCTGAAT 307  
 QY 331 GAGAGATTTGCTGGAAGGGGGTCCCACTGATAGCAACCAATGAGTGAAGCCCTAGC 390  
 DB 308 GAGAGATTTGCTGGAAGGGGGTCCCACTGATAGCAACCAATGAGTGAAGCCCTAGC 367  
 QY 391 ATTGTTGTTGAAAAATGATCTCTACCCCGAAGAGTATCTGATGCTGCTGACTGAA 450  
 DB 368 ATTGTTGTTGAAAAATGATCTCTACCCCGAAGAGTATCTGATGCTGCTGACTGAA 427  
 QY 451 CTTCAATGATTTGGCAACAACCTGAGCTATCATGATGTTCTTGGCTCCCTGGAAGGAT 510  
 DB 428 CTTCAATGATTTGGCAACAACCTGAGCTATCATGATGTTCTTGGCTCCCTGGAAGGAT 487  
 QY 511 ACCAGTCCGACACATACTTACTCTTACTATTGGACAGAACCTGGAATAAATTCAT 570  
 DB 488 ACCAGTCCGACACATACTTACTCTTACTATTGGACAGAACCTGGAATAAATTCAT 547  
 QY 571 CAATGTGAAAAACATCTTTAGAGAGGCCAATACCTTGGTGTCTTGTGATGACCAAA 630  
 DB 548 CAATGTGAAAAACATCTTTAGAGAGGCCAATACCTTGGTGTCTTGTGATGACCAAA 607  
 QY 631 GTGAGAGATTCAGTTTGAACAACAACAGTGCCTCAATTAATGTCAGAGTAAATGACGA 690  
 DB 608 GTGAGAGATTCAGTTTGAACAACAACAGTGCCTCAATTAATGTCAGAGTAAATGACGA 667  
 QY 691 AAAATTAACCATCTTCAATATATAGTCCCTTTAACTTCCGCTGGAACCTGATCTCCA 750  
 DB 668 AAAATTAACCATCTTCAATATATAGTCCCTTTAACTTCCGCTGGAACCTGATCTCCA 727  
 QY 751 CATATTAAAAACCTCTCTCTCC 772  
 DB 728 CATATTAAAAACCTCTCTCTTC 749

RESULT 14  
 CRO00442 842 bp mRNA linear EST 26-NOV-2003  
 LOCUS AGENCOURT\_16363365 NIH\_MGC\_221 Homo sapiens cDNA clone  
 DEFINITION IMAGE:30708826 5', mRNA sequence.  
 CRO00442  
 CRO00442.1 GI:38526476  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 1 (bases 1 to 842)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics / NIH  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgsdbs-f@mail.nih.gov  
 Tissue Procurement: James Martin, University of Iowa  
 cDNA Library Preparation: M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 http://image.linl.gov  
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 Site 2: NotI; Library is oligo-dT primed and directionally  
 cloned. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to RNA size fraction, ligated with  
 EcoR I adaptor, digested with Not I and then cloned  
 directionally into pYX-Ase vector. Average insert size  
 4-5kb. Adaptors 5' (AATTCGACAGAG) 3' and 5' d  
 (CCTGATGCTG) 3'. 3' linker sequence - GCGCCGCTGAGAGCC T18.  
 Sequencing primers 3' end: T3 promoter primer 5' d  
 (ATTAACTCTCACTAAGGAG) 3'. 5' End: T7 promoter primer 5' d  
 (TAATCGACTCACTATAGAG) 3'. Library was constructed in the  
 laboratory of M. Bento Soares. Note: this is a NIH\_MGC  
 Library"

QY 729 CCGTGTGAAACCTGATCTCTCAATATTAACCTCTCTTCCACATGATGACTTATA 788  
 DB 26 CCGTGTGAAACCTGATCTCTCAATATTAACCTCTCTTCCACATGATGACTTATA 85  
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 QY 849 CAATAACAGCAACAGTACAGACATATATGTTTCTACGTCACAAAGAGCTTAATGTAGAA 908  
 DB 146 CAATAACAGCAACAGTACAGACATATATGTTTCTACGTCACAAAGAGCTTAATGTAGAA 205  
 QY 909 TCCAGAAATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTC 968  
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 QY 1329 AGCCTCTCAGTGTGAGATATTTATTTTACCTTCACTGTGACTTGAAGA 1383  
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RESULT 15  
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 LOCUS CA391344

DEFINITION cs14a05.y1 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs Homo sapiens cDNA clone cs14a05  
5', mRNA sequence.

ACCESSION CA391344  
VERSION CA391344.1 GI:24723148  
KEYWORDS EST.

SOURCE  
ORGANISM Homo sapiens (human)  
Homosapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 633)

REFERENCE  
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NIH Bank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)

JOURNAL  
PUBMED 12107410  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: grame@helix.nih.gov  
Plate: 14 row: a column: 05  
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Location/Qualifiers  
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/lab\_host="EMDHL0B"  
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(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>). The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

ORIGIN  
Query Match 45.7%; Score 631.4; DB 4; Length 633;  
Best Local Similarity 99.8%; Pred. No. 5; Se-161;  
Matches 633; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 1 GCCTACGGAAGCTGACCTGTGACAAATTGAGTCTCTGTGAAAACTCTGCAC 60  
QY 198 AGTAATATGACATGGAATCACCAGGAGGAGCCAGCTCAATGTAGTCTATGTATT 257  
DB 61 AGTAATATGACATGGAATCACCAGGAGGAGCCAGCTCAATGTAGTCTATGTATT 120  
QY 258 TAGTCATTTTGGGACAAACAGATAAGAAATAGCTCCGAAACTGCTTCAATAGA 317  
DB 121 TAGTCATTTTGGGACAAACAGATAAGAAATAGCTCCGAAACTGCTTCAATAGA 180  
QY 318 AGTACCCCTGAATGAGAGATTGTCTGCAAGTGGGGTCCAGTGAGCAACCAATGAG 377  
DB 181 AGTACCCCTGAATGAGAGATTGTCTGCAAGTGGGGTCCAGTGAGCAACCAATGAG 240

QY 378 TGAGAGCCTAGCATTTTGGTTGAAAAATGATCTCAACCCAGAGGTGATCCTGAGTC 437  
DB 241 TGAGAGCCTAGCATTTTGGTTGAAAAATGATCTCAACCCAGAGGTGATCCTGAGTC 300  
QY 438 TGCTGTGACTGAATCTGATGATGATTTGGCAACACCTGAGTACATGAGTGTCTGGCT 497  
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DB 361 CCTGTGAAGATTCAGTCCGACACTACTACTACTACTACTACTACTACTACTACTACT 420  
QY 558 GGAATAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 617  
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DB 541 GGATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGTCTTAATCTCCGTGAA 600  
QY 738 ACCGTATCCTCCATATATTAATAAACCCTCTCCT 770  
DB 601 ACCGTATCCTCCATATATTAATAAACCCTCTCCT 633

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Job time : 6251 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

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IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 1          | 1383   | 100.0       | 1383   | US-09-688-286D-3    | Sequence 3, Appli  |
| 2          | 1333.8 | 96.4        | 3999   | US-09-543-679A-2902 | Sequence 2902, Ap  |
| 3          | 1333.8 | 96.4        | 4038   | US-08-969-125-8     | Sequence 8, Appli  |
| 4          | 1333.8 | 96.4        | 4038   | US-09-545-002-8     | Sequence 8, Appli  |
| 5          | 1333.8 | 96.4        | 4039   | US-09-949-016-223   | Sequence 223, App  |
| 6          | 1333.8 | 96.4        | 4039   | US-09-880-107-3856  | Sequence 3856, Ap  |
| 7          | 1333.8 | 96.4        | 4039   | US-09-543-679A-2903 | Sequence 2903, Ap  |
| 8          | 1333.8 | 96.4        | 11927  | US-09-193-707-5     | Sequence 5, Appli  |
| 9          | 1333.8 | 96.4        | 14978  | US-09-543-679A-2905 | Sequence 2905, Ap  |
| 10         | 1012   | 73.2        | 1547   | US-09-828-995B-49   | Sequence 49, Appli |
| 11         | 1012   | 73.2        | 1547   | US-09-828-995B-51   | Sequence 51, Appli |
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| 13         | 1009.8 | 73.0        | 2382   | US-10-282-162-31    | Sequence 31, Appli |
| 14         | 983    | 71.1        | 1215   | US-09-828-995B-52   | Sequence 52, Appli |
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## ALIGNMENTS

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; Sequence 3, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicola, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding san
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688, 286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PN6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PN7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PP2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (61)..(1338)
; OTHER INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 GCGCGGGGCGCGCGCGCGCTTACGGAACCTGACGACCTGTGACCAATTGAGTGTCT 180
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| Db | 121  | GGCGGAGGCGGGGGGCGGCTTAACGAAAACCTGAGCAACCTGTGACAAATTTGAGTGTCTCT | 180  |
| Oy | 181  | GTGAAAACTCTGCAACGTAATATGACATGGAATCCACCCGAGGGACCACTTCAAT        | 240  |
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| Db | 481  | ATGAAGTGTCTTGGGCTCCCTGSAAGAAATCCAGTCCCGACATTAATACTCTAC         | 540  |
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| Oy | 1021 | GAGGATGCAAACTCTGAGTATTTGGAGCCAAAGAAATGAGTATTAAGTAAAGACGCAAT    | 1080 |
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| Oy | 1261 | TACGACATCTATGATGAGACAAACCAAGSAGAAACGACTCTGTAGCTGATAGAAAC  | 1320 |
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| Oy | 1321 | CTGAGAAAGCCTCTCAGTANTGAGATTAATTTATTTTACTTCACTGTGACCTTGAGA | 1380 |
| Db | 1321 | CTGAGAAAGCCTCTCAGTANTGAGATTAATTTATTTTACTTCACTGTGACCTTGAGA | 1380 |
| Oy | 1381 | AGA   | 1383 |
| Db | 1381 | AGA   | 1383 |

```

RESULT 2
US-09-543-679A-2902
: Sequence 2902, Application US/09543679A
: Patent No. 7034007
: GENERAL INFORMATION:
: APPLICANT: NYCE, Jonathan W.
: TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
: COMPOSITIONS, KIT & METHOD FOR TREATMENT
: OF AIRWAY DISORDERS ASSOCIATED WITH
: BRONCHOCONSTRICITION, LUNG INFLAMMATION,
: NUMBER OF SEQUENCES: 3111
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
: STREET: 7 Clarke Drive
: City: Cranbury
: STATE: NJ
: COUNTRY: USA
: ZIP: 08512
: COMPUTER READABLE FORM:
: MEDIUM TYPE: CD-R
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: N/A
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/543, 679A
: FILING DATE: 13-Apr-2000
: CLASSIFICATION: UNKNOWN
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/127,958
: FILING DATE: 1998-08-03
: ATTORNEY/AGENT INFORMATION:
: NAME: Amzel, Viviana
: REGISTRATION NUMBER: 30,930
: REFERENCE/DOCKET NUMBER: EPI-0067191B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 609-409-3035
: TELEFAX: 413-254-9245
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 2902:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3999 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 2902:
US-09-543-679A-2902

Query Match          96.4%; Score 1333.8; DB 5; Length 3999;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY      34  CGCGCCGGGTTCCGAGGCGAGAGGCTGATGATGAGTGGCCCGGCGCGGCTTGTGGGGCTGTGG  93
      |||||||
DB       7  CGGCGCGGCTCCGAGGCGAGAGGCTGCATGAGTGAGCGCCGCGCGCTGTGGGGCTGTGG  66
      |||||||

QY      94  GCGCTGCTGCTCTGCGCGCGCGCGCGGGGGCGGGGGCGGGGG---CGGCGCTACGGAAGT  150
      |||||||
DB       6  GCGCTGCTGCTCTGCGCGCGCGCGCGGGGGCGGGGGCGGGGGCGCGCGCGCTTACGGAAGT  126
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151 CAGCACCCTGTGACAAATTGATGTCTCTGTGAAAACTCTGACAGTAATATGACA 210  
127 CAGCACCCTGTGACAAATTGATGTCTCTGTGAAAACTCTGACAGTAATATGACA 186  
211 TGGATTCACCCGAGGGGAGCGACGTAATTTGATGCTATAGTATTTTATGATTTGGC 270  
187 TGGATTCACCCGAGGGGAGCGACGTAATTTGATGCTATAGTATTTTATGATTTGGC 246  
271 GACAAACAGATAGAAAAATAGCTCCGGAACCTGTCGTTCAATAGAAAGTACCCCTGAT 330  
247 GACAAACAGATAGAAAAATAGCTCCGGAACCTGTCGTTCAATAGAAAGTACCCCTGAT 306  
331 GAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGCCTTAGC 390  
307 GAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGCCTTAGC 366  
391 ATTTTGGTTGAAAAATGATTCACCCCGAAGAGTATCTGTGCTGCTGTGACTGAA 450  
367 ATTTTGGTTGAAAAATGATTCACCCCGAAGAGTATCTGTGCTGCTGTGACTGAG 426  
451 CTTCATGCAATTTGGGCAACACCTGAGCTACATGAAGTCTTGGCTCCCTGGAAGGAT 510  
427 CTTCATGCAATTTGGGCAACACCTGAGCTACATGAAGTCTTGGCTCCCTGGAAGGAT 486  
511 ACCAGTCCGACACTAATCTACTCTACTATTGGACAGAAAGCTGGAAGAAATTCAT 570  
487 ACCAGTCCGACACTAATCTACTCTACTATTGGACAGAAAGCTGGAAGAAATTCAT 546  
571 CAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTTGGTTGCTTTGATCTGACCAA 630  
547 CAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTTGGTTGCTTTGATCTGACCAA 606  
631 GTGAGAGATTCAGTTTGAACAAACAGAGTCCAAATATGTCAGAGATTAAGCAGGA 690  
607 GTGAGAGATTCAGTTTGAACAAACAGAGTCCAAATATGTCAGAGATTAAGCAGGA 666  
691 AAAATTAACCATCTCTCAATATAGTCCCTTAACTCCGCTGGAACCTGATCTCTCA 750  
667 AAAATTAACCATCTCTCAATATAGTCCCTTAACTCCGCTGGAACCTGATCTCTCA 726  
751 CATATTAAAAAAGCTCTCTCTGACATGATGACCTATATGTGCAATGGAGAAATCCA 810  
727 CATATTAAAAAAGCTCTCTCTGACATGATGACCTATATGTGCAATGGAGAAATCCA 786  
811 AATTTATATGAGAGTCTATTTATGAGTGAAGTCAATTAACAGCAAACTGAGACA 870  
787 AATTTATATGAGAGTCTATTTATGAGTGAAGTCAATTAACAGCAAACTGAGACA 846  
871 CATATGTTTTCTACGTCCAAAGGCTAAATGTGAGATCCAGAAATTTGAGAAATGTG 930  
847 CATATGTTTTCTACGTCCAAAGGCTAAATGTGAGATCCAGAAATTTGAGAAATGTG 906  
931 GAGAAATCATCTGTTTCAATGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 990  
907 GAGAAATCATCTGTTTCAATGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 966  
991 ATAAGAGTCAAAACAAATAGTATGCTATGAGATGACAACTCTGAGATTAATGAGC 1050  
967 ATAAGAGTCAAAACAAATAGTATGCTATGAGATGACAACTCTGAGATTAATGAGC 1026  
1051 CAGAAATGAGTATAGTATGAGAGCGCAATTCACACTATACATACATGTTACTGAT 1110  
1027 CAGAAATGAGTATAGTATGAGAGCGCAATTCACACTATACATACATGTTACTGAT 1086  
1111 GTTCCAGTCAATGCTGAGGCTGCAATATAGTATCTCTGCTTTTAACTTAAAGGCTC 1170  
1087 GTTCCAGTCAATGCTGAGGCTGCAATATAGTATCTCTGCTTTTAACTTAAAGGCTC 1146  
1171 ATTATATATATTCCTGCAATTCCTGATCTGGGCAAGATTTTAAAGAAAGTTTGGAGAC 1230  
1147 ATTATATATATTCCTGCAATTCCTGATCTGGGCAAGATTTTAAAGAAAGTTTGGAGAC 1206  
1231 CAGAAATGATATCTGCACTGGAAAGATGACACATCTATGAGAAAGCAAACTGAGAG 1290

1207 CAGAAATGATATCTGCACTGAGAGATGACACATCTATGAGAAAGCAAACTGAGAG 1266  
1291 GAAACCGACTCTGAGAGTCTGATGATGAAACCTGAAAGAAAGCTCTGATGATGAGATTA 1350  
1267 GAAACCGACTCTGAGAGTCTGATGATGAAACCTGAAAGAAAGCTCTGATGATGAGATTA 1326  
1351 TTTATTTTACCTTCACTGATGACCTTGAAGA 1383  
1327 TTTATTTTACCTTCACTGATGACCTTGAAGA 1359

RESULT 3  
US-08-969-125-8  
Sequence 8, Application US/08969125B  
Patent No. 6143871  
GENERAL INFORMATION:  
APPLICANT: BONNEFOY, JEAN-YVES  
GAUCHAT, JEAN-FRANCOIS  
TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/969,125B  
FILING DATE: 12-No. 6143871-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9625899.1  
FILING DATE: 13-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1430-179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 8  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4038 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FRAGMENT TYPE: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..1323  
SEQUENCE DESCRIPTION: SEQ ID NO: 8  
US-08-969-125-8  
Query Match 96.4%; Score 1333.8; DB 3; Length 4038;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

34 CGGCCGGGCTCCGAGCGAGAGGCTGATGATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 93  
16 CGGCCGGGCTCCGAGCGAGAGGCTGATGATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 75  
94 GCGCTGTCTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 150  
76 GCGCTGTCTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 135



| Query | Match | 96.4%   | Score 1333.8 | DB 3        | Length 4039  |   |
|-------|-------|---|--------------|-------------|--------------|---|
| Db    | 17    | CGGCGGGGCTCGAGGCGAGAGGCTGATGAGTGGCCGGCGGCTCTGGGGGCTGTGG     | 99.6%        | Pred. No. 0 | Matches 1348 | Conservative 0; Mismatches 2; Indels 3; Gaps 1; |
| Qy    | 34    | CGGCGGGGCTCGAGGCGAGAGGCTGATGAGTGGCCGGCGGCTCTGGGGGCTGTGG     |              |             |              |   |
| Db    | 94    | GCCTGCTGCTCTCGCGCGCGGCGGGGGCGGGGGCGGGG---CGCGCTTACGGAACT    |              |             |              |   |
| Qy    | 77    | GCCTGCTGCTCTCGCGCGCGGCGGGGGCGGGGGCGGGGGCGCGGCGCTTACGGAACT   |              |             |              |   |
| Db    | 151   | CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGACA |              |             |              |   |
| Qy    | 137   | CAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTGCACAGTAATATGACA |              |             |              |   |
| Db    | 211   | TGGAATCACCCGAGGGGAGCAGCTCAAAATTTGATGTCTATGATTTTATGATTTTGGC  |              |             |              |   |
| Qy    | 197   | TGGAATCACCCGAGGGGAGCAGCTCAAAATTTGATGTCTATGATTTTATGATTTTGGC  |              |             |              |   |
| Db    | 271   | GACAAACAAGTAAAGAAATAGCTCCGGAACCTGTCGTTCAATAGAAATACCCCTGAT   |              |             |              |   |
| Qy    | 257   | GACAAACAAGTAAAGAAATAGCTCCGGAACCTGTCGTTCAATAGAAATACCCCTGAT   |              |             |              |   |
| Db    | 331   | GAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATAGAGTGAAGAGCTTAGC   |              |             |              |   |
| Qy    | 317   | GAGAGGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATAGAGTGAAGAGCTTAGC   |              |             |              |   |
| Db    | 391   | ATTTGGTTGAAAAATCATCTCACCCCAAGAGTGAATCTGAGTCTGCTGTGACTGAA    |              |             |              |   |
| Qy    | 377   | ATTTGGTTGAAAAATCATCTCACCCCAAGAGTGAATCTGAGTCTGCTGTGACTGAA    |              |             |              |   |
| Db    | 451   | CTTCATGATTTGGCAACCTGAGCTACATGAAGTGTCTTGGCTCCCTGGAAGGAT      |              |             |              |   |
| Qy    |       |   |              |             |              |   |



|   |      |   |      |
|---|------|---|------|
| QY  | 811  | AATTTATTTAGCAGATGCTATTTTATTAAGAGTAAGCAATTAACAGCCAACTGAGCA   | 870  |
| Db  | 797  | AATTTATTTAGCAGATGCTATTTTATTAAGAGTAAGCAATTAACAGCCAACTGAGCA   | 856  |
| QY  | 871  | CATAATGTTTTCTACGTCCAGAGGCTAAATGTGGAATCCAGAAATTTGAGAAATGTG   | 930  |
| Db  | 857  | CATAATGTTTTCTACGTCCAGAGGCTAAATGTGGAATCCAGAAATTTGAGAAATGTG   | 916  |
| QY  | 921  | GAGAAATACATCTGTTTTATGAGTCCCTGCTGTCTTCCGTGATACCTTAACAACATCGA | 990  |
| Db  | 917  | GAGAAATACATCTGTTTTATGAGTCCCTGCTGTCTTCCGTGATACCTTAACAACATCGA | 976  |
| QY  | 991  | ATAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACTCTGGAGTATTGGAGC  | 1056 |
| Db  | 977  | ATAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACTCTGGAGTATTGGAGC  | 1036 |
| QY  | 1051 | CAAGAAATGAGTATAGTATGTAAGAGCGCAATTCACACTCTACATAACCATGTTACTCA | 1110 |
| Db  | 1037 | CAAGAAATGAGTATAGTATGTAAGAGCGCAATTCACACTCTACATAACCATGTTACTCA | 1098 |
| QY  | 1111 | GTTCCAGTCATCGTGCAGAGTGCAATCAATAGTACCTGCTTACTTAAAAAGGCTCAAG  | 1170 |
| Db  | 1097 | GTTCCAGTCATCGTGCAGAGTGCAATCAATAGTACCTGCTTACTTAAAAAGGCTCAAG  | 1156 |
| QY  | 1171 | ATTATTAATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTGGAGAC | 1230 |
| Db  | 1157 | ATTATTAATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTGGAGAC | 1216 |
| QY  | 1231 | CAGAAATGATGATACCTGTCGACATGGAAGAAATGACATCTATGAGAACCAACCAAGAG | 1296 |
| Db  | 1217 | CAGAAATGATGATACCTGTCGACATGGAAGAAATGACATCTATGAGAACCAACCAAGAG | 1276 |
| QY  | 1291 | GAAACCGACTCTGTAGTGTCTGATAGAAACCTGAAAGAAAGCTCTCAGTGTGAGATAA  | 1356 |
| Db  | 1277 | GAAACCGACTCTGTAGTGTCTGATAGAAACCTGAAAGAAAGCTCTCAGTGTGAGATAA  | 1336 |
| QY  | 1351 | TTTATTTTTCACCTTCACCTGTAAGCTTGAAGAA                          | 1383 |
| Db  | 1337 | TTTATTTTTCACCTTCACCTGTAAGCTTGAAGAA                          | 1369 |
| RESULT 7  |      |   |      |
| US-09-543-679A-2903   |      |   |      |
| Sequence 2903, Application US/09543679A                       |      |   |      |
| Patent No. 7034007  |      |   |      |
| GENERAL INFORMATION:  |      |   |      |
| APPLICANT: NVCE, Jonathan W.                                  |      |   |      |
| TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE, |      |   |      |
| COMPOSITIONS, KIT & METHOD FOR TREATMENT                      |      |   |      |
| OF AIRWAY DISORDERS ASSOCIATED WITH                           |      |   |      |
| BRONCHOCONSTRICTION, LUNG INFLAMMATION,                       |      |   |      |
| NUMBER OF SEQUENCES: 3111                                     |      |   |      |
| CORRESPONDENCE ADDRESS:                                       |      |   |      |
| ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.                   |      |   |      |
| STREET: 7 Clarke Drive  |      |   |      |
| CITY: Cranbury  |      |   |      |
| STATE: NJ   |      |   |      |
| COUNTRY: USA  |      |   |      |
| ZIP: 08512  |      |   |      |
| COMPUTER READABLE FORM:                                       |      |   |      |
| MEDIUM TYPE: CD-R   |      |   |      |
| COMPUTER: IBM Compatible                                      |      |   |      |
| OPERATING SYSTEM: DOS   |      |   |      |
| SOFTWARE: N/A   |      |   |      |
| CURRENT APPLICATION DATA:                                     |      |   |      |
| APPLICATION NUMBER: US/09/543,679A                            |      |   |      |
| FILING DATE: 13-Apr-2000                                      |      |   |      |
| CLASSIFICATION: UNKNOWN                                       |      |   |      |
| PRIOR APPLICATION DATA:                                       |      |   |      |
| APPLICATION NUMBER: 60/127,958                                |      |   |      |
| FILING DATE: 1998-08-03                                       |      |   |      |
| ATTORNEY/AGENT INFORMATION:                                   |      |   |      |
| NAME: Amzel, Viviana  |      |   |      |

[illegible]









Db 2477 CAGATGATGATATCTGTGCACTGGAAAGAGTACATCTATGAGAGCAAAACCAAGAG 2536  
Qy 1291 GAAACGACTCTGTAGTGTGATAGAAAACTGGAAGAAAGCTCTCAGTATGAGATTA 1350  
Db 2537 GAAACGACTCTGTAGTGTGATAGAAAACTGGAAGAAAGCTCTCAGTATGAGATTA 2596  
Qy 1351 TTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
Db 2597 TTTATTTTACCTTCACTGTGACCTTGAGAGA 2629

RESULT 10  
US-09-828-995B-49  
; Sequence 49, Application US/09828995B  
; Patent No. 6703360  
; GENERAL INFORMATION:  
; APPLICANT: Heska Corporation  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Tang, Liang A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13  
; FILE REFERENCE: AL-7  
; CURRENT APPLICATION NUMBER: US/09/828,995B  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 49  
; LENGTH: 1547  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1215)  
; OTHER INFORMATION:  
US-09-828-995B-49

Query Match 73.2%; Score 1012; DB 3; Length 1547;  
Best Local Similarity 87.7%; Pred. No. 2.6e-288;  
Matches 1105; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

Qy 124 GGGGGGGGGGGCGCGCGCTACGGAAGTCAAGCACTGTGCAAAATTTGAGTGTCTGT 183  
Db 1 GGGGGGGTGGCGCGCACCCGAACTCAGCCACTGTGACGAAATTTGAGTGTCTGT 60  
Qy 184 GAAAACTCTGCACTAATATGACATGGAATCCAGGAGGAGCCAGCTCAATTGT 243  
Db 61 GAAAACTCTGCACTAATATGACATGGAATCCAGGAGGAGCCAGCTCAATTGT 120  
Qy 244 AGTCATGATATTTAGTCAATTTTGGGACAAACAGATTAAGTAATAGCTCCGGAAT 303  
Db 121 ACCTTACGGATATTTAGTCAATTTTGGGACAAACAGATTAAGTAATAGCTCCGGAAT 180  
Qy 304 CGTCGTTCAATAGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAGT 363  
Db 181 CATCGTTCAAAAGAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAGT 240  
Qy 364 AGCAACCAATGAGAGTGAAGAGCTAGCATTTTGGTAAAAATGCACTTCAACCCCAAA 423  
Db 241 AGCAACCAATGAGAGTGAAGAGCTAGCATTTTGGTAAAAATGCACTTCAACCCCAAA 300  
Qy 424 GGTGATCTGAGTCTGTGACTGAGTCAATGCAATTTGGGACAAACCTGAGTCAAG 483  
Db 301 GGTGATCTGAGTCTGTGACTGAGTCAATGCAATTTGGGACAAACCTGAGTCAAG 360  
Qy 484 AAGTGTCTTGGCTCCCTGGAAGAAATCCAGTCCGACACTAATTAATCTCTACTAT 543  
Db 361 AAGTGTCTTGGCTCCCTGGAAGAAATCCAGTCCGACACTAATTAATCTCTACTAT 420  
Qy 544 TGGCAGAGAGCTGGAAAAATTTCAATGTAATGAAAACTTTTGAAGAGCCAAATAC 603  
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Db 421 TGGCAGAGAGCTGGAAAAATTTCAATGCAAGACATCTATAGAGAGGTCAACAC 480  
Qy 604 TTTGGTGTTCCTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTG 663  
Db 481 ATTGGTGTTCCTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTG 540  
Qy 664 CAATTAATGTCAGAGTAATGCAAGAAAAATTAACATCTTCAATATAGTGCCTTA 723  
Db 541 CAATTAATGTCAGAGTAATGCAAGAAAAATTAACATCTTCAATATAGTGCCTTA 600  
Qy 724 ACTTCCCGTGAACCTGATCTCCACATTAATAAACCTCTCCCTCAAGATGATGAC 783  
Db 601 ACTTCCCGTGAACCTGATCTCCCGCAATTAAGCTCTTCTTCCAAATGGATAC 660  
Qy 784 CTATATGTCGAATGGAGATCCACAGATTTTATAGAGATGCTATTTATAGAA 843  
Db 661 TTGTATGTGCAATGGAAGATCCACAAATTTTATAGAGATGCTATTTATAGAA 720  
Qy 844 GAAGTCAATPAACAGCCAACTGAGACACATTAATGTTTGTACGTCGAAGAGCTAAATG 903  
Db 721 GAAGTCAATPAACAGCCAGCTGAGACAGATGATATATCTACGTTGAAGAGCCAAATG 780  
Qy 904 GAGATCCGAATTTGAGAGAAATGAGAAATACATCTTGTTCATGTTCCCTGAT 963  
Db 781 CAGAAATTCAGAAATTTGAGAGAAATCCGAGGGGATCAATTTGTTCAATGGTCCCGGCGTT 840  
Qy 964 CTTCCTGATACCTTTGACACAGTCAAGATTAAGTCAAAACAAATAGTATGCTATGAG 1023  
Db 841 CTTCCTGATACCTTTGACACAGTCAAGATTAAGTCAAAACAAATAGTATGCTATGAG 900  
Qy 1024 GATGACAACTCTGAGTAATTTGAGCCCAAGAAATGATATAGTAAGAGCCAAATTC 1083  
Db 901 GATGACAACTCTGAGTAATTTGAGCCCAAGATGATATAGTAAGTAAGAGCCAAATTC 960  
Qy 1084 ACACTTCAATPAACATGTTATCTATCTATGTTCCAGTATGTTGCGAGGTCATATAGTA 1143  
Db 961 AGCTTCAATPAACATGTTATCTGCGCACTCAAGTATGTTGCGAGGTCATATAGTA 1020  
Qy 1144 CTTCCTGTTTACCTTAAGAAAGCTCAAGATTAATTAATTTCCCTCAATTCCTGATCCTGGC 1203  
Db 1021 CTTCCTGTTTATCTCAAAAGGCTCAAGATTAATTAATTTCCCTCAATTCCTGATCCTGGC 1080  
Qy 1204 AAGATTTTAAAGAAATGTTTGGAGCCAGAAATGATATCTCTGCACTGGAAGATAC 1263  
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Qy 1264 GACATCTATGAGAGAGCAACCAAGAGAAACCGACTGTAGTGTGCTGATAGAAACCTG 1323  
Db 1141 GACATCTATGAGAGAGCAACCAAGAGAAACCGACTGTAGTGTGCTGATAGAAACCTG 1200  
Qy 1324 AAGAAAGCTCTCAGTATGAGATTAATTTTACCTTCACTGCTGACCTTGAGAGA 1383  
Db 1201 AAGAAAGCTCTCAGTATGAGATTAATTTTACCTTCACTGCTGACCTTGAGAGA 1260  
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RESULT 11  
US-09-828-995B-51/c  
; Sequence 51, Application US/09828995B  
; Patent No. 6703360  
; GENERAL INFORMATION:  
; APPLICANT: Heska Corporation  
; APPLICANT: McCall, Catherine A.  
; APPLICANT: Tang, Liang A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13  
; FILE REFERENCE: AL-7  
; CURRENT APPLICATION NUMBER: US/09/828,995B  
; PRIOR FILING DATE: 2001-04-09  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.1

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:10:57 ; Search time 1701 Seconds  
(without alignments)  
9990.476 Million cell updated/sec

Title: US-09-051-843D-3

Perfect score: 1383  
Sequence: 1 gagcttaacacgcagcaag.....tcactgtcacttcagaga 1383

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
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- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description         |
|------------|--------|-------------|--------|----|---------------------|
| 1          | 1376.6 | 99.5        | 1383   | 6  | US-10-036-568-3     |
| 2          | 1333.8 | 96.4        | 4009   | 15 | US-11-185-230-3     |
| 3          | 1333.8 | 96.4        | 4009   | 16 | US-11-182-384A-3    |
| 4          | 1333.8 | 96.4        | 4009   | 16 | US-11-183-599A-3    |
| 5          | 1333.8 | 96.4        | 4038   | 8  | US-10-671-697-8     |
| 6          | 1333.8 | 96.4        | 4039   | 3  | US-09-962-832-160   |
| 7          | 1333.8 | 96.4        | 4039   | 3  | US-09-880-107-3856  |
| 8          | 1333.8 | 96.4        | 4039   | 7  | US-10-172-118-633   |
| 9          | 1333.8 | 96.4        | 4039   | 8  | US-10-342-887-633   |
| 10         | 1333.8 | 96.4        | 4039   | 10 | US-10-843-641A-6046 |
| 11         | 1333.8 | 96.4        | 4466   | 3  | US-09-971-392-58    |
| 12         | 1330.6 | 96.2        | 1572   | 9  | US-10-278-698-6     |
| 13         | 1330.6 | 96.2        | 1572   | 9  | US-10-278-698-6     |
| 14         | 1264.8 | 91.5        | 1284   | 10 | US-10-850-270-3     |
| 15         | 1238.4 | 89.5        | 3880   | 3  | US-09-822-846-109   |
| 16         | 1236.8 | 89.4        | 3906   | 12 | US-10-745-586-32    |
| 17         | 1181.4 | 85.4        | 1680   | 3  | US-09-822-846-110   |

|    |        |      |      |    |                   |                   |
|----|--------|------|------|----|-------------------|-------------------|
| 18 | 1012.8 | 73.2 | 2343 | 3  | US-09-935-868-33  | Sequence 33, Appl |
| 19 | 1012.8 | 73.2 | 2343 | 6  | US-10-287-035-33  | Sequence 33, Appl |
| 20 | 1012   | 73.2 | 1547 | 3  | US-09-828-995B-49 | Sequence 49, Appl |
| 21 | 1012   | 73.2 | 1547 | 3  | US-09-828-995B-51 | Sequence 51, Appl |
| 22 | 1012   | 73.2 | 1547 | 8  | US-10-753-159-51  | Sequence 49, Appl |
| 23 | 1012   | 73.2 | 1547 | 8  | US-10-753-159-51  | Sequence 51, Appl |
| 24 | 1011.2 | 73.1 | 2343 | 3  | US-09-935-868-37  | Sequence 37, Appl |
| 25 | 1011.2 | 73.1 | 2343 | 6  | US-10-287-035-17  | Sequence 37, Appl |
| 26 | 1011.2 | 73.1 | 2349 | 3  | US-09-935-868-31  | Sequence 31, Appl |
| 27 | 1011.2 | 73.1 | 2349 | 6  | US-10-287-035-51  | Sequence 51, Appl |
| 28 | 1011.2 | 73.1 | 2349 | 6  | US-10-287-035-57  | Sequence 57, Appl |
| 29 | 1009.8 | 73.0 | 2382 | 3  | US-09-313-942-31  | Sequence 31, Appl |
| 30 | 1009.8 | 73.0 | 2382 | 3  | US-09-935-868-31  | Sequence 31, Appl |
| 31 | 1009.8 | 73.0 | 2382 | 6  | US-10-287-035-11  | Sequence 31, Appl |
| 32 | 1009.8 | 73.0 | 2382 | 7  | US-10-282-162-31  | Sequence 31, Appl |
| 33 | 1009.8 | 73.0 | 2382 | 13 | US-11-134-114-31  | Sequence 31, Appl |
| 34 | 1008   | 72.9 | 2343 | 3  | US-09-935-868-31  | Sequence 41, Appl |
| 35 | 1008   | 72.9 | 2343 | 6  | US-10-287-035-41  | Sequence 41, Appl |
| 36 | 1008   | 72.9 | 2349 | 3  | US-09-935-868-47  | Sequence 47, Appl |
| 37 | 1008   | 72.9 | 2349 | 6  | US-10-287-035-47  | Sequence 47, Appl |
| 38 | 1008   | 72.9 | 2349 | 6  | US-10-287-035-53  | Sequence 53, Appl |
| 39 | 983    | 71.1 | 1215 | 3  | US-09-828-995B-52 | Sequence 52, Appl |
| 40 | 983    | 71.1 | 1215 | 3  | US-09-828-995B-53 | Sequence 53, Appl |
| 41 | 983    | 71.1 | 1215 | 8  | US-10-753-159-52  | Sequence 52, Appl |
| 42 | 983    | 71.1 | 1215 | 8  | US-10-753-159-53  | Sequence 53, Appl |
| 43 | 959.4  | 69.4 | 2355 | 3  | US-09-313-942-29  | Sequence 29, Appl |
| 44 | 959.4  | 69.4 | 2355 | 3  | US-09-935-868-29  | Sequence 29, Appl |
| 45 | 959.4  | 69.4 | 2355 | 6  | US-10-287-035-29  | Sequence 29, Appl |

## ALIGNMENTS

RESULT 1  
US-10-036-568-3  
Sequence 3, Application US/10036568  
Publication No. US20020090682A1  
GENERAL INFORMATION:  
APPLICANT: Willson, Tracy  
APPLICANT: Nicola, Nicos A.  
APPLICANT: Hilton, Douglas J.  
APPLICANT: Metcalf, Donald  
APPLICANT: Zhang, Jian G.  
TITLE OF INVENTION: NOVEL HAEMOPLETIN RECEPTOR AND GENETIC SEQUENCES  
TITLE OF INVENTION: ENCODING SAME  
FILE REFERENCE: Davies cc  
CURRENT APPLICATION NUMBER: US/10/036,568  
CURRENT FILING DATE: 2001-11-07  
PRIOR APPLICATION NUMBER: US/09/051,843  
PRIOR FILING DATE: 1998-06-29  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 3  
LENGTH: 1383  
TYPE: DNA  
ORGANISM: Human IL-13 receptor alpha-chain  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (61)..(1338)  
US-10-036-568-3

Query Match 99.5%; Score 1376.6; DB 6; Length 1383;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 1379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCTTAACACGACCAAGAGATTAAACAGTCGCGCCGAGTTCGAGCGAGAGGCTGC 60  
DB 1 GAGCTTAACACGACCAAGAGATTAAACAGTCGCGCCGAGTTCGAGCGAGAGGCTGC 60  
QY 61 ATGAGTGGCGCGCGCGCTCTGCGGCGCTGCGGCGCTGCTGCTGCGCGCGCGG 120  
DB 61 ATGAGTGGCGCGCGCGCTCTGCGGCGCTGCGGCGCTGCTGCTGCGCGCGCGG 120

|    |      |  |      |
|----|------|--|------|
| QY | 121  | GGCGGGGGGGGGGGGGGGGCGGCGCTACAGGAACTCAGGCACTCGTGACAAATTTGAGTGCTCT | 180  |
| Db | 121  | GGCGGGGGGGGGGGGGGGGCGGCGCTACAGGAACTCAGGCACTCGTGACAAATTTGAGTGCTCT | 180  |
| QY | 181  | GTTGAAAACCTCTGCACAGTAAATATGACATGGAATCCACCAGGGAGCGAGCTCAAT        | 240  |
| Db | 181  | GTTGAAAACCTCTGCACAGTAAATATGACATGGAATCCACCAGGGAGCGAGCTCAAT        | 240  |
| QY | 241  | TGTAGCTATAGGTATTTTATGTCATTTTGGCGACAAACAAGTAAAGAAATAGCTTCGGAA     | 300  |
| Db | 241  | TGTAGCTATAGGTATTTTATGTCATTTTGGCGACAAACAAGTAAAGAAATAGCTTCGGAA     | 300  |
| QY | 301  | ACTGTCGTCCTCAATAGAGTACCCCTGGAATGAGAGGATTTGTCGCAAGTGGGGTCCGAG     | 360  |
| Db | 301  | ACTGTCGTCCTCAATAGAGTACCCCTGGAATGAGAGGATTTGTCGCAAGTGGGGTCCGAG     | 360  |
| QY | 361  | TGTAGCAACAATGAGAGTGAAGAGCTGACATTTTGGTTGTAAGAAATGATGATCAACCCCA    | 420  |
| Db | 361  | TGTAGCAACAATGAGAGTGAAGAGCTGACATTTTGGTTGTAAGAAATGATGATCAACCCCA    | 420  |
| QY | 421  | GAAAGTGATCCTGAGTCTGCTGTGACTGAACCTTCAATGCAATTTGGCAACAACCTGAGCTAC  | 480  |
| Db | 421  | GAAAGTGATCCTGAGTCTGCTGTGACTGAACCTTCAATGCAATTTGGCAACAACCTGAGCTAC  | 480  |
| QY | 481  | ATGAAGTCTTCTGGCTCCCTGGAGAGAAATACAGTCCCGACACTAATACCTCTAC          | 540  |
| Db | 481  | ATGAAGTCTTCTGGCTCCCTGGAGAGAAATACAGTCCCGACACTAATACCTCTAC          | 540  |
| QY | 541  | TATTGGCACAGAAAGCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAA      | 600  |
| Db | 541  | TATTGGCACAGAAAGCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAA      | 600  |
| QY | 601  | TACTTTGGTGTCTCTTTGATCTGACCAAGTGAAGATTCGAGTTTGAACAACAGT           | 660  |
| Db | 601  | TACTTTGGTGTCTCTTTGATCTGACCAAGTGAAGATTCGAGTTTGAACAACAGT           | 660  |
| QY | 661  | GTCCAAATAAATAGTGTCAAGATTAATGACAGAAAAATTAACATCCTTCAATATAGTGCT     | 720  |
| Db | 661  | GTCCAAATAAATAGTGTCAAGATTAATGACAGAAAAATTAACATCCTTCAATATAGTGCT     | 720  |
| QY | 721  | TTAATCTCCCGGTGAAACCTGATCCTCAATATTAAGAACCTCTCTCCACAAATGAT         | 780  |
| Db | 721  | TTAATCTCCCGGTGAAACCTGATCCTCAATATTAAGAACCTCTCTCCACAAATGAT         | 780  |
| QY | 781  | GACCTATAATGTGCAATGAGAGATCCACAGATTTTATTAACAGATGCTTATTTATGAA       | 840  |
| Db | 781  | GACCTATAATGTGCAATGAGAGATCCACAGATTTTATTAACAGATGCTTATTTATGAA       | 840  |
| QY | 841  | GTAGAAGTCAATACAGCCAAACTGAGACATATGTTTTCTATAGCTCAAGAGCTTAA         | 900  |
| Db | 841  | GTAGAAGTCAATACAGCCAAACTGAGACATATGTTTTCTATAGCTCAAGAGCTTAA         | 900  |
| QY | 901  | TGTGGAATCCAGAAATTTGAGGAAATGTGGAATACATCTTGTTCATGTGCTCCGT          | 960  |
| Db | 901  | TGTGGAATCCAGAAATTTGAGGAAATGTGGAATACATCTTGTTCATGTGCTCCGT          | 960  |
| QY | 961  | GTTCTTCCCTGATCTTTGAAACAAGTCAAGATTAAGTCAAAACAATTAAGTTATGCTAT      | 1020 |
| Db | 961  | GTTCTTCCCTGATCTTTGAAACAAGTCAAGATTAAGTCAAAACAATTAAGTTATGCTAT      | 1020 |
| QY | 1021 | GAGATGACAAACTTGGAGTAAATTTGGAGCCAAAGAAATGAGTATBTGGTAAGAGCCAT      | 1080 |
| Db | 1021 | GAGATGACAAACTTGGAGTAAATTTGGAGCCAAAGAAATGAGTATBTGGTAAGAGCCAT      | 1080 |
| QY | 1081 | TCCACACTCTCATACACATGTTACTCATTTGTCACAGTACCTGTGCGCAGGTGCATCATTA    | 1140 |
| Db | 1081 | TCCACACTCTCATACACATGTTACTCATTTGTCACAGTACCTGTGCGCAGGTGCATCATTA    | 1140 |
| QY | 1141 | GTACTCCCTGCTTAACTTAAAAAGCTCAAGATTTATTAATTCCTCCCAATTCCTGATCCT     | 1200 |
| Db | 1141 | GTACTCCCTGCTTAACTTAAAAAGCTCAAGATTTATTAATTCCTCCCAATTCCTGATCCT     | 1200 |
| QY | 1201 | GGCAAGATTTTAAAGAAATGTTTGGAGACCAAGATGATGATCTTGCACTGGAGAG          | 1260 |

|  |      |  |      |
|--|------|--|------|
| Dd   | 1201 | GGCAAGATTTTAAAGAATGTTTGAGACCGAATAATGACTCTGCACGTGAAGAAG       | 1260 |
| Qy   | 1261 | TAGCACAATCTATGAGAAACCAACCAGAGAAAACGACTCTGTAGTGTGATAGAAAC     | 1320 |
| Dd   | 1261 | TACACACATCTATGAGAGAACCAACCAGAGAAAACGACTGTGATGTGATAGAAAC      | 1320 |
| Qy   | 1321 | CTGAAGAAAGCCTCTCAGTAGTAGAGATTAATTATTTTACCTTCACCTGTGACCTTGAGA | 1380 |
| Dd   | 1321 | CTGAAGAAAGCCTCTCAGTAGTAGAGATTAATTATTTTACCTTCACCTGTGACCTTGAGA | 1380 |
| Qy   | 1381 | AGA 1383<br>   |      |
| Dd   | 1381 | AGA 1383   |      |
| RESULT 2   |      |  |      |
| US-11-185-230-3  |      |  |      |
| ; Sequence 3, Application US/11185230                                      |      |  |      |
| ; Publication No. US20050282216A1  |      |  |      |
| ; GENERAL INFORMATION:   |      |  |      |
| ; APPLICANT: Caput, Daniel   |      |  |      |
| ; APPLICANT: Ferrera, Pascual  |      |  |      |
| ; APPLICANT: Laurent, Patrick  |      |  |      |
| ; APPLICANT: Vite, Narcilio  |      |  |      |
| ; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity |      |  |      |
| ; FILE REFERENCE: IVD924 US CNT 1  |      |  |      |
| ; CURRENT APPLICATION NUMBER: US/11/185,230                                |      |  |      |
| ; CURRENT FILING DATE: 2005-07-18  |      |  |      |
| ; PRIOR APPLICATION NUMBER: PCT/FR96/01756                                 |      |  |      |
| ; PRIOR FILING DATE: 1996-11-07  |      |  |      |
| ; NUMBER OF SEQ ID NOS: 15   |      |  |      |
| ; SOFTWARE: PatentIn Ver. 2.0  |      |  |      |
| ; SEQ ID NO 3  |      |  |      |
| ; LENGTH: 4009   |      |  |      |
| ; TYPE: DNA  |      |  |      |
| ; ORGANISM: Homo sapiens   |      |  |      |
| ; FEATURE:   |      |  |      |
| US-11-185-230-3  |      |  |      |
| Query Match            96.4%; Score 1333.8; DB 15; Length 4009;            |      |  |      |
| Best Local Similarity   99.6%; Pred. No. 0;                                |      |  |      |
| Matches 1348; Conservative   0; Mismatches   2; Indels   3; Gaps   1;      |      |  |      |
| Qy   | 34   | CGGCCGGGTTCCGAGCGAGAGGCTGATGAGTGGCCGGCGGGCTCTGGGGCTGTGG      | 93   |
| Dd   | 7    | CGCCGGGGCTCCGAGCGAGAGGCTGATGAGTGGCCGGCGGGCTCTGGGGCTGTGG      | 66   |
| Qy   | 94   | GCGCTGCTGCTCTCGCCGGCGGGCGGGGGCGGGGGCGGGGG--CGGGCTTACGGAACT   | 150  |
| Dd   | 67   | GCGCTGCTGCTCTCGCCGGCGGGCGGGGGCGGGGGCGGGGGCGGGGGCTTACGGAACT   | 126  |
| Qy   | 151  | CAGCACCTGTGACAAATTTGAGTGTCTGTGTAAAACTCTGCACAGTAAATYGACA      | 210  |
| Dd   | 127  | CAGCACCTGTGACAAATTTGAGTGTCTGTGTAAAACTCTGCACAGTAAATYGACA      | 186  |
| Qy   | 211  | TGGAATCCACCGAGGAGCCAGCTCAAATTTGATAGTATGATATTTAGTCAATTTGGC    | 270  |
| Dd   | 187  | TGGAATCCACCGAGGAGCCAGCTCAAATTTGATAGTATGATATTTAGTCAATTTGGC    | 246  |
| Qy   | 271  | GACAAACAGATTAAGAAATATGCTCCGAAACTGTGTCTTAATAGAAATCCCCGTGAT    | 330  |
| Dd   | 247  | GACAAACAGATTAAGAAATATGCTCCGAAACTGTGTCTTAATAGAAATCCCCGTGAT    | 306  |
| Qy   | 331  | GAGAGGATTTCTGCAAGTGGGGTCCCAGTGTAGCAACAAATGAGATGAGAGGCTAGC    | 390  |
| Dd   | 307  | GAGAGGATTTCTGCAAGTGGGGTCCCAGTGTAGCAACAAATGAGATGAGAGGCTAGC    | 366  |
| Qy   | 391  | ATTTTGGTTGAAAAATGCATCTCACCCCAGAAAGTATCCTGAGTGTGCTGTGACTGAA   | 450  |
| Dd   | 367  | ATTTTGGTTGAAAAATGCATCTCACCCCAGAAAGTATCCTGAGTGTGCTGTGACTGAG   | 426  |
| Qy   | 451  | CTTCATGCAATTTGGCAACACTTGAGCTACATGAAGTGTCTTGAGCTCCCTGGAAGAT   | 510  |

427 CTTAAATGATTTGGACACACCTGAGCTACATGAAGTCTTGGCTCCCTGGAAGAAAT 486  
486  
511 ACCAGTCCCGACACTATATCTCTACTATTGGGACACAAAGCTGGAAAAATTCAT 570  
570  
487 ACCAGTCCCGACACTATATCTCTACTATTGGGACACAAAGCTGGAAAAATTCAT 546  
546  
571 CAATGTGAAAAACATCTTTAGAGAAAGGCAATATCTTGGTGTCTCTTGATCTGACAAA 630  
630  
547 CAATGTGAAAAACATCTTTAGAGAAAGGCAATATCTTGGTGTCTCTTGATCTGACAAA 606  
606  
631 GTGAAGATTCAGTTTGAACAAACAGTGTCCAAATTAATGTCAAGATTAATGACAGA 690  
690  
607 GTGAAGATTCAGTTTGAACAAACAGTGTCCAAATTAATGTCAAGATTAATGACAGA 666  
666  
691 AAAATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 750  
750  
667 AAAATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 726  
726  
751 CATATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 810  
810  
727 CATATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 786  
786  
811 AATTTATAGCAGATGCTATTTATAGAGTAGAAGTCAATTAACGCAAACTGAGACA 870  
870  
787 AATTTATAGCAGATGCTATTTATAGAGTAGAAGTCAATTAACGCAAACTGAGACA 846  
846  
871 CATATATGTTTCTACGTCACAGAGGCTTAAATGTGAGAAATCCAGATTTGAGAAATGTG 930  
930  
847 CATATATGTTTCTACGTCACAGAGGCTTAAATGTGAGAAATCCAGATTTGAGAAATGTG 906  
906  
931 GAGAAATCATCTTGTTCATGATGCTCCGCTGTCTCTCTGATCTTGAACACAGTCA 990  
990  
907 GAGAAATCATCTTGTTCATGATGCTCCGCTGTCTCTCTGATCTTGAACACAGTCA 966  
966  
991 AATAGAGTCAAAACAAATTAAGTTATGTATGAGATGACAACTCTGAGTAAATGAGC 1050  
1050  
967 AATAGAGTCAAAACAAATTAAGTTATGTATGAGATGACAACTCTGAGTAAATGAGC 1026  
1026  
1051 CAAGAAATGAGTATAGGTAAGAGAGGCAATTCACACTTACATTAACCATGTTCTCAT 1110  
1110  
1027 CAAGAAATGAGTATAGGTAAGAGAGGCAATTCACACTTACATTAACCATGTTCTCAT 1086  
1086  
1111 GTTCAGATCATCTGTCGAGGAGTGAATGATGATCTCTGCTTAAAGGCTCAAG 1170  
1170  
1087 GTTCAGATCATCTGTCGAGGAGTGAATGATGATCTCTGCTTAAAGGCTCAAG 1146  
1146  
1171 AATATTATATTCCTCCCAATTCCTGATCTGCGCAAGATTTTAAAGAAATGTTGAGAC 1230  
1230  
1147 AATATTATATTCCTCCCAATTCCTGATCTGCGCAAGATTTTAAAGAAATGTTGAGAC 1206  
1206  
1231 CAGATATGATGATCTGTCGACTGGAAGAGTGAACATCTATGAGAAACCAAGAGAG 1290  
1290  
1207 CAGATATGATGATCTGTCGACTGGAAGAGTGAACATCTATGAGAAACCAAGAGAG 1266  
1266  
1291 GAAACCGACTCTGAGTGTGATGAGAAACCTGGAAGAAAGCTCTCAGTGTGAGATTA 1350  
1350  
1267 GAAACCGACTCTGAGTGTGATGAGAAACCTGGAAGAAAGCTCTCAGTGTGAGATTA 1326  
1326  
1351 TTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
1383  
1327 TTTATTTTACCTTCACTGTGACCTTGAGAGA 1359  
1359

RESULT 3  
US-11-182-384A-3  
; Sequence 3, Application US/11182384A  
; Publication No. US20060035855A1  
; GENERAL INFORMATION:  
; APPLICANT: Caput, Daniel  
; APPLICANT: Ferrera, Pascual  
; APPLICANT: Laurent, Patrick  
; APPLICANT: Vita, Natalio

FILE REFERENCE: IVD924 US DIV 2  
CURRENT FILING DATE: 2005-07-15  
PRIOR APPLICATION NUMBER: 09/077,817  
PRIOR FILING DATE: 1998-09-14  
PRIOR APPLICATION NUMBER: PCT/FR96/01756  
PRIOR FILING DATE: 1996-11-07  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3  
LENGTH: 4009  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-11-182-384A-3

Query Match 96.4%; Score 133.8; DB 16; Length 4009;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

34 CGGCGGGGTTCCGAGGCGAGAGGCTGCATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 93  
7 CGGCGGGGCTCCGAGGCGAGAGGCTGCATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 66  
94 GCGCTGCTGCTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 150  
67 GCGCTGCTGCTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 126  
151 CAGCACCCTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTGACAGTAAATGAGCA 210  
127 CAGCACCCTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTGACAGTAAATGAGCA 186  
211 TGAATCAACCCGAGGAGGAGCCAGCTCAATTTGATGTCTATGTATTTTATGATTTGGC 270  
187 TGAATCAACCCGAGGAGGAGCCAGCTCAATTTGATGTCTATGTATTTTATGATTTGGC 246  
271 GACAAACAGATTAAGAAATATGCTCCGGAACCTGTGTTCAATAGAAAGTACCCCTGAT 330  
247 GACAAACAGATTAAGAAATATGCTCCGGAACCTGTGTTCAATAGAAAGTACCCCTGAT 306  
331 GAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGACCAATGAGTGAAGAGCTTAGC 390  
307 GAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGACCAATGAGTGAAGAGCTTAGC 366  
391 ATTTGGTGAAGAAATGATCTCAACCCGAGAGGATGCTGTGATCTGTGATCTGAA 450  
367 ATTTGGTGAAGAAATGATCTCAACCCGAGAGGATGCTGTGATCTGTGATCTGAA 426  
451 CTTCAATGCAATTTGGCAACCTGAGCTACATGAAAGTGTCTTGGCTCCGGAAGGAT 510  
427 CTTCAATGCAATTTGGCAACCTGAGCTACATGAAAGTGTCTTGGCTCCGGAAGGAT 486  
511 ACCAGTCCCGACACTATATCTCTACTATTGGGACACAAAGCTGGAAAAATTCAT 570  
487 ACCAGTCCCGACACTATATCTCTACTATTGGGACACAAAGCTGGAAAAATTCAT 546  
571 CAATGTGAAAAACATCTTTAGAGAAAGGCAATATCTTGGTGTCTCTTGATCTGACAAA 630  
547 CAATGTGAAAAACATCTTTAGAGAAAGGCAATATCTTGGTGTCTCTTGATCTGACAAA 606  
631 GTGAAGATTCAGTTTGAACAAACAGTGTCCAAATTAATGTCAAGATTAATGACAGA 690  
607 GTGAAGATTCAGTTTGAACAAACAGTGTCCAAATTAATGTCAAGATTAATGACAGA 666  
691 AAAATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 750  
667 AAAATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 726  
751 CATATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 810  
727 CATATTAACCATCTTCAATATATAGTGTCTTAACTCCGCTGGAACCTGATCTTCA 786  
811 AATTTATAGCAGATGCTATTTATAGAGTAGAAGTCAATTAACGCAAACTGAGACA 870



[illegible]

|    |      |   |      |
|----|------|---|------|
| QY | 151  | CAGCCACCGGACAAATTGAGTGTCTGTGTGAAAACCTGTGACAGTAAATATGAGCA      | 21   |
| Db | 136  | CAGCCACCTGTGACAAATTGAGTGTCTGTGTGAAAACCTGTGACAGTAAATATGAGCA    | 195  |
| QY | 211  | TGGAATCCACCCGAGGAGCCAGCTCAAAATTGTAGTCTAATGGTATTTTATGATATTTGGC | 270  |
| Db | 196  | TGGAATCCACCCGAGGAGCCAGCTCAAAATTGTAGTCTAATGGTATTTTATGATATTTGGC | 255  |
| QY | 271  | GACAAACAAGATAGAAAATAGCTCCGAAAACCTGTCGTAATGAAATACCCCTGAAT      | 330  |
| Db | 256  | GACAAACAAGATAGAAAATAGCTCCGAAAACCTGTCGTAATGAAATACCCCTGAAT      | 315  |
| QY | 331  | GAGAGATTTTGTCTCAAGTGGGGTCCAGAGTACACCAATGAGAAGAGAGGCTGAG       | 390  |
| Db | 316  | GAGAGATTTTGTCTCAAGTGGGGTCCAGAGTACACCAATGAGAAGAGAGGCTGAG       | 375  |
| QY | 391  | ATTTTGTGTGAAAAATGATCTCACCCCGAAGGTGATTCCTGATCTGCTGTGACTGNA     | 450  |
| Db | 376  | ATTTTGTGTGAAAAATGATCTCACCCCGAAGGTGATTCCTGATCTGCTGTGACTGAG     | 435  |
| QY | 451  | CTTCATGCAATTTGGCACAACCTGAGCTACATGAAGTGTCTTGCTCCCTGAGAGAT      | 510  |
| Db | 436  | CTTCATGCAATTTGGCACAACCTGAGCTACATGAAGTGTCTTGCTCCCTGAGAGAT      | 495  |
| QY | 511  | AACGATCCCGACACTAATATATCTATCTATATTGGGACADAAGCTGGAAAAAATTGAT    | 570  |
| Db | 496  | AACGATCCCGACACTAATATATCTATCTATATTGGGACADAAGCTGGAAAAAATTGAT    | 555  |
| QY | 571  | CAATGTGAAAAACATCTTAGAGAGAGGCCAATACTTTGGTTGTCTTGTGATCTGACCAA   | 630  |
| Db | 556  | CAATGTGAAAAACATCTTTAGAGAGGCCAATATCTTTGGTTGTCTTGTGATCTGACCAA   | 615  |
| QY | 631  | GTGAAGATTCAGTTTGAACAACAAGTCCAAATPATGTGTCAAGATPATGACGAGA       | 690  |
| Db | 616  | GTGAAGATTCAGTTTGAACAACAAGTCCAAATPATGTGTCAAGATPATGACGAGA       | 675  |
| QY | 691  | AAATTTAACAATCCCTTCAATATATGTGCTTAACTCCCGGTGAAACCTGATCTCTCA     | 750  |
| Db | 676  | AAATTTAACAATCCCTTCAATATATGTGCTTAACTCCCGGTGAAACCTGATCTCTCA     | 735  |
| QY | 751  | CATATTTAAAAACCTCTCCCTTCCAAATGATACCTATATGTGCAATGGAGAAATCCAG    | 810  |
| Db | 736  | CATATTTAAAAACCTCTCCCTTCCAAATGATACCTATATGTGCAATGGAGAAATCCAG    | 795  |
| QY | 811  | AATTTATTTAGCAGATGCTATATTTTATGAAGTAGAAAGTCAATPAAACGCAAACTGAGCA | 870  |
| Db | 796  | AATTTATTTAGCAGATGCTATATTTTATGAAGTAGAAAGTCAATPAAACGCAAACTGAGCA | 855  |
| QY | 871  | CATATGTTTTCTACGTCCAAAGAGGCTPAAATGTGAAATCCAGAAATTTGAGAGAAATGTG | 930  |
| Db | 856  | CATATGTTTTCTACGTCCAAAGAGGCTPAAATGTGAAATCCAGAAATTTGAGAGAAATGTG | 915  |
| QY | 931  | GAGAAATACATCTTGTTCATGTGCTCCGTGTTCTTCCGTATCTTTGAAACACAGTCAGA   | 990  |
| Db | 916  | GAGAAATACATCTTGTTCATGTGCTCCGTGTTCTTCCGTATCTTTGAAACACAGTCAGA   | 975  |
| QY | 991  | ATAAGAGTCAAAACAAATTAAGTTATGCTATGAGANTGACAACTCTGAGATTAATTGAGC  | 1050 |
| Db | 976  | ATAAGAGTCAAAACAAATTAAGTTATGCTATGAGANTGACAACTCTGAGATTAATTGAGC  | 1035 |
| QY | 1051 | CAAGAAATGATATATAGGTAAAGAACCGCAATTCACACTCTACATPAAACATGTACTATT  | 1110 |
| Db | 1036 | CAAGAAATGATATATAGGTAAAGAACCGCAATTCACACTCTACATPAAACATGTACTATT  | 1095 |
| QY | 1111 | GTTCACAGTCATGTCGAGAGGTGCAATCATAGTACTCCGTGCTTAACTTAAAGAGCTCAAG | 1170 |
| Db | 1096 | GTTCACAGTCATGTCGAGAGGTGCAATCATAGTACTCCGTGCTTAACTTAAAGAGCTCAAG | 1155 |
| QY | 1171 | ATTATTTATATTCCTCCCAATTCCTGATCTGTGGCAAGATTTTAAAGAAATGTTTGGAGAC | 1230 |
| Db | 1156 | ATTATTTATATTCCTCCCAATTCCTGATCTGTGGCAAGATTTTAAAGAAATGTTTGGAGAC | 1215 |







```

; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 3856
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y10659
US-09-880-107-3856

Query Match          96.4%; Score 1333.8; DB 3; Length 4039;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 34 CGGCCGGGTTCCGAGCGAGAGGCTGATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 93
    |||||
DB 17 CGGCCGGGCTCCGAGCGAGAGGCTGATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 76
    |||||

QY 94 GGCCTGCTGCTGCGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 150
    |||||
DB 77 GGCCTGCTGCTGCGCGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 136
    |||||

QY 151 CAGCCACCTGTGACCAATTTGAGTGTCTGTTGAAACCTGTGACAGATTAATGAGCA 210
    |||||
DB 137 CAGCCACCTGTGACCAATTTGAGTGTCTGTTGAAACCTGTGACAGATTAATGAGCA 196
    |||||

QY 211 TGAATTCACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 270
    |||||
DB 197 TGAATTCACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 256
    |||||

QY 271 GACAAACAGATTAAGAAATAGCTCCGAGAACTGTGTTCAATGAGTACCCTGAT 330
    |||||
DB 257 GACAAACAGATTAAGAAATAGCTCCGAGAACTGTGTTCAATGAGTACCCTGAT 316
    |||||

QY 331 GAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGAGTGAAGAGCTAGC 390
    |||||
DB 317 GAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGAGTGAAGAGCTAGC 376
    |||||

QY 391 ATTTGGTTGAAAAATGATCTCAACCCGAGAAAGTATCTGTGCTGTGACTGAA 450
    |||||
DB 377 ATTTGGTTGAAAAATGATCTCAACCCGAGAAAGTATCTGTGCTGTGACTGAA 436
    |||||

QY 451 CTTCATGCAATTTGGCAACACTGAGTCAATGAGTGTCTGTGCTCTGAGAGGAT 510
    |||||
DB 437 CTTCATGCAATTTGGCAACACTGAGTCAATGAGTGTCTGTGCTCTGAGAGGAT 496
    |||||

QY 511 ACCAGTCCGAGCACTAATCTACTCTACTATTGGGACAGAAAGCTGGAATAATTCAT 570
    |||||
DB 497 ACCAGTCCGAGCACTAATCTACTCTACTATTGGGACAGAAAGCTGGAATAATTCAT 556
    |||||

QY 571 CAATGTGAAAAATCTTTAGAGAAAGGCAATACCTTTGTTGCTTTGATCTGACCAA 630
    |||||
DB 557 CAATGTGAAAAATCTTTAGAGAAAGGCAATACCTTTGTTGCTTTGATCTGACCAA 616
    |||||

QY 631 GTGAAGATTCAGTTTGAACAACAAGTGTCCAAATAATGCAAGATTAATGACGA 690
    |||||
DB 617 GTGAAGATTCAGTTTGAACAACAAGTGTCCAAATAATGCAAGATTAATGACGA 676
    |||||

QY 691 AAAATTAACCACTCTTCAATATAGTCCCTTAATCCGCTGGAACCTGATCTCTCA 750
    |||||
DB 677 AAAATTAACCACTCTTCAATATAGTCCCTTAACTCCGCTGGAACCTGATCTCTCA 726
    |||||

QY 751 CATATTAAAAACCTCTCTTCCACAATGATGACCTATATGCAATGGAATTCACAG 810
    |||||
DB 737 CATATTAAAAACCTCTCTTCCACAATGATGACCTATATGCAATGGAATTCACAG 796
    |||||

QY 811 AATTTTATTTGAGATGCTTATTTTATGAGTGAAGTCAATAACGCAAACTGAGACA 870
    |||||
DB 797 AATTTTATTTGAGATGCTTATTTTATGAGTGAAGTCAATAACGCAAACTGAGACA 856
    |||||
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QY 871 CATATGTTTCTACGTCCAAAGGCTAAATGTGAGAAATCAGAAATTTGAGAAATGTG 930
    |||||
DB 857 CATATGTTTCTACGTCCAAAGGCTAAATGTGAGAAATCAGAAATTTGAGAAATGTG 916
    |||||

QY 931 GAGAAATCATCTGTTTCAATGCTCCCTGTGTCTTCTGATTAATTTGAACACAGTCA 990
    |||||
DB 917 GAGAAATCATCTGTTTCAATGCTCCCTGTGTCTTCTGATTAATTTGAACACAGTCA 976
    |||||

QY 991 ATAGAGTCAAAACAAATTAATGTTATGCTATGAGAGTACAACACTGAGTAATTTGAGC 1050
    |||||
DB 977 ATAGAGTCAAAACAAATTAATGTTATGCTATGAGAGTACAACACTGAGTAATTTGAGC 1036
    |||||

QY 1051 CAAGAAATGAGTATAGGTAAGAAAGCGCAATTCACACTTCAATACATGTTACTCAT 1110
    |||||
DB 1037 CAAGAAATGAGTATAGGTAAGAAAGCGCAATTCACACTTCAATACATGTTACTCAT 1096
    |||||

QY 1111 GTTCAGTCAATCGTGGAGGTGCAATGATGATCTCTGCTTTAATTAAGAGCTCAAG 1170
    |||||
DB 1097 GTTCAGTCAATCGTGGAGGTGCAATGATGATCTCTGCTTTAATTAAGAGCTCAAG 1156
    |||||

QY 1171 ATATTATATTTCCCTCCAAATTCCTGATCTGTGCAAGATTTTAAAGAAATGTTGAGAC 1230
    |||||
DB 1157 ATATTATATTTCCCTCCAAATTCCTGATCTGTGCAAGATTTTAAAGAAATGTTGAGAC 1216
    |||||

QY 1231 CAGAAATGATATCTGCACTGGAAGAGTACATGAGAGCAATGAGCAAAACCAAGAG 1290
    |||||
DB 1217 CAGAAATGATATCTGCACTGGAAGAGTACATGAGAGCAATGAGCAAAACCAAGAG 1276
    |||||

QY 1291 GAAACGAGCTGTAGTGTGATGATGAAAGCTGGAAGAGCTCTGAGTGAAGATTA 1350
    |||||
DB 1277 GAAACGAGCTGTAGTGTGATGATGAAAGCTGGAAGAGCTCTGAGTGAAGATTA 1336
    |||||

QY 1351 TTTATTTTACCTTCACTGATGACCTTGAAGA 1383
    |||||
DB 1337 TTTATTTTACCTTCACTGATGACCTTGAAGA 1369
    |||||

RESULT 8
US-10-172-118-633
; Sequence 633, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 633
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001560
; DATABASE ENTRY DATE: 2001-06-18
; US-10-172-118-633

Query Match          96.4%; Score 1333.8; DB 7; Length 4039;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 34 CGGCCGGGTTCCGAGCGAGAGGCTGATGAGTGGCCGGCGGCTCTGCGGGCTGTGG 93
    |||||
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|   |      |   |      |
|---|------|---|------|
| OY  | 811  | AAATTATATAGCAGATGCGCTATTTTATAGATGAGAAAGTCAATPAACGCCAACTGAGACA   | 870  |
| Db  | 834  | AAATTATATAGCAGATGCGCTATTTTATAGATGAGAAAGTCAATPAACGCCAACTGAGACA   | 893  |
| OY  | 871  | CATPAATGTTTTCTACGTCGAAGGCTAAATGTGAAATCCAGAAATTTGAGAGAAATGTG     | 930  |
| Db  | 894  | CATPAATGTTTTCTACGTCGAAGGCTAAATGTGAAATCCAGAAATTTGAGAGAAATGTG     | 953  |
| OY  | 931  | GAGAAATACATCTTTGTTTCATGTCGCTCGTGTGTTCTTCTGATACCTTTGAACACAGTCKGA | 990  |
| Db  | 954  | GAGAAATACATCTTTGTTTCATGTCGCTCGTGTGTTCTTCTGATACCTTTGAACACAGTCKGA | 1012 |
| OY  | 991  | ATPAAGAGTCAAAAACAAATTAAGTTATGCTATGAGATGACAAACCTGGAGTAATTTGAGAC  | 1050 |
| Db  | 1014 | ATPAAGAGTCAAAAACAAATTAAGTTATGCTATGAGATGACAAACCTGGAGTAATTTGAGAC  | 1073 |
| OY  | 1051 | CAAGAAATGAGATATAGTATGAGAAAGGCGCAATTCACACTCTACATPAACCATGTTACTAAT | 1110 |
| Db  | 1074 | CAAGAAATGAGATATAGTATGAGAAAGGCGCAATTCACACTCTACATPAACCATGTTACTAAT | 1133 |
| OY  | 1111 | GTTCCAGTCATCTGTGCGAGGTGCATCATATGATCTCTGCTTTACTTAAAAAGGCTCAAG    | 1170 |
| Db  | 1134 | GTTCCAGTCATCTGTGCGAGGTGCATCATATGATCTCTGCTTTACTTAAAAAGGCTCAAG    | 1193 |
| OY  | 1171 | ATTATTTAATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTTTAAAGAAATGTTTGGAGAC | 1230 |
| Db  | 1194 | ATTATTTAATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTTTAAAGAAATGTTTGGAGAC | 1253 |
| OY  | 1231 | CAGAAATGATGATACTCTGCACTGGAAGATGACGATCTATGAGAACCAACCAAGGAG       | 1290 |
| Db  | 1254 | CAGAAATGATGATACTCTGCACTGGAAGATGACGATCTATGAGAACCAACCAAGGAG       | 1313 |
| OY  | 1291 | GAAACCGACCTGTGATGTCGTGATGAAAAAAGCTGAAAGAAAGCTCTCAAGTATGAGATPA   | 1350 |
| Db  | 1314 | GAAACCGACCTGTGATGTCGTGATGAAAAAAGCTGAAAGAAAGCTCTCAAGTATGAGATPA   | 1373 |
| OY  | 1351 | TTTATTTTAACTTCACTGTGCACTTGGAGAGA                                | 1383 |
| Db  | 1374 | TTTATTTTAACTTCACTGTGCACTTGGAGAGA                                | 1406 |
| RESULT 12                                   |      |   |      |
| US-10-278-698-6                             |      |   |      |
| : Sequence 6, Application US/10278698       |      |   |      |
| : Publication No. US20050037344A1           |      |   |      |
| : GENERAL INFORMATION:                      |      |   |      |
| : APPLICANT: Patnarray GmbH                 |      |   |      |
| : APPLICANT: Stuhlmüller, Bruno             |      |   |      |
| : TITLE OF INVENTION: Nucleic Acid Array    |      |   |      |
| : FILE REFERENCE: 030027US                  |      |   |      |
| : CURRENT APPLICATION NUMBER: US/10/278,698 |      |   |      |
| : NUMBER OF SEQ ID NOS: 1050                |      |   |      |
| : SOFTWARE: PatentIn version 3.2            |      |   |      |
| : SEQ ID NO 6                               |      |   |      |
| : LENGTH: 1572                              |      |   |      |
| : TYPE: DNA                                 |      |   |      |
| : ORGANISM: Homo sapiens                    |      |   |      |
| : US-10-278-698-6                           |      |   |      |

|                       |              |              |              |             |
|-----------------------|--------------|--------------|--------------|-------------|
| Query Match           | 96.2%        | Score 1330.6 | DB 9         | Length 1572 |
| Best Local Similarity | 99.5%        | Pred. No. 0  |              |             |
| Matches 1346          | Conservative | 0            | Mismatches 4 | Indels 3    |
|                       |              |              | Gaps         | 1           |

  

|    |   |     |
|----|---|-----|
| QY | CGGCGGGTTCCGAGCGAGCGCTGCTGTGAGATGCCCCGCGGCTCTGGGGCTGTGG   | 93  |
|    |   |     |
| DB | CGGCGGGGCTCGAGCGAGAGCGCTGCTGTGAGATGCCCCGCGGCTCTGGGGCTGTGG | 117 |
|    |   |     |
| QY | CGCGTGTGCTCTGTGGCGCGCGCGGGGCGGGGG--CGCGCTTACGGAACCT       | 150 |
|    |   |     |
| DB | GGCGTGTGCTCTGTGGCGCGCGCGGGGCGGGGGCGCGCGCTTACGGAACCT       | 177 |
|    |   |     |

|    |      |   |      |
|----|------|---|------|
| QY | 151  | CAGCCACCTGTGACAAATTTTGAGTGTCTCTGTGAAAACCTCTGCACAGTAATATGACAC  | 210  |
| Db | 178  | CAGCCACCTGTGACAAATTTTGAGTGTCTCTGTGAAAACCTCTGCACAGTAATATGACAC  | 237  |
| QY | 211  | TGSAATCCACCCGAGGGAGCAGCTCAATTTGTAGTCTATGATATTTTAGTCATTTGGC    | 270  |
| Db | 238  | TGSAATCCACCCGAGGGAGCAGCTCAATTTGTAGTCTATGATATTTTAGTCATTTGGC    | 297  |
| QY | 271  | GACAAACAAGTAAAGAAAATAGCTTCGGAAACTGTCGTTCAATTGAAATACCCCTGAAT   | 330  |
| Db | 298  | GACAAACAAGTAAAGAAAATAGCTTCGGAAACTGTCGTTCAATTGAAATACCCCTGAAT   | 357  |
| QY | 331  | GAGAGGATTTGTCTGCAAGTGGGGGTCCAGAGTAGCAACAATGAGAGTGAAGAGCTGAC   | 390  |
| Db | 358  | GAGAGGATTTGTCTGCAAGTGGGGGTCCAGAGTAGCAACAATGAGAGTGAAGAGCTGAC   | 417  |
| QY | 391  | ATTTTGGTTGAAAAATGCACTCAACCCAGAAAGTGATCCTGAGTCTGCTGTGACTGA     | 450  |
| Db | 418  | ATTTTGGTTGAAAAATGCACTCAACCCAGAAAGTGATCCTGAGTCTGCTGTGATGAG     | 477  |
| QY | 451  | CTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAAGTGTCTTGGCTCCCTGGAAAGAT | 510  |
| Db | 478  | CTTCAATGCAATTTGGCAACAACCTGAGCTACATGAAAGTGTCTTGGCTCCCTGGAAAGAT | 537  |
| QY | 511  | ACCAGTCCGACACTAACCTACTCTCTACTATTGGACAGAAAGCCTGGAAAAAATTCAT    | 570  |
| Db | 538  | ACCAGTCCGACACTAACCTACTCTCTACTATTGGACAGAAAGCCTGGAAAAAATTCAT    | 597  |
| QY | 571  | CAATGTGAAAACATCTTTAGAGAAAGGCCAATPACTTTGGTGTCTCTTGATCTGACAA    | 630  |
| Db | 598  | CAATGTGAAAACATCTTTAGAGAAAGGCCAATPACTTTGGTGTCTCTTGATCTGACAA    | 657  |
| QY | 631  | GTGAAGAGTTCCAGTTTGAACAACAGCTGTCCAAATTAATGTCAAAGATPAAATGACAGA  | 690  |
| Db | 658  | GTGAAGAGTTCCAGTTTGAACAACAGCTGTCCAAATTAATGTCAAAGATPAAATGACAGA  | 717  |
| QY | 691  | AAAATTAAACCATCTTCAATATATAGTGCCTTAACTTCCGATGTGAAACCTGATCCTCA   | 750  |
| Db | 718  | AAAATTAAACCATCTTCAATATATAGTGCCTTAACTTCCGATGTGAAACCTGATCCTCA   | 777  |
| QY | 751  | CATATTTAAAAACCTCTCTCTTCCACATATATGACTATATGTGCAATGSGAATTCACAG   | 810  |
| Db | 778  | CATATTTAAAAACCTCTCTCTTCCACATATATGACTATATGTGCAATGSGAATTCACAG   | 837  |
| QY | 811  | AATTTTATTTAGCAGATGCTATTTTATGAATAGAGTCAATTAACAGCAAACTGAGACA    | 870  |
| Db | 838  | AATTTTATTTAGCAGATGCTATTTTATGAATAGAGTCAATTAACAGCAAACTGAGACA    | 897  |
| QY | 871  | CATAATGTTTCTACGTCCAAAGAGCTTAATGTGAGAAATCCAGAAATTTGAGAAATGTG   | 930  |
| Db | 898  | CATAATGTTTCTACGTCCAAAGAGCTTAATGTGAGAAATCCAGAAATTTGAGAAATGTG   | 957  |
| QY | 931  | GAGAAATCATTTGTTCATATGTCCTCCGAGGTCTTCTCTGATPACTTTGAACACAGCTGAG | 990  |
| Db | 958  | GAGAAATCATTTGTTCATATGTCCTCCGAGGTCTTCTCTGATPACTTTGAACACAGCTGAG | 1011 |
| QY | 991  | ATAAGAGTCAAAACAAATAAGTTATGCTATGAGANTGACAAACTCTGAGATTAATTGAGC  | 1056 |
| Db | 1018 | ATAAGAGTCAAAACAAATAAGTTATGCTATGAGANTGACAAACTCTGAGATTAATTGAGC  | 1077 |
| QY | 1051 | CAAAATAATGATATATGTTAAGAAAGCGCAATTCACACTTACATTAACCATGTCTACTTT  | 1118 |
| Db | 1078 | CAAAATAATGATATATGTTAAGAAAGCGCAATTCACACTTACATTAACCATGTCTACTTT  | 1137 |
| QY | 1111 | GTTCACAGTCATCGTCGAGGTGCATCATATAGTACTCTCTGCTTTACCTTAAAGGCTCAAG | 1170 |
| Db | 1138 | GTTCACAGTCATCGTCGAGGTGCATCATATAGTACTCTCTGCTTTACCTTAAAGGCTCAAG | 1197 |
| QY | 1171 | ATTATTTATTTCCCTCCAAATTCCTGATCTCGGCAAGATTTTAAAGAAATGTTTGAGAC   | 1230 |
| Db | 1198 | ATTATTTATTTCCCTCCAAATTCCTGATCTCGGCAAGATTTTAAAGAAATGTTTGAGAC   | 1257 |





PRIOR APPLICATION NUMBER: AU 2003900437  
PRIOR FILING DATE: 2003-02-03  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn Version 3.1  
SEQ ID NO 3  
LENGTH: 1284  
TYPE: DNA  
ORGANISM: human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)-(1284)  
OTHER INFORMATION:  
US-10-850-270-3

Query Match 91.5%; Score 1264.8; DB 10; Length 1284;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1279; Conservative 0; Mismatches 2; Indels 3; Gaps 1;  
QY 61 ATGAGAGTGGCGCGCGCGCTCTGCGGGCTGTGGCGCTGCTCTGCGCGCGCGCGG 120  
DB 1 ATGAGAGTGGCGCGCGCGCTCTGCGGGCTGTGGCGCTGCTCTGCGCGCGCGCGG 60  
QY 121 GGG 177  
DB 61 GGG 120  
QY 178 TCTGTGAAAACTCTGCAAGTAATATGAGCATGGAATCACCCGAGGAGCGAGTCA 237  
DB 121 TCTGTGAAAACTCTGCAAGTAATATGAGCATGGAATCACCCGAGGAGCGAGTCA 180  
QY 238 AATTGTAGTCTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTT 297  
DB 181 AATTGTAGTCTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTATGATTT 240  
QY 298 GAAACTCTGCTCTCATAGAGTAACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCC 357  
DB 241 GAAACTCTGCTCTCATAGAGTAACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCC 300  
QY 358 CAGGTAGACCAATGAGTGAAGAGCCCTGATTTTGTGAAAAATGCACTCAAGCC 417  
DB 301 CAGGTAGACCAATGAGTGAAGAGCCCTGATTTTGTGAAAAATGCACTCAAGCC 360  
QY 418 CCAGAGGTGATCTGATGCTGCTGATGAACTTCAATGCAATTTGGCAAACTGAGC 477  
DB 361 CCAGAGGTGATCTGATGCTGCTGATGAACTTCAATGCAATTTGGCAAACTGAGC 420  
QY 478 TACATGAGTGTCTTGGCTCCCTGAGAGATTAACGATCCGACACTAACTATCTC 537  
DB 421 TACATGAGTGTCTTGGCTCCCTGAGAGATTAACGATCCGACACTAACTATCTC 480  
QY 538 TACTATTGGACAGAGCCCTGAAAAATTCATCATATGCAAAATCTTTAAGAAAGC 597  
DB 481 TACTATTGGACAGAGCCCTGAAAAATTCATCATATGCAAAATCTTTAAGAAAGC 540  
QY 598 CAATATCTTGGTGTCTTGGTCTGACCAAGTGAAGATTCAGTTTGAACAAC 657  
DB 541 CAATATCTTGGTGTCTTGGTCTGACCAAGTGAAGATTCAGTTTGAACAAC 600  
QY 658 AGTGTCCAAATAATGTCAGAGTAATGCAAGAAAAATTAACATCTTCAATATAGT 717  
DB 601 AGTGTCCAAATAATGTCAGAGTAATGCAAGAAAAATTAACATCTTCAATATAGT 660  
QY 718 CCTTAACTCCCGTGTGAAGCTGATCTCCCAATTTAAAAAATCTTCTCCCAAT 777  
DB 661 CCTTAACTCCCGTGTGAAGCTGATCTCCCAATTTAAAAAATCTTCTCCCAAT 720  
QY 778 GATGACCTATATGTCAGATGGAGATTCACAGATTTTATGAGAGATCTATTTAT 837  
DB 721 GATGACCTATATGTCAGATGGAGATTCACAGATTTTATGAGAGATCTATTTAT 780  
QY 838 GAAATGAAAGTCAATTAACGCAAACTGAGACATATATTTTCTTCAAGAGGCT 897  
DB 781 GAAATGAAAGTCAATTAACGCAAACTGAGACATATATTTTCTTCAAGAGGCT 840

QY 898 AAATGTGAGATCCAGATTTTGAAGAAATGTGAGAAATCATCTTGTTCATGTCCT 957  
DB 841 AAATGTGAGATCCAGATTTTGAAGAAATGTGAGAAATCATCTTGTTCATGTCCT 900  
QY 958 GGTGTCTTCTGATCTTGTGAACACAGTCAAGTAATAGTCAAAATTAAGTTATGC 1017  
DB 901 GGTGTCTTCTGATCTTGTGAACACAGTCAAGTAATAGTCAAAATTAAGTTATGC 960  
QY 1018 TATGAGATGACAACTCTGAGAAATTTGAGCCAAATTAAGTATAGTAAGAACGC 1077  
DB 961 TATGAGATGACAACTCTGAGAAATTTGAGCCAAATTAAGTATAGTAAGAACGC 1020  
QY 1078 AATTCACACTCTACATTAACATATGTTCTGATGTCAGTCAATGTCAGGAGCAATC 1137  
DB 1021 AATTCACACTCTACATTAACATATGTTCTGATGTCAGTCAATGTCAGGAGCAATC 1080  
QY 1138 ATAGTACTCTGCTTAACTTAAAGGCTCAAGTATATATTTCCCTCAATTCCTGAT 1197  
DB 1081 ATAGTACTCTGCTTAACTTAAAGGCTCAAGTATATATTTCCCTCAATTCCTGAT 1140  
QY 1198 CTTGGCAAGTTTAAAGAAATGTTGGAGACCAATGATGATCTTGCATGAGAG 1257  
DB 1141 CTTGGCAAGTTTAAAGAAATGTTGGAGACCAATGATGATGATCTTGCATGAGAG 1200  
QY 1258 AAGTACGACATCTATGAGAGCAAAACCAAGAGGAAACGACTGTGATGCTGATGAA 1317  
DB 1201 AAGTACGACATCTATGAGAGCAAAACCAAGAGGAAACGACTGTGATGCTGATGAA 1260  
QY 1318 AACCTGAGAAAGCTCTCAAGTGA 1341  
DB 1261 AACCTGAGAAAGCTCTCAAGTGA 1284

RESULT 15  
US-09-822-846-109  
Sequence 109, Application US/09822846  
Publication No. US20030027139A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
APPLICANT: McCoy, John M.  
APPLICANT: Lavallee, Edward R.  
APPLICANT: Collins-Racie, Lisa A.  
APPLICANT: Evans, Cheryl  
APPLICANT: Merberg, David  
APPLICANT: Treacy, Maurice  
APPLICANT: Agostino, Michael J.  
APPLICANT: Steininger II, Robert J.  
APPLICANT: Bowman, Michael R.  
APPLICANT: Spaulding, Vikki  
APPLICANT: Wong, Gordon G.  
APPLICANT: Clark, Hilary  
APPLICANT: Fehchel, Kim  
APPLICANT: Howes, Steven H.  
APPLICANT: Resnick, Richard J.  
APPLICANT: Gulukota, Kamalakar  
APPLICANT: Graham, James R.  
APPLICANT: Genetics Institute, Inc.  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS  
FILE REFERENCE: GIN 6400  
CURRENT APPLICATION NUMBER: US/09/822,846  
PRIORITY FILING DATE: 2001-03-29  
PRIOR APPLICATION NUMBER: 60/195,605  
PRIORITY FILING DATE: 2000-04-06  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 109  
LENGTH: 3880  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-822-846-109  
Query Match 89.5%; Score 1238.4; DB 3; Length 3880;



Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

144 GGAATCTGACCACTGCTGACAAATTTGAGTGTCTGTTGAAACCTCTGCACTAAT 203  
Db 2 GGAATCTGACCACTGCTGACAAATTTGAGTGTCTGTTGAAACCTCTGCACTAAT 61  
QY 204 ATGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTGATCTATGATATTGTGCA 263  
Db 62 ATGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTGATCTATGATATTGTGCA 121  
QY 264 TTTTGGCGCAAAACAAGATAGAAAAATAGCTCCGAAACTGTCGTTCAATAGAGTAC 323  
Db 122 TTTTGGCGCAAAACAAGATAGAAAAATAGCTCCGAAACTGTCGTTCAATAGAGTAC 181  
QY 324 CCTGATGAGAGATTTGCTGCAAGTGGGTCCAGTGTAGACCAATAGAGTAGAA 383  
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Job time : 1705 secs

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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:18:40 ; Search time 210 Seconds  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 844069 seqs, 650066433 residues

Total number of hits satisfying chosen parameters: 1668138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID                    | Description        |
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| 1          | 1333.8 | 96.4        | 2139   | US-11-266-748A-25722  | Sequence 25722, A  |
| 2          | 1333.8 | 96.4        | 4006   | US-11-266-748A-56241  | Sequence 56241, A  |
| 3          | 1011   | 73.1        | 2741   | US-11-266-748A-185183 | Sequence 185183, A |
| 4          | 978.2  | 70.7        | 1016   | US-11-266-748A-54658  | Sequence 54658, A  |
| 5          | 972.4  | 70.3        | 975    | US-11-266-748A-192679 | Sequence 192679, A |
| 6          | 972.4  | 70.3        | 975    | US-11-266-748A-226550 | Sequence 226550, A |
| 7          | 927.6  | 67.1        | 1294   | US-11-266-748A-73628  | Sequence 73628, A  |
| 8          | 927.6  | 67.1        | 1294   | US-11-266-748A-107924 | Sequence 107924, A |
| 9          | 927.6  | 67.1        | 1294   | US-11-266-748A-126439 | Sequence 126439, A |
| 10         | 601    | 43.5        | 902    | US-11-266-748A-54614  | Sequence 54614, A  |
| 11         | 334.4  | 24.2        | 1297   | US-11-266-748A-73627  | Sequence 73627, A  |
| 12         | 334.4  | 24.2        | 1297   | US-11-266-748A-107923 | Sequence 107923, A |
| 13         | 334.4  | 24.2        | 1297   | US-11-266-748A-126438 | Sequence 126438, A |
| 14         | 63     | 4.6         | 583    | US-11-266-748A-51095  | Sequence 51095, A  |
| 15         | 44.6   | 3.2         | 2566   | US-11-266-748A-26705  | Sequence 26705, A  |
| 16         | 41.8   | 3.0         | 642    | US-11-266-748A-219120 | Sequence 219120, A |
| 17         | 41.4   | 3.0         | 1337   | US-10-449-902-2338    | Sequence 2338, Ap  |
| 18         | 41.4   | 3.0         | 1377   | US-10-449-902-21352   | Sequence 21352, A  |
| 19         | 41.4   | 3.0         | 152331 | US-11-175-714-86      | Sequence 86, Appl  |
| 20         | 41.2   | 3.0         | 4620   | US-11-266-748A-30060  | Sequence 30060, A  |
| 21         | 41.2   | 3.0         | 4620   | US-11-266-748A-27561  | Sequence 27561, A  |
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| 28 | 39.6 | 2.9 | 9223   | US-10-449-902-2516    | Sequence 2516, Ap  |
| 29 | 39.6 | 2.9 | 4563   | US-10-196-749-311     | Sequence 311, App  |
| 30 | 39.4 | 2.8 | 1211   | US-11-174-307B-3379   | Sequence 3379, Ap  |
| 31 | 39.4 | 2.8 | 1426   | US-11-218-305-16740   | Sequence 16740, A  |
| 32 | 39.4 | 2.8 | 1687   | US-10-449-902-20855   | Sequence 20855, A  |
| 33 | 39.4 | 2.8 | 1948   | US-10-449-902-2790    | Sequence 2790, Ap  |
| 34 | 38.4 | 2.8 | 1146   | US-11-266-748A-366840 | Sequence 366840, A |
| 35 | 38.4 | 2.8 | 1146   | US-11-266-748A-388660 | Sequence 388660, A |
| 36 | 38.4 | 2.8 | 1146   | US-11-266-748A-450219 | Sequence 450219, A |
| 37 | 38.4 | 2.8 | 2472   | US-11-266-748A-329032 | Sequence 29032, A  |
| 38 | 38.4 | 2.8 | 3913   | US-11-266-748A-29031  | Sequence 29031, A  |
| 39 | 38.2 | 2.8 | 148828 | US-11-266-748A-24893  | Sequence 24893, A  |
| 40 | 38   | 2.7 | 1507   | US-10-449-902-11785   | Sequence 11785, A  |
| 41 | 37.8 | 2.7 | 1817   | US-10-449-902-20981   | Sequence 20981, A  |
| 42 | 37.8 | 2.7 | 3279   | US-11-266-748A-32299  | Sequence 32299, A  |
| 43 | 37.6 | 2.7 | 1152   | US-10-449-902-14304   | Sequence 14304, A  |
| 44 | 37.6 | 2.7 | 1597   | US-10-449-902-12119   | Sequence 12119, A  |
| 45 | 37.4 | 2.7 | 1000   | US-11-266-748A-294949 | Sequence 294949, A |

## ALIGNMENTS

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RESULT 1
US-11-266-748A-25722
; Sequence 25722, Application US/11266748A
; Publication No. US2006013463A1
; GENERAL INFORMATION:
; APPLICANT: Hartkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE OF INVENTION: Methods of using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25722
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-25722

Query Match 96.4%; Score 1333.8; DB 8; Length 2139;
Best Local Similarity Pred. No. 0;
Matches 1348; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
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; Publication No. US2006013463A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR APPLICATION NUMBER: EP 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR APPLICATION NUMBER: EP 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR FILING DATE: 2004-11-03  
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; PRIOR FILING DATE: 2005-03-14  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR FILING DATE: 2005-07-18  
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Sequence 54658, Application US/11266748A  
Publication No. US20060134663A1  
GENERAL INFORMATION:  
APPLICANT: Harkin, Paul  
APPLICANT: Johnson, Patrick  
APPLICANT: Mulligan, Karl  
TITLE OF INVENTION: Transcriptome Microarray Technology and  
FILE REFERENCE: 55815-0102 (319189)  
CURRENT APPLICATION NUMBER: US/11/266, 748A  
CURRENT FILING DATE: 2005-11-03  
PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105483.4  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105507.0  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105484.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662,276

QY PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
QY PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 48396  
QY SOFTWARE: Patent version 3.3  
SEQ ID NO 54658  
LENGTH: 1016  
QY TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (60)..(60)  
QY OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-54658

Query Match 70.7%; Score 978.2; DB 8; Length 1016;  
Best Local Similarity 98.1%; Pred. No. 8.8e-280;  
Matches 997; Conservative 3; Mismatches 12; Indels 4; Gaps 1;

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QY 237 AAATGTAGTCTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 296  
Db 181 AAATGTAGTCTATGATTTTATGATTTTATGATTTTATGATTTTATGATTTTAT 240  
QY 297 GGAATCTCGTCTTCAATGAGTACCTCTGAAATGAGAGATTTGCTGAATGGGCTC 336  
Db 241 GGAATCTCGTCTTCAATGAGTACCTCTGAAATGAGAGATTTGCTGAATGGGCTC 300  
QY 357 CCAGTATGAGCAACCAAGAGAGTGAAGGCTTACATTTTGTGAAATGATCTCAC 416  
Db 301 CCAGTATGAGCAACCAAGAGAGTGAAGGCTTACATTTTGTGAAATGATCTCAC 360  
QY 417 CCCAGAGGTGATCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476  
Db 361 CCCAGAGGTGATCTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
QY 477 CTACATGAGTGTCTTGGCTCCCTGAAAGAAATACAGTCCGACACTATATCTCT 536  
Db 421 CTACATGAGTGTCTTGGCTCCCTGAAAGAAATACAGTCCGACACTATATCTCT 480  
QY 537 CTACTATGAGCAAGAGGCTGGAAGAAATTCATCAATGAGAAACATCTTTGAGAGG 596  
Db 481 CTACTATGAGCAAGAGGCTGGAAGAAATTCATCAATGAGAAACATCTTTGAGAGG 540  
QY 597 CCAATCTTGTGTTGTTCTCTTGTATCTGACCAAGTGAAGATTCAGTTTGAACACA 656  
Db 541 CCAATCTTGTGTTGTTCTCTTGTATCTGACCAAGTGAAGATTCAGTTTGAACACA 600  
QY 657 CAGTGTCCAAATATATGATGAGAGATCCAGATTTTAAACATCTCTCAATATAGT 716  
Db 601 CAGTGTCCAAATATATGATGAGAGATCCAGATTTTAAACATCTCTCAATATAGT 660  
QY 717 GCCTTAACTTCCCGGTGAGAAACCTATCTCCACATTTAAACCTCTCTTCCACAA 736  
Db 661 GCCTTAACTTCCCGGTGAGAAACCTATCTCCACATTTAAACCTCTCTTCCACAA 720  
QY 777 TGATGACCTATATGATGAGAGATCCAGATTTTAAATGAGAGATGCTATTTTA 836  
Db 721 TGATGACCTATATGATGAGAGATCCAGATTTTAAATGAGAGATGCTATTTTA 780  
QY 837 TGAAGTGAAGATCAATTAACGCAACCTGAGACATTAATGTTTCTACGCTCAAGAGC 896

Db 781 TGAAGTAGAAGTCAATTAACACCAACTGAGACACATTAATGTTTTCTACGTCACAGAGGC 840  
 Qy 897 TAAATGTAGAAATCCAGAAATTTGAGAGAAATGTGAGAAATACATCTTGTTTCATGTCCTC 956  
 Db 841 TAAATGTAGAAATCCAGAAATTTGAGAGAAATGTGAGAAATACATCTTGTTTCATGTCCTC 900  
 Qy 957 TGTGTTCTTCTGATATCTTTGAAACAGTCAGAAATAGAGTCAAAACAAATTAAGTTATG 1016  
 Db 901 TGTGTTCTTCTGATATCTTTGAAACAGTCAGAAATAGAGTCAAAACAAATTAAGTTATG 960  
 Qy 1017 CTATGAGATGACAACTCTGAGTAAATTTGAGCCCAAGAAATGATAGTTAGTAAGA 1072  
 Db 961 CTATGAGATGACAACTCTGAGTAAATTTGAGCCCAAGAAATGATAGTTAGTTAGTAAGA 1016

## RESULT 5

US-11-266-748A-192679  
 ; Sequence 192679, Application US/11266748A  
 ; Publication No. US20060134663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harkin, Paul  
 ; APPLICANT: Johnston, Patrick  
 ; APPLICANT: Mulligan, Karl  
 ; TITLE OF INVENTION: Transcription Microarray Technology and  
 ; FILE REFERENCE: 55815-0102 (319189)  
 ; CURRENT APPLICATION NUMBER: US/11/266,748A  
 ; CURRENT FILING DATE: 2005-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105479.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105482.6  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105483.4  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105507.0  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105485.9  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105484.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: US 60/662,276  
 ; PRIOR FILING DATE: 2005-03-14  
 ; PRIOR APPLICATION NUMBER: US 60/700,293  
 ; PRIOR FILING DATE: 2005-07-18  
 ; NUMBER OF SEQ. ID NOS: 48396  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ. ID NO 192679  
 ; LENGTH: 975  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; US-11-266-748A-192679

Query Match 70.3%; Score 972.4; DB 8; Length 975;  
 Best Local Similarity 99.9%; Pred. No. 4,5e-278;  
 Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 135 CGGGCCATACGGAACCTGACCACTGTGACAAATTTAGAGTCTCTGTGAAAACTCTG 194  
 Db 2 CGGGCCATACGGAACCTGACCACTGTGACAAATTTAGAGTCTCTGTGAAAACTCTG 61  
 Qy 195 CACAGTAATATGACATGATCCACCCGAGGAGCAGCTCAATATGATGATGTA 254  
 Db 62 CACAGTAATATGACATGATCCACCCGAGGAGCAGCTCAATATGATGATGTA 121  
 Qy 255 TTTTATGATTTTGGGCAAAACAGTAAGAAATGCTCCGGAACCTGCTGTAAT 314  
 Db 122 TTTTATGATTTTGGGCAAAACAGTAAGAAATGCTCCGGAACCTGCTGTAAT 181  
 Qy 315 AGAAGTACCCCTGATGAGAGATTTGCTGCAAGTGGGCTCCAGTGTAGCAACATGA 374  
 Db 182 AGAAGTACCCCTGATGAGAGATTTGCTGCAAGTGGGCTCCAGTGTAGCAACATGA 241  
 Qy 375 GAGTGAGAGCCTTAGCATTTTGTGTAATAATGATCTACCCCAAGAGGTGATCTGA 434

Db 242 GAGTGAGAGCCTTAGCATTTTGTGTAATAATGATCTACCCCAAGAGGTGATCTGA 301  
 Qy 435 GTCTGCTGATGATGATCTTCAATGATCTTTGGCAACCTGATGATGATGATCTG 494  
 Db 302 GTCTGCTGATGATGATCTTCAATGATCTTTGGCAACCTGATGATGATGATCTG 361  
 Qy 495 GCTCCCTGAGAGAAATACAGTCCCGACATCAATATGATCTTACTATGATGAGAG 554  
 Db 362 GCTCCCTGAGAGAAATACAGTCCCGACATCAATATGATCTTACTATGATGAGAG 421  
 Qy 555 CTTGAGAAAAATTCATCAATGATGAAAAATCTTTAGAGAGCCAAATCTTTGTTTC 614  
 Db 422 CTTGAGAAAAATTCATCAATGATGAAAAATCTTTAGAGAGCCAAATCTTTGTTTC 481  
 Qy 615 CTTGATCTGACCAAGATGAGATTCAGTTTGAACACACAGTGTCCAAATATGAT 674  
 Db 482 CTTGATCTGACCAAGATGAGATTCAGTTTGAACACACAGTGTCCAAATATGAT 541  
 Qy 675 CAAGATATGACAGAAAAATTAACCATCTTCATATATGATGCTTTAATCTCCGCT 734  
 Db 542 CAAGATATGACAGAAAAATTAACCATCTTCATATATGATGCTTTAATCTCCGCT 601  
 Qy 735 GAAACCTGATCTCCACATATTAATAAACTCTCTCCACAAATGATGATCTATATGCA 794  
 Db 602 GAAACCTGATCTCCACATATTAATAAACTCTCTCCACAAATGATGATCTATATGCA 661  
 Qy 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTATTTATGATGAGATGAT 854  
 Db 662 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTATTTATGATGAGATGAT 721  
 Qy 855 CAGCCAACTGAGACACATATGTTTCTACGTCACAGAGGCTAAATGTGAAATCCAG 914  
 Db 722 CAGCCAACTGAGACACATATGTTTCTACGTCACAGAGGCTAAATGTGAAATCCAG 781  
 Qy 915 ATTTGAGAAATGTGAGAAATATCATCTTTGATGATGCTGCTGTTCTCTGATAC 974  
 Db 782 ATTTGAGAAATGTGAGAAATATCATCTTTGATGATGCTGCTGTTCTCTGATAC 841  
 Qy 975 TTTGACACAGTCAATTAAGATCAAAACAAATTAAGTATGATGATGATCAAACT 1034  
 Db 842 TTTGACACAGTCAATTAAGATCAAAACAAATTAAGTATGATGATGATCAAACT 901  
 Qy 1035 CTGAGTAATTTGAGCCCAAGAAATGATTAAGTAAGGCAATCCACATCTCAT 1094  
 Db 902 CTGAGTAATTTGAGCCCAAGAAATGATTAAGTAAGGCAATCCACATCTCAT 961  
 Qy 1095 AACCATGTACTCA 1108  
 Db 962 AACCATGTACTCA 975

## RESULT 6

US-11-266-748A-226550  
 ; Sequence 226550, Application US/11266748A  
 ; Publication No. US20060134663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harkin, Paul  
 ; APPLICANT: Johnston, Patrick  
 ; APPLICANT: Mulligan, Karl  
 ; TITLE OF INVENTION: Transcription Microarray Technology and  
 ; FILE REFERENCE: 55815-0102 (319189)  
 ; CURRENT APPLICATION NUMBER: US/11/266,748A  
 ; CURRENT FILING DATE: 2005-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105479.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105482.6  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105483.4  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105507.0  
 ; PRIOR FILING DATE: 2004-11-03

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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 226550
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-226550

Query Match      70.3%; Score 972.4; DB 8; Length 975;
Best Local Similarity 99.9%; Pred. No. 4,5e-278;
Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CCGGCTACGGAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAAACTCTG 194
DB 2 CCGGCTACGGAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAAACTCTG 61

QY 195 CACAGTAATATGACATGGAATCCACCCGGGAGGAGCCAGCTCAATTTGATGCTATGCTA 254
DB 62 CACAGTAATATGACATGGAATCCACCCGGGAGGAGCCAGCTCAATTTGATGCTATGCTA 121

QY 255 TTTTATGATCTTTTGGGACAAACAGATAGAAAATAGCTCCGGAAAATCTGTGTTCAAT 314
DB 122 TTTTATGATCTTTTGGGACAAACAGATAGAAAATAGCTCCGGAAAATCTGTGTTCAAT 181

QY 315 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 374
DB 182 AGAAGTACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 241

QY 375 GAGTGAAGACCTTAGCATTTTGTGTAATAATGATCTCACCCCGAGAGGTGATCTCTGA 434
DB 242 GAGTGAAGACCTTAGCATTTTGTGTAATAATGATCTCACCCCGAGAGGTGATCTCTGA 301

QY 435 GTCTGCTGATGCTGAATCTTCAATGCAATTTGGCAACCTGAGCTACATGAAAGTCTTG 494
DB 302 GTCTGCTGATGCTGAATCTTCAATGCAATTTGGCAACCTGAGCTACATGAAAGTCTTG 361

QY 495 GCTCCCTGGAAGGAATACAGTCCCGACACTAACTATCTCTACTATTTGGCAGAGA 554
DB 362 GCTCCCTGGAAGGAATACAGTCCCGACACTAACTATCTCTACTATTTGGCAGAGA 421

QY 555 CCTGGAATAATTCATCATATGTGAAAACATCTTTAGGAAAGGCCAATCTTTGGTGTTC 614
DB 422 CCTGGAATAATTCATCATATGTGAAAACATCTTTAGGAAAGGCCAATCTTTGGTGTTC 481

QY 615 CTTTATGCTGACCAAGGTGAAGATTCAGTTTGTGAACAACACAGTGTCCAAATATGCT 674
DB 482 CTTTATGCTGACCAAGGTGAAGATTCAGTTTGTGAACAACACAGTGTCCAAATATGCT 541

QY 675 CAAGATTAATGCGAAGAAAATTAACCATCTTCAATATATAGTGCCTTTAATCCGCTG 734
DB 542 CAAGATTAATGCGAAGAAAATTAACCATCTTCAATATATAGTGCCTTTAATCCGCTG 601

QY 735 GAAACTGATCTCCCATATTTAAACCTCTCTCTCCACAAATGATGACCTATATGTGCA 794
DB 602 GAAACTGATCTCCCATATTTAAACCTCTCTCTCCACAAATGATGACCTATATGTGCA 661

QY 795 ATGGGGAATCCACAGAAATTTTATAGCAGATGCGTATTTTATGAAGTAAAGTCATTA 854
DB 662 ATGGGGAATCCACAGAAATTTTATAGCAGATGCGTATTTTATGAAGTAAAGTCATTA 721

QY 855 CAGCCAAACTGAGACACATTAATGTTTCTACGTCCAGAGGCTAAATGTGAGATCCAGA 914
DB 722 CAGCCAAACTGAGACACATTAATGTTTCTACGTCCAGAGGCTAAATGTGAGATCCAGA 781

QY 915 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGATGCTCCGTGATGCTCTCTGATAC 974
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DB 782 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGATGCTCCGTGATGCTCTCTGATAC 841
QY 975 TTGGAACACAGTCAGAAATAGAGTCAAAACAAATAGTATGCTATGAGATGACAAACT 1034
DB 842 TTGGAACACAGTCAGAAATAGAGTCAAAACAAATAGTATGCTATGAGATGACAAACT 901
QY 1035 CTGAGTAATTTGAGCCCAAGAAATGAGTATAGGTAAAGAGGCAATTCACACTTACAT 1094
DB 902 CTGAGTAATTTGAGCCCAAGAAATAGTATAGGTAAAGAGGCAATTCACACTTACAT 961
QY 1095 AACCATGTTACTCA 1108
DB 962 AACCATGTTACTCA 975
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RESULT 7
US-11-266-748A-73628/c
; Sequence 73628, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73628
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-73628

Query Match      67.1%; Score 927.6; DB 8; Length 1294;
Best Local Similarity 98.4%; Pred. No. 1.1e-264;
Matches 990; Conservative 0; Mismatches 9; Indels 7; Gaps 5;

QY 385 CTTAGCATTTTGGTTGAAAAA--TGCATCTCACCCCAAGAGTGAATCTGAGTCTGCTG 442
DB 1294 CTTAGCATTTTGGTTGAAAAAAGTGCATCTCACCCCAAGAGTGAATCTGAGTCTGCTG 1235
QY 443 TGACTGAATCTTCA--TGCATTTGGCACAACCTGAGCTACTAATAGTGTCTTGCT-CC 499
DB 1234 TGACTGAATCTTCAATAGGAGTGGGCAACAACCTGAGCTACTAATAGTGTCTTGCTCC 1175
QY 500 CTGGAAGAAATACAGTCCGACACTAATATATCTCTC--TACTATTGGCAGAGAAGCTG 558
DB 1174 CTGGAAGAAATACAGTCCGACACTAATATATCTCTCCTGACTATTGGCAGAGAAGCTG 1115
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QY 559 GAAAAATTCATCA-ATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 617  
 |||||  
 Db 1114 GAGAAAAATTCATCATATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 1055  
 |||||  
 QY 618 TGATCTGACCAAAATGAAAGATTCAGTTTGGAAACAACAGGTGCTCAAAATATAGTGC 677  
 |||||  
 Db 1054 TGATCTGACCAAAATGAAAGATTCAGTTTGGAAACAACAGGTGCTCAAAATATAGTGC 995  
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 QY 678 GGAATATGCAAGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTTCCGCTG 737  
 |||||  
 Db 994 GGAATATGCAAGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTTCCGCTG 935  
 |||||  
 QY 738 ACTGATCTCTCAATATTAATAAACTCTCTCTTCAACATGATGACCTATATGTCATG 797  
 |||||  
 Db 934 ACTGATCTCTCAATATTAATAAACTCTCTCTTCAACATGATGACCTATATGTCATG 875  
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 QY 798 GGAATATCCACAGAAATTTTATAGCAATGCTTATTTATGAAATAGTGCATTAAC 857  
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 Db 874 GGAATATCCACAGAAATTTTATAGCAATGCTTATTTATGAAATAGTGCATTAAC 815  
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 QY 858 CCAAACTGAGACACATATGTTTCTAGCTCCAAAGAGCTAAATGAGAAATCCAGAA 917  
 |||||  
 Db 814 CCAAACTGAGACACATATGTTTCTAGCTCCAAAGAGCTAAATGAGAAATCCAGAA 755  
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 QY 918 TGAGAGAAATGTGAGAAATACATCTGTTTCACTGCTCTGTTCTTCCGATACCTT 977  
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 Db 754 TGAGAGAAATGTGAGAAATACATCTGTTTCACTGCTCTGTTCTTCCGATACCTT 695  
 |||||  
 QY 978 GAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACTCTG 1037  
 |||||  
 Db 694 GAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACTCTG 635  
 |||||  
 QY 1038 GAGTAATTTGAGCCCAAGAAATAGTATGAGTAAGAGCAATTCACACCTTACATAC 1097  
 |||||  
 Db 634 GAGTAATTTGAGCCCAAGAAATAGTATGAGTAAGAGCAATTCACACCTTACATAC 575  
 |||||  
 QY 1098 CATGTTACTCATGTTTCCAGTCACTGTCGAGGTGTCATCATAGTACTCCTGCTTTA 1157  
 |||||  
 Db 574 CATGTTACTCATGTTTCCAGTCACTGTCGAGGTGTCATCATAGTACTCCTGCTTTA 515  
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 QY 1158 AAAAAAGCTCAAGATTTATTAATTTCCCTCAATTCCTGATCTGCGAAAGATTTTAA 1217  
 |||||  
 Db 514 AAAAAAGCTCAAGATTTATTAATTTCCCTCAATTCCTGATCTGCGAAAGATTTTAA 455  
 |||||  
 QY 1218 AATGTTGAGACCAAGATATGATATCTGCACTGGAAGAATGACATCTATAGGA 1277  
 |||||  
 Db 454 AATGTTGAGACCAAGATATGATATCTGCACTGGAAGAATGACATCTATAGGA 395  
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 QY 1278 GCAAAACCAAGAGAAACCGACTCTGATGTCGATGAGAAACCTGAAAGAGCTCTCA 1337  
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 Db 394 GCAAAACCAAGAGAAACCGACTCTGATGTCGATGAGAAACCTGAAAGAGCTCTCA 335  
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 QY 1338 GTGATGAGATTAATTTATTTTACCTTCACTGTCGACCTTGAGAGA 1393  
 |||||  
 Db 334 GTGATGAGATTAATTTATTTTACCTTCACTGTCGACCTTGAGAGA 289  
 |||||

## RESULT 8

US-11-266-748A-107924/c  
 ; Sequence 107924, Application US/11266748A  
 ; Publication No. US20060134663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harkin, Paul  
 ; APPLICANT: Johnston, Patrick  
 ; APPLICANT: Mulligan, Karl  
 ; TITLE OF INVENTION: Transcription Microarray Technology and  
 ; FILE REFERENCE: 55815-0102 (319189)  
 ; CURRENT APPLICATION NUMBER: US/11/266, 748A  
 ; CURRENT FILING DATE: 2005-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105479.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105482.6

; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105483.4  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105507.0  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105485.9  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: EP 04105484.2  
 ; PRIOR FILING DATE: 2004-11-03  
 ; PRIOR APPLICATION NUMBER: US 60/662,276  
 ; PRIOR FILING DATE: 2005-03-14  
 ; PRIOR APPLICATION NUMBER: US 60/700,293  
 ; PRIOR FILING DATE: 2005-07-18  
 ; NUMBER OF SEQ ID NOS: 48396  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ ID NO 107924  
 ; LENGTH: 1294  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (30)..(30)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; US-11-266-748A-107924

Query Match 67.1%; Score 927.6; DB 8; Length 1294;  
 Best Local Similarity 98.4%; Pred. No. 1.1e-264;  
 Matches 990; Conservative 0; Mismatches 9; Indels 7; Gaps 5;

QY 385 CTTAGCATTTTGGTTGAAAA--TGCACTCCACCCGAGAGGTGATCTGAGTCTGCTG 442  
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 Db 1294 CTTAGCATTTTGGTTGAAAAAGTGCATCTACCCGAGAGGTGATCTGAGTCTGCTG 1235  
 |||||  
 QY 443 TGACTGAACTTCAA--TGCACTTGGCAACCTGAGCTAATGAAGTCTTGGCT-CC 499  
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 Db 1234 TGACTGAGCTTCAAATGGCATGGGGCAACCTGAGCTAATGAAGTCTTGGCTGCC 1175  
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 QY 500 CTGGAAGAAATACAGTCCCGGACACTTATATCTC--TACTTGGGCAAGAGCTG 558  
 |||||  
 Db 1174 CTGGAAGAAATACAGTCCCGGACACTTATATCTCCTGTACTATGCGACAGAGCTG 1115  
 |||||  
 QY 559 GAAAAATTCATCA-ATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 617  
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 Db 1114 GAAAAATTCATCATATGTGAAAAATCTTTAGAGAAAGCCAAATACCTTTGGTTCCTT 1055  
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 QY 618 TGATCTGACCAAGAGATTCAGTTTGAACAACAAGTGTCCAAATATAGTCAA 677  
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 Db 1054 TGATCTGACCAAGAGATTCAGTTTGAACAACAAGTGTCCAAATATAGTCAA 995  
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 QY 678 GGAATATGCAAGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTTCCGCTG 737  
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 Db 994 GGAATATGCAAGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTTCCGCTG 935  
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 QY 738 ACTGATCTCTCAATATTAATAAACTCTCTTCAACATGATGACCTATATGTCATG 797  
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 Db 934 ACTGATCTCTCAATATTAATAAACTCTCTTCAACATGATGACCTATATGTCATG 875  
 |||||  
 QY 798 GGAATATCCACAGAAATTTATAGCAATGCTTATTTATGAAATAGTGCATTAAC 857  
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 Db 874 GGAATATCCACAGAAATTTATAGCAATGCTTATTTATGAAATAGTGCATTAAC 815  
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 QY 858 CCAAACTGAGACACATATGTTTCTAGCTCCAAAGAGCTAAATGAGAAATCCAGAA 917  
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 Db 814 CCAAACTGAGACACATATGTTTCTAGCTCCAAAGAGCTAAATGAGAAATCCAGAA 755  
 |||||  
 QY 918 TGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGATGTTCTTCCGATACCTT 977  
 |||||  
 Db 754 TGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGATGTTCTTCCGATACCTT 695  
 |||||  
 QY 978 GAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACTCTG 1037  
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 Db 694 GAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAACTCTG 635  
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QY 1038 GAGTAATTGGAGCCAGAAATGAGTATAGGTAAGAAAGCCAACTTCCACTCTTACATAC 1097  
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Db 634 GAGTAATTGGAGCCAGAAATGAGTATAGGTAAGAAAGCCAACTTCCACTCTTACATAC 575  
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|  
QY 1098 CATGTACTCATCTGTTCCAGTCATCGTCGAGGAGGCAATCATATGTCCTGCTTAACT 1157  
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Db 574 CATGTACTCATCTGTTCCAGTCATCGTCGAGGAGGCAATCATATGTCCTGCTTAACT 515  
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QY 1158 AAAAGGCTCAAGATTATATATATTCCTCCAACTTCCGATCTGGCAAGATTTTAAAGA 1217  
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Db 514 AAAAGGCTCAAGATTATATATATTCCTCCAACTTCCGATCTGGCAAGATTTTAAAGA 455  
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QY 1218 AATGTTGGAGACCAAGATGATATCTCTGCACTGGAGAAGTAGACAATCTATAGAA 1277  
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Db 454 AATGTTGGAGACCAAGATGATATCTCTGCACTGGAGAAGTAGACAATCTATAGAA 395  
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QY 1278 GCAAACCAAGAGAGAACCGACTCTGTAGTGTGATGAGAAACCTGAGAAAGCCTCTCA 1337  
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Db 394 GCAAACCAAGAGAGAAACCGACTCTGTAGTGTGATGAGAAACCTGAGAAAGCCTCTCA 335  
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QY 1338 GTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAAGA 1383  
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|  
Db 334 GTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAAGA 289  
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RESULT 9  
US-11-266-748A-126439  
; Sequence 126439, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcription Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
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; TYPE: DNA  
; ORGANISM: Homo Sapiens  
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; NAME/KEY: misc.feature  
; LOCATION: (1265)..(1265)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-126439

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; Sequence 54614, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick

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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 54614
LENGTH: 902
TYPE: DNA
ORGANISM: Homo Sapiens
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NAME/KEY: misc_feature
LOCATION: (872)..(872)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
LOCATION: (902)..(902)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-54614
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Query Match 43.5%; Score 601; DB 8; Length 902;

Best Local Similarity 99.8%; Pred. No. 7.6e-168; Matches 612; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Sequence 73627, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
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PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 73627
LENGTH: 1297
TYPE: DNA
ORGANISM: Homo Sapiens
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PRIOR APPLICATION NUMBER: EP 04105485.9

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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## SUMMARIES

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| 22 | 1198 | 86.6 | 4039  | 13 | ACN41073  | Acn41073 Tumour-as |
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| KW       | NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine; |
| KW       | allergy; asthma; therapy; ss.   |
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| OS       | Homo sapiens.   |
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| PD       | 01-MAY-1997.  |
| XX       |   |
| PF       | 23-OCT-1996; 96MO-AU000668.   |
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| PR       | 23-OCT-1995; 95AU-00006135.   |
| PR       | 22-DEC-1995; 95AU-00007276.   |
| PR       | 09-SEP-1996; 96AU-00002208.   |
| XX       |   |
| PA       | (AMRA-) AMRAD OPERATIONS PTY LTD.                                     |
| PI       | Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;                 |
| XX       |   |
| DR       | WPI; 1997-259018/23.  |
| DR       | P-PSDB; AA009822.   |
| XX       |   |
| PT       | DNA encoding animal haemopoietin receptor which interacts with        |

PT interleukin-13 - useful to treat asthma, allergy or condition exacephated  
 PT by IGE production.

PS Claim 6; Page 52-54; 93pp; English.

CC DNA sequences (AAT6164 and AAT6165) respectively code for novel mouse  
 CC and human haemopoietin receptors (AAW09821 and AAW09822) designated NR4  
 CC that comprise the interleukin-13 (IL-13) receptor alpha-chain. A human  
 CC bone marrow cDNA library was screened with probes comprising nucleotides  
 CC 82-840 and 840-1270 of murine NR4 cDNA, and a composite sequence for  
 CC human NR4 was produced from isolated clones. The availability of genetic  
 CC sequences for NR4 permits the development of a range of agents capable of  
 CC modulating the activity of IL-13 and related cytokines such as  
 CC interleukin-4 for the treatment of allergy, asthma and other conditions  
 CC relating to IGE. The genetic sequences can also be used in prodn. of  
 CC recombinant NR4 or fusion proteins including NR4

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Query Match 100.0%; Score 1383; DB 2; Length 1383;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 841 GTTGAAGTCAATPACAGCCAACTGAGACACATATGTTTGTACGTCCAGAGCTTAA 900  
 DB 841 GTTGAAGTCAATPACAGCCAACTGAGACACATATGTTTGTACGTCCAGAGCTTAA 900  
 QY 901 TGTGGAATCCGAATTTGAGAGAAATGAGAAATACATCTGTTTCAATGTCCTGAT 960  
 DB 901 TGTGGAATCCGAATTTGAGAGAAATGAGAAATACATCTGTTTCAATGTCCTGAT 960  
 QY 961 GTTCTTCTGATACCTTTGAACACAGTCAAGATTAAGTCAAAA CAATAAGTTATGCTAT 1020  
 DB 961 GTTCTTCTGATACCTTTGAACACAGTCAAGATTAAGTCAAAA CAATAAGTTATGCTAT 1020  
 QY 1021 GAGGATGACAAACTGTGAGTAATTTGAGCCCAAGAAATGATATGTAAGAGCCCAAT 1080  
 DB 1021 GAGGATGACAAACTGTGAGTAATTTGAGCCCAAGAAATGATATGTAAGAGCCCAAT 1080  
 QY 1081 TCCACACTTACATTAACCAATGTTACTCATTTTCCAGTATGTCGAGGTGCATCAT 1140  
 DB 1081 TCCACACTTACATTAACCAATGTTACTCATTTTCCAGTATGTCGAGGTGCATCAT 1140  
 QY 1141 GTACTCTCTTACTTAAAGAAAGGCTCAAGATTAATATATTCCTTCAATTCCTGATCCT 1200  
 DB 1141 GTACTCTCTTACTTAAAGAAAGGCTCAAGATTAATATATTCCTTCAATTCCTGATCCT 1200  
 QY 1201 GGCAGATTTTAAAGAAATGTTTGGAGACCAAGATGATATCTGTGACCTGGAAG 1260  
 DB 1201 GGCAGATTTTAAAGAAATGTTTGGAGACCAAGATGATATCTGTGACCTGGAAG 1260  
 QY 1261 TACGATCTATGAGAGAGAAACCAAGAGAAACCGACTGTGATGCTGATAGAAAC 1320  
 DB 1261 TACGATCTATGAGAGAGAAACCAAGAGAAACCGACTGTGATGCTGATAGAAAC 1320  
 QY 1321 CTGAAGAAAGCCTCTGAGTATGAGATATTTATTTTACCTTCACTGTGACCTTGAGA 1380  
 DB 1321 CTGAAGAAAGCCTCTGAGTATGAGATATTTATTTTACCTTCACTGTGACCTTGAGA 1380  
 QY 1381 AGA 1383  
 DB 1381 AGA 1383  
 RESULT 2  
 AAA35213  
 ID AAA35213 standard; DNA; 3999 BP.  
 XX  
 XX AAA35213;  
 AC  
 AC 28-JUL-2000 (first entry)  
 DT  
 XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO: 87.  
 DE  
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 XX phosphorothioate; impaired respiration; inflammation; allergy;  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammation;  
 KW anti-allergic; antiasthmatic; cyostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 OS MO200009525-A2.  
 PN  
 PN 24-FEB-2000.  
 PD  
 PD 03-AUG-1999; 99MO-US017712.  
 PF

XX 03-AUG-1998; 98US-0095212P.  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX  
 PI Nyce JW;  
 XX  
 XX WPI; 2000-205971/18.  
 DR  
 XX  
 PT New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 XX  
 PS Disclosure; Page 1252-1253; 1343pp; English.  
 CC  
 CC The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antispasmodic, cytosolic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasize to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA3233 to AAA5312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA2333 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 XX  
 SQ Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;  
 Query Match 86.6%; Score 1198; DB 3; Length 3999;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 471 GCTCCCTGGAAGAAATACAGTCCCGACATCACTATCTCTACTATGACAGAG 530  
 QY 555 CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGCCAAATCTTGTGTTTC 614  
 Db 531 CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGCCAAATCTTGTGTTTC 590  
 QY 615 CTTGATCTGACCAAGAGTGAAGATTCAGTTTGAACACAGAGTGCCTTAATATAGT 674  
 Db 591 CTTGATCTGACCAAGAGTGAAGATTCAGTTTGAACACAGAGTGCCTTAATATAGT 650  
 QY 675 CAAGATTAATGACAGAAAAATTAACATCTTCAATATAGTGCCTTAATATAGT 734  
 Db 651 CAAGATTAATGACAGAAAAATTAACATCTTCAATATAGTGCCTTAATATAGT 710  
 QY 735 GAAACCTGATCTCCCAATATTAATAAATCTCTCTCCCAATATAGTGCCTTAATATAGT 794  
 Db 711 GAAACCTGATCTCCCAATATTAATAAATCTCTCTCCCAATATAGTGCCTTAATATAGT 770  
 QY 795 ATGGAGAAATCCACAGAAATTTATAGAGATGCTATTTATAGAGAGAAATCAATTA 854  
 Db 771 ATGGAGAAATCCACAGAAATTTATAGAGATGCTATTTATAGAGAGAAATCAATTA 830  
 QY 855 CAGCCAAATCTGACACATATATGTTTCTAAGTCCAAAGAGCTAAATGTGAATCCAGA 914  
 Db 831 CAGCCAAATCTGACACATATATGTTTCTAAGTCCAAAGAGCTAAATGTGAATCCAGA 890  
 QY 915 ATTTGAAGAAATGTGAGAAATATACATCTTGTTCATGCTCCCTGCTGTTCTCTGATAC 974  
 Db 891 ATTTGAAGAAATGTGAGAAATATACATCTTGTTCATGCTCCCTGCTGTTCTCTGATAC 950  
 QY 975 TTTGAACAGTCAAGTGAATAGAGTCAAAACAAATAGTTATGATAGAGTGAACAACT 1034  
 Db 951 TTTGAACAGTCAAGTGAATAGAGTCAAAACAAATAGTTATGATAGAGTGAACAACT 1010  
 QY 1035 CTGAGATTAATTTGAGCCCAAGAAATAGATATAGTGAAGAGCAATTCACACTCTACAT 1094  
 Db 1011 CTGAGATTAATTTGAGCCCAAGAAATAGATATAGTGAAGAGCAATTCACACTCTACAT 1070  
 QY 1095 AACCATGTTACTATTTGTCAGTCAATGCTGCGAGGTGCAATCAATGACTCTGCTTTA 1154  
 Db 1071 AACCATGTTACTATTTGTCAGTCAATGCTGCGAGGTGCAATCAATGACTCTGCTTTA 1130  
 QY 1155 CCTAAAAGGCTCAAGATTAATTAATCCCTCCAAATCTCGATCTGCGAAATTTTAA 1214  
 Db 1131 CCTAAAAGGCTCAAGATTAATTAATCCCTCCAAATCTCGATCTGCGAAATTTTAA 1190  
 QY 1215 AGAAATGTTTGAAGACAGATGATGATCTGCACTGGAAGAATGACATCTATGA 1274  
 Db 1191 AGAAATGTTTGAAGACAGATGATGATCTGCACTGGAAGAATGACATCTATGA 1250  
 QY 1275 GAAGCAAAACCAAGAGAAAAACGACTGTAGTGTGATGAAAAAAGCTGAAGAAAGCTC 1334  
 Db 1251 GAAGCAAAACCAAGAGAAAAACGACTGTAGTGTGATGAAAAAAGCTGAAGAAAGCTC 1310  
 QY 1335 TCAGTGAATGAGATTAATTTTAACTTCACTGTAACCTTGAGAA 1383  
 Db 1311 TCAGTGAATGAGATTAATTTTAACTTCACTGTAACCTTGAGAA 1359

RESULT 3  
 AAF21335  
 ID AAF21335 standard; DNA; 3999 BP.  
 XX AAF21335;  
 AC  
 XX  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human low adenosine antisense oligonucleotide related sequence #2902.  
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KM human; airway disorder; bronchoconstriction; lung inflammation;  
 KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;



immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens.

MO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US008020.

06-APR-1999; 99US-0127958P.

(UYEC-) UNIV EAST CAROLINA.

(NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure, Page 1336-1337; 1592pp; English.

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, anti-inflammatory, analgesic, immunosuppressive, antiepileptic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulin and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 3; Length 3999;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

135 CGGCGCTACGAACTCAGCCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 194  
111 CGGCGCTACGAACTCAGCCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 170  
195 CACAGTAATATGACATGGAATCACCAGGAGGACGAGTCAAAATTGTATGTATGTA 254

171 CACAGTAATATGACATGGAATCACCAGGAGGACGAGTCAAAATTGTATGTATGTA 230  
255 TTTTACGATTTTGGGACAAACAAATAGATAGCTCCGGAATCGTGTCAAT 314  
231 TTTTACGATTTTGGGACAAACAAATAGATAGCTCCGGAATCGTGTCAAT 230  
315 AGAAGTACCCCTGAATGAAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374  
291 AGAAGTACCCCTGAATGAAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 350  
375 GAGTGAAGACCCGATAGATTTTGGTTGAAATAAGCATCTACCCCGAAGGTGATCTCTGA 434  
351 GAGTGAAGACCCGATAGATTTTGGTTGAAATAAGCATCTACCCCGAAGGTGATCTCTGA 410  
435 GTCTGCTGTGATGAGTCAATGCAATTTGGGACAACTGAGCTACATGAGTGTCTTG 494  
411 GTCTGCTGTGATGAGTCAATGCAATTTGGGACAACTGAGCTACATGAGTGTCTTG 470  
495 GCTCCCTGGAAGGATACAGTCCGACATTAATCTTCTGATCTTCTGATTTGGACAGAA 554  
471 GCTCCCTGGAAGGATACAGTCCGACATTAATCTTCTGATCTTCTGATTTGGACAGAA 530  
555 CCTGGAATAATTCATCAATGCAATTTGGGACAACTGAGCTACATGAGTGTCTTG 614  
531 CTTGGAATAATTCATCAATGCAATTTGGGACAACTGAGCTACATGAGTGTCTTG 590  
615 CTTGATCTGACCAAGATGAGATTCAGTTTGAACAACACAGTGTCCAAATATNGT 674  
591 CTTGATCTGACCAAGATGAGATTCAGTTTGAACAACACAGTGTCCAAATATNGT 650  
675 CAAAGATATGACAGAAATAATTAACCATCTTCAATATATGTCCTTTAACTTCCGTGT 734  
651 CAAAGATATGACAGAAATAATTAACCATCTTCAATATATGTCCTTTAACTTCCGTGT 710  
735 GAAACCTGATCTCCCATATTAATAAAGCTCTTCCCAATGATGACCTATATGTC 794  
711 GAAACCTGATCTCCCATATTAATAAAGCTCTTCCCAATGATGACCTATATGTC 770  
795 ATGGAGAAATCCACAGAAATTTTATGACAGATGCTATTTATGAGTGAAGTCAATTA 854  
771 ATGGAGAAATCCACAGAAATTTTATGACAGATGCTATTTATGAGTGAAGTCAATTA 830  
855 CAGCCAACTGACACATATATGTTTCTACGTCGAAGGCTAAATGTGAGATTCAGA 914  
831 CAGCCAACTGACACATATATGTTTCTACGTCGAAGGCTAAATGTGAGATTCAGA 890  
915 ATTTGAGAAATATGAGAAATATCATCTGTTCAAGTCCCGGTGTTCTCTGATAC 974  
891 ATTTGAGAAATATGAGAAATATCATCTGTTCAAGTCCCGGTGTTCTCTGATAC 950  
975 TTTGAACACAGTCAGATTAAGTCAAAACAATAAGTATGATGAGATGACAAACT 1034  
951 TTTGAACACAGTCAGATTAAGTCAAAACAATAAGTATGATGAGATGACAAACT 1010  
1035 CTGAGTAATTTGAGGCAAGAAATGATATAGTAAAGACCAATTCACACTTACAT 1094  
1011 CTGAGTAATTTGAGGCAAGAAATGATATAGTAAAGACCAATTCACACTTACAT 1070  
1095 AACCATGTTACTCATGTTCCAGTCACTGTCGAGGTGCAATCATATGTAATCTCTGCTTTA 1154  
1071 AACCATGTTACTCATGTTCCAGTCACTGTCGAGGTGCAATCATATGTAATCTCTGCTTTA 1130  
1155 CCTAATAAGGCTCAAGATTAATATTCCTCCCAATTCCTGATCCGGAAGATTTTAA 1214  
1131 CCTAATAAGGCTCAAGATTAATATTCCTCCCAATTCCTGATCCGGAAGATTTTAA 1190  
1215 AGAATGTTTGGAGACCAAGATGATATCTCTGCACTGGAAGATGACATCTATGA 1274  
1191 AGAATGTTTGGAGACCAAGATGATATCTCTGCACTGGAAGATGACATCTATGA 1250  
1275 GAAAGCAACCAAGAGGAAACCGACTCTGTATGCTGATAGAAACCACTGAAGAAAGCTTC 1334  
1251 GAAAGCAACCAAGAGGAAACCGACTCTGTATGCTGATAGAAACCACTGAAGAAAGCTTC 1310

QY 1335 TCAGTGAATGAGATTAATTTTACCTTCAGTGAACCTTGAGAGA 1383  
 DB 1311 TCAGTGAATGAGATTAATTTTACCTTCAGTGAACCTTGAGAGA 1359

RESULT 4  
 AB297029 standard; DNA; 3999 BP.

AB297029;

17-OCT-2003 (first entry)

Human nucleic acid sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;  
 antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;  
 antiasthmatic; hypotensive; immunosuppressive; cytosolic; gene therapy;  
 antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIC-) EPIGENESIS PHARM INC.

Nyce JM, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D,  
 Miller S, Tang L, Shahbuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired  
 respiration, has oligo(s) antisense to specific gene(s) or its  
 corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 ubiquinone.

Disclosure; SEQ ID NO 12271; 872bp; English.

The invention relates to a novel pharmaceutical composition, which has a  
 first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 junctions of genes encoding a polypeptide associated with lung and/or  
 nasal airway dysfunction and a second active agent comprising an  
 antiinflammatory steroid and ubiquinone. A composition of the invention  
 has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,  
 immunosuppressive, and cytosolic activity. The composition may have a  
 use in antisense gene therapy. The composition is useful for treating or  
 preventing a respiratory, lung or malignant disease or condition, also  
 for enhancing the prophylactic or therapeutic respiratory effect of an  
 antiinflammatory steroid in a subject, for reducing or depleting levels  
 of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 receptor, producing bronchodilation, increasing levels of ubiquinone or  
 lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 lung inflammation, lung allergies, or a respiratory disease or condition.  
 Note: The sequence data for this patent is not represented in the printed  
 specification, but was obtained in electronic format directly from WIPO  
 at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 10; Length 3999;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1246; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |      |   |      |
|----|------|---|------|
| QY | 135  | CGCGCTACGGAACCTGAGCCAGCTGACAAATTTGAGTGTCTCTGTTGAAAACTCTG    | 194  |
| DB | 111  | CGCGCTACGGAACCTGAGCCAGCTGAGCAAAATTTGAGTGTCTCTGTTGAAAACTCTG  | 170  |
| QY | 195  | CACAGTAATATGACATGGAATCCACCGAGGGAGCCAGCTCAATATTGACTATGAGTA   | 254  |
| DB | 171  | CACAGTAATATGACATGGAATCCACCGAGGGAGCCAGCTCAATATTGACTATGAGTA   | 230  |
| QY | 255  | TTTTAGCATTTTGGCGCAACAAGATTAAGAAATATGCTCCGGAACTCGTCCGTCAAT   | 314  |
| DB | 231  | TTTTAGCATTTTGGCGCAACAAGATTAAGAAATATGCTCCGGAACTCGTCCGTCAAT   | 290  |
| QY | 315  | AGAAGTACCCCTGAAATGAGAGATTTGCTGCAAGTGGGGTCCAGGTGACCAATGA     | 374  |
| DB | 291  | AGAAGTACCCCTGAAATGAGAGATTTGCTGCAAGTGGGGTCCAGGTGACCAATGA     | 350  |
| QY | 375  | GAGTGAAGCTTGAATTTTGGTGAATAATGATCTCACCCGAGAGGTGATCTCTGA      | 434  |
| DB | 351  | GAGTGAAGCTTGAATTTTGGTGAATAATGATCTCACCCGAGAGGTGATCTCTGA      | 410  |
| QY | 435  | GTCGCTGTGACTGAATCTTCAATGCAATTTGGCAACACTGAGCTACATGAAGTGTCTTG | 494  |
| DB | 411  | GTCGCTGTGACTGAATCTTCAATGCAATTTGGCAACACTGAGCTACATGAAGTGTCTTG | 470  |
| QY | 495  | GCTCCCTGGAAGAAATACAGTCCCGACACTAACTACTCTACTATTGGCACAAG       | 554  |
| DB | 471  | GCTCCCTGGAAGAAATACAGTCCCGACACTAACTACTCTACTATTGGCACAAG       | 530  |
| QY | 555  | CCTGGAATAAATTCATCATGTGAAAACATCTTTAGAGAGGCCAATATCTTGGTGTTC   | 614  |
| DB | 531  | CCTGGAATAAATTCATCATGTGAAAACATCTTTAGAGAGGCCAATATCTTGGTGTTC   | 590  |
| QY | 615  | CTTTGATCTGACCAATGGAAGATTCAGTTTGAACACACAGTGTCCAAATATGCT      | 674  |
| DB | 591  | CTTTGATCTGACCAATGGAAGATTCAGTTTGAACACACAGTGTCCAAATATGCT      | 650  |
| QY | 675  | CAAGATTAATGACGAGAAAATTAACCATCTTCAATATGCTTAACTCCCGGT         | 734  |
| DB | 651  | CAAGATTAATGACGAGAAAATTAACCATCTTCAATATGCTTAACTCCCGGT         | 710  |
| QY | 735  | GAAACCTGATCTTCCATATTAATAAACCCTCTCTTCCAGATGATGACCTATATGCA    | 794  |
| DB | 711  | GAAACCTGATCTTCCATATTAATAAACCCTCTCTTCCAGATGATGACCTATATGCA    | 770  |
| QY | 795  | ATGGAGAAATCCACAGAAATTTTATAGCAATGCTTATTTTGAAGTGAATCAATAA     | 854  |
| DB | 771  | ATGGAGAAATCCACAGAAATTTTATAGCAATGCTTATTTTGAAGTGAATCAATAA     | 830  |
| QY | 855  | CAGCAAACTGAGACATATATGTTTCTACGTCGCAAGAGCTAAATGAGAAATCCAGA    | 914  |
| DB | 831  | CAGCAAACTGAGACATATATGTTTCTACGTCGCAAGAGCTAAATGAGAAATCCAGA    | 890  |
| QY | 915  | ATTGAGAGAAATGAGAAATATCATCTTTTCATGTCCTGCTGTTCTCTGATAC        | 974  |
| DB | 891  | ATTGAGAGAAATGAGAAATATCATCTTTTCATGTCCTGCTGTTCTCTGATAC        | 950  |
| QY | 975  | TTTGAACACGTCAGAAATTAAGTCAAAATTAAGTATGCTATGAGATGCAAACT       | 1034 |
| DB | 951  | TTTGAACACGTCAGAAATTAAGTCAAAATTAAGTATGCTATGAGATGCAAACT       | 1010 |
| QY | 1035 | CTGAGAAATTTGAGCAAAATTAAGTATGAGTAAAGAGCAATTCACACTCTCAT       | 1094 |
| DB | 1011 | CTGAGAAATTTGAGCAAAATTAAGTATGAGTAAAGAGCAATTCACACTCTCAT       | 1070 |
| QY | 1095 | AACCATTTTACTATTTTCTCAGTCAATGTCGAGGTGCAATGATGATCTCTCTTA      | 1154 |
| DB | 1071 | AACCATTTTACTATTTTCTCAGTCAATGTCGAGGTGCAATGATGATCTCTCTTA      | 1130 |
| QY | 1155 | CTTAAAAAGGCTCAAGATTTATATTTCTCTCAATTTCTGATCTCTGCAAGATTTTAA   | 1214 |
| DB | 1131 | CTTAAAAAGGCTCAAGATTTATATTTCTCTCAATTTCTGATCTCTGCAAGATTTTAA   | 1190 |

QY 1215 AGAATGTTTGGAGACCGAGATGATGATCTGCACTGGAGAGATGACATCTTATGA 1274  
CC |  
CC |  
DB 1191 AGAAATGTTTGGAGACCGAGATGATGATCTGCACTGGAGAGATGACATCTTATGA 1250  
CC |  
QY 1275 GAAGCAACCAAGAGAGAAACCGACCTGTGAGTGCATGATGAAACCTGAAAGAAAGCTC 1334  
CC |  
DB 1251 GAAGCAACCAAGAGAGAAACCGACCTGTGAGTGCATGATGAAACCTGAAAGAAAGCTC 1310  
CC |  
QY 1335 TCAGTGTGAGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
CC |  
DB 1311 TCAGTGTGAGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1359  
CC |  
RESULT 5  
ABD20878  
ID ABD20878 standard; DNA; 3999 BP.  
XX  
AC ABD20878;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human pulmonary and inflammatory target DNA #489.  
XX  
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;  
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;  
KW surfactant depletion; anti-allergic; anti-inflammatory; anti-asthmatic;  
KW analgesic; hypotensive; immunosuppressive; cyostatic; cystic fibrosis;  
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;  
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;  
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;  
KW pulmonary transplantation rejection; ds.  
XX  
OS Homo sapiens.  
XX  
PN MO200285309-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 23-APR-2002; 2002MO-US013143.  
XX  
PR 24-APR-2001; 2001US-0286036P.  
XX  
PA (EPIC-) EPIDEMESIS PHARM INC.  
XX  
PI Myce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
PI Miller S, Tang L, Shahbuddin S;  
XX  
DR MPI; 2003-093058/08.  
XX  
PT Pharmaceutical composition for treating asthma, has antisense  
PT oligonucleotide containing less percentage of adenosine, targeted to  
PT nucleic acids associated with lung airway or lung dysfunction, and  
PT bronchodilating agent.  
XX  
PS Claim 15; SEQ ID NO 12271; 763bp; English.  
XX  
CC This invention describes a novel composition (a) a first active agent,  
CC comprising oligonucleotides, effective for alleviating  
CC bronchoconstriction, respiratory tract inflammation, allergies and  
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,  
CC surfactant depletion or hyposecretion, when administered to a mammal. The  
CC oligonucleotides are derived from a gene encoding or regulating  
CC expression of a target polypeptide associated with lung airway or lung  
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.  
CC The invention also describes a kit, that comprises: (a) a delivery  
CC device, in separate containers, (b) the oligonucleotides, (c)  
CC instructions for adding a carrier and for use of the kit. The composition  
CC of the invention has anti-allergic, anti-inflammatory, anti-asthmatic,  
CC analgesic, hypotensive, immunosuppressive and cyostatic activity, is a  
CC beta-adrenergic agonist. The composition is useful for preventing or  
CC treating a respiratory, lung or malignant disease. The administered  
CC composition comprises oligo and is administered to reduce the production  
CC or availability, or to increase the degradation of the target mRNA or to

CC reduce the amount of target polypeptide present in the lungs. The  
CC pulmonary obstruction, and/or bronchoconstriction and/or lung  
CC inflammation, allergies and/or surfactant hypoproduction are associated  
CC with a disease or condition such as pulmonary vasoconstriction,  
CC inflammation, allergies, asthma, impeded respiration, respiratory  
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary  
CC hypertension, emphysema, chronic obstructive pulmonary disease, cancer.  
CC transplantation rejection, pulmonary infections, bronchitis or cancer.  
CC The reduced adenosine content of the anti-sense oligos corresponding to  
CC thymides present in the target RNA serves to prevent the breakdown of  
CC the oligonucleotides into products that free adenosine into the system  
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to  
CC prevent any unwanted effects due to it  
XX  
SQ Sequence 3999 BP; 1127 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;  
Query Match 86.6%; Score 1198; DB 11; Length 3999;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CGGCTTACGAGAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 194  
DB 111 CGGCTTACGAGAACTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 170  
QY 195 CACAGTAATATGACATGGAATCCACCGAGAGCCACGCTCAATTTAGTCTATGTA 254  
DB 171 CACAGTAATATGACATGGAATCCACCGAGAGCCACGCTCAATTTAGTCTATGTA 230  
QY 255 TTTTATCATTTTGGGACAAACAAATTAAGAAATTTGCTCCGGAACCTGCTGTCAT 314  
DB 231 TTTTATCATTTTGGGACAAACAAATTAAGAAATTTGCTCCGGAACCTGCTGTCAT 290  
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACATGA 374  
DB 291 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACATGA 350  
QY 375 GAGTGAAGAGCTTGAATTTTGGTGAATAATGATCTGACCCCGAAGGTGATCTCTGA 434  
DB 351 GAGTGAAGAGCTTGAATTTTGGTGAATAATGATCTGACCCCGAAGGTGATCTCTGA 410  
QY 435 GTCTGCTGTGACCTGAACTTCAATGATTTTGGGCAACCTGAGCTAATGAAAGTCTTCTG 494  
DB 411 GTCTGCTGTGACCTGAACTTCAATGATTTTGGGCAACCTGAGCTAATGAAAGTCTTCTG 470  
QY 495 GTCCTCGGAAGAAATACCAAGTCCGACACTAATCTTACTCTTACTATTTGGACAGAG 554  
DB 471 GTCCTCGGAAGAAATACCAAGTCCGACACTAATCTTACTCTTACTATTTGGACAGAG 530  
QY 555 CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTTGGTTTTC 614  
DB 531 CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAAAGCCAAATCTTTGGTTTTC 590  
QY 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAAATATGTGT 674  
DB 591 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAAATATGTGT 650  
QY 675 CAAGATTAATGCAAGAAAAATTTAAACATCTTCAATATAGTCCCTTAACTCCCGTGT 734  
DB 651 CAAGATTAATGCAAGAAAAATTTAAACATCTTCAATATAGTCCCTTAACTCCCGTGT 710  
QY 735 GAAACCTGATCTTCCATATTAATAAATCTTCTTCCCAATATGATGACCTATATGTGA 794  
DB 711 GAAACCTGATCTTCCATATTAATAAATCTTCTTCCCAATATGATGACCTATATGTGA 770  
QY 795 ATGGAGATCCACAGAAATTTTATTTAGCAGATGCTTATTTATGAAGTATGAATCAATA 854  
DB 771 ATGGAGATCCACAGAAATTTTATTTAGCAGATGCTTATTTATGAAGTATGAATCAATA 830  
QY 855 CAGCCAAATGAGACATATATTTTCTACGCTCAAGAGGCTTAATATGAGAAATCCAGA 914  
DB 831 CAGCCAAATGAGACATATATTTTCTACGCTCAAGAGGCTTAATATGAGAAATCCAGA 890  
QY 915 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTGCTCCGTGTCTTCTCTGATAC 974

|||||  
Db 891 ATTGAGAGAAATGTGAGATATACATCTGTTTCATGGTCCCTGGTGTCTTCTGATAC 950  
Qy 975 TTGGAACAGAGTCGAATPAAGAGTCAAAACAAATPAAGTATGATAGAGATGCAAACT 1034  
Db 951 TTGGAACAGAGTCGAATPAAGAGTCAAAACAAATPAAGTATGATAGAGATGCAAACT 1010  
Qy 1035 CTGAGATTAATTTGAGCCAGAAATAGATATAGTATAGAGAGGCAATTCACACTCTACAT 1094  
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Qy 1095 AACCATGTTACTACTGTTTCCAGTCATGTCGACAGTGCACATCAATGACTCTGCTTTA 1154  
Db 1071 AACCATGTTACTACTGTTTCCAGTCATGTCGACAGTGCACATCAATGACTCTGCTTTA 1130  
Qy 1155 CCTAAAGAGGCTCAAGATTAATTAATTCCTCCCAATTCCTGATCCCTGCAAGATTTTAA 1214  
Db 1131 CCTAAAGAGGCTCAAGATTAATTAATTCCTCCCAATTCCTGATCCCTGCAAGATTTTAA 1190  
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Db 1191 AGAAATGTTTGGAGACCAAGATGATGATCTGTCACATGGAAGAGTACGATCTATGA 1250  
Qy 1275 GAAGCAAAACCAAGAGGAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1334  
Db 1251 GAAGCAAAACCAAGAGGAAACCGACTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1310  
Qy 1335 TCAGTGTGAGATTAATTTTACCTTCACTGATGATGAAAACCTGAAGAAAGCTC 1383  
Db 1311 TCAGTGTGAGATTAATTTTACCTTCACTGATGATGAAAACCTGAAGAAAGCTC 1359

## RESULT 6

ACF87407 standard; DNA; 4006 BP.

ACF87407;

02-JUN-2005 (first entry)

Human SIRS/sepsis diagnostic marker DNA fragment 6267.

Systemic inflammatory response syndrome; SIRS; antibacterial;

Immunosuppressive; antiinflammatory; diagnosis; sepsis; ds.

Homo sapiens.

WO2004087949-A2.

14-OCT-2004.

31-MAR-2004; 2004MO-EP003419.

02-APR-2003; 2003DE-01015031.

08-AUG-2003; 2003DE-01036511.

02-SEP-2003; 2003DE-01040395.

(SIRS-) SIRS LAB GMBH.

Rueswurm S, Reinhart K, Saluz H, Straube E, Zipfel PF, Deigner H;

WPI; 2004-748070/73.

In vitro detection of systemic inflammatory response syndrome and related conditions, for e.g. monitoring progression, comprises detecting abnormal expressions of disease-related genes.

Disclosure; Page; 75pp; German.

The invention relates to a novel method for in vitro detection of systemic inflammatory response syndrome (SIRS). The method comprises detecting abnormal expression of disease-related genes, or their associated peptides. The method of the invention demonstrates

CC antibacterial, immunosuppressive and antiinflammatory applications and  
CC may be used for early differential diagnosis, monitoring progression,  
CC assessing risk, assessing the likely response to treatment and for post  
CC mortem diagnosis of systemic inflammatory response syndrome, sepsis and  
CC sepsis-like conditions. The recombinant or synthetic nucleic acid  
CC sequences of the invention, or derived proteins or peptides, may be  
CC useful as calibrants in assays for the specified diseases, for evaluating  
CC activity or toxicity in screening for active agents and/or for  
CC preparation of agents for treatment or prevention of the specified  
CC diseases. The current sequence is that of a human SIRS/sepsis diagnostic  
CC marker DNA fragment of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at ftd.wipo.int/pub/publicated  
CC pct sequences. Furthermore, a number of arbitrary SEQ ID NO.s are  
CC disclosed within the specification, however, these have not been taken  
CC into account during indexing due to inconsistencies in application and  
CC format

SQ Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 13; Length 4006;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Gaps 0;

Matches 1248; Conservative 0; Indels 0; Gaps 0;

Qy 135 CGGCGCTACCGAAACTCAGCCACTGTGACAAATTTAGTGTCTGTGTAACCTCTG 194  
Db 121 CGGCGCTACCGAAACTCAGCCACTGTGACAAATTTAGTGTCTGTGTAACCTCTG 180  
Qy 195 CACAGTAATATGACATGAAATCCACCGAGGAGCCAGCTCAATTTGATGATGTA 254  
Db 181 CACAGTAATATGACATGAAATCCACCGAGGAGCCAGCTCAATTTGATGATGTA 240  
Qy 255 TTTTATGATTTTGGGACAAACAAATTAAGTATGCTCCGAAATCTGCTTCAAT 314  
Db 241 TTTTATGATTTTGGGACAAACAAATTAAGTATGCTCCGAAATCTGCTTCAAT 300  
Qy 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA 374  
Db 301 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA 360  
Qy 375 GAGTGAGAACCTAGACATTTTGGTGAATAATGATCTACCCCGAGAGGTGATCTGA 434  
Db 361 GAGTGAGAACCTAGACATTTTGGTGAATAATGATCTACCCCGAGAGGTGATCTGA 420  
Qy 435 GTCTGCTGTGACGAACTTAATGCAATTTGGGACAACTGACTACATGAAGTCTTG 494  
Db 421 GTCTGCTGTGACGAACTTAATGCAATTTGGGACAACTGACTACATGAAGTCTTG 480  
Qy 495 GCTCCCTGGAAGAAATACAGTCCCGACATACTACTCTACTATTTGGGACAGAG 554  
Db 481 GCTCCCTGGAAGAAATACAGTCCCGACATACTACTCTACTATTTGGGACAGAG 540  
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Db 541 CTTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATCTTTGGTGTTC 600  
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Db 601 CTTTGTATCTGACCAAGAGTTCAGTTTGAACAACAAGTGTCCAATATAGT 660  
Qy 675 CAGGATTAATGACGAAAAATTAACCATCTTCAATATATGAGCTTTAACTCCGCTG 734  
Db 661 CAGGATTAATGACGAAAAATTAACCATCTTCAATATATGAGCTTTAACTCCGCTG 720  
Qy 735 GAAACCTGATCTTCAATATTAACCTCTCTTTCACAAATGATGATATATGCA 794  
Db 721 GAAACCTGATCTTCAATATTAACCTCTCTTTCACAAATGATGATATATGCA 780  
Qy 795 ATGGAGATTCACAGAAATTTTATGAGATGCTATTTTATGAGATTAAGTATTA 854  
Db 781 ATGGAGATTCACAGAAATTTTATGAGATGCTATTTTATGAGATTAAGTATTA 840  
Qy 855 CAGCCAAACTGACACATTAATGTTTCTACGTCAAGAGGCTAATATGAGATTCAGA 914

|||||  
Db 841 CAGCCAAACGAGACACATATCTTTCTACGTCGAAGAGCTAAATGTGAGATCCAGA 900  
QY 915 ATTGAGAGAAATGTGAGAGATACATCTGTGTTACGAGTCCCTGGTCTTCTCTGATAC 974  
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QY 975 TTTGAAACAGTCAGATAGATAGATCAAAACAAATAGATTATGCTATGAGATGACAAACT 1034  
Db 961 TTTGAAACAGTCAGATAGATAGATCAAAACAAATAGATTATGCTATGAGATGACAAACT 1020  
QY 1035 CTGAGATTAATTGAGAGCCAGAAATGAGTATAGGTAGAGACGCATTTCCACCTTACAT 1094  
Db 1021 CTGAGATTAATTGAGAGCCAGAAATGAGTATAGGTAGAGACGCATTTCCACCTTACAT 1080  
QY 1095 AACCATGTTACTGATTTGTTCCAGTCATCGTCGAGAGGCAATCATAGTACTCTCGCTTTA 1154  
Db 1081 AACCATGTTACTGATTTGTTCCAGTCATCGTCGAGAGGCAATCATAGTACTCTCGCTTTA 1140  
QY 1155 CCTAAAGAGCTCAAGATTAATTATTTCCCTCCAAATTCCTGATCTCGCAAGATTTTAA 1214  
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QY 1215 AGAAATGTTTGAGACCCAGATGATGATCTTGCACTGAGAGAGATGACATCTATGA 1274  
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Db 1261 GAGCAAAACCAAGAGAGAAACGACCTGTAGTGCTGATGAGAAACCTGAGAAAGCTC 1320  
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Db 1321 TCAGTATGAGATTAATTATTTTACCTTCACTGTGACCTTGAGAGA 1369  
RESULT 7  
AECL5897  
ID AECL5897 standard; RNA; 4006 BP.  
XX  
AC AECL5897;  
XX  
DT 20-OCT-2005 (first entry)  
XX  
DE Human interleukin-13 receptor alpha 1 (IL-13RA1) cDNA.  
XX  
KW RNA interference; gene silencing; cancer; hyperproliferation; neoplasm;  
KW cytosolic; viral infection; infection; virucide; inflammation;  
KW antiinflammatory; autoimmune disease; immune disorder; immunosuppressive;  
KW pulmonary disease; respiratory disease; respiratory-gen.;  
KW cardiovascular disease; cardiovascular-gen.; neurological disease;  
KW neuroprotective; renal disease; endocrine disease; gastrointestinal disease;  
KW nephrotropic; endocrine-gen.; liver disease; gastrointestinal disease;  
KW hepatotropic; ocular disease; ophthalmological; reproductive disorder;  
KW infertility; antiinfertility; gynecology and obstetrics; andrology;  
KW mitochondrial disease; prion disease; degeneration;  
KW interleukin-13 receptor alpha 1; IL-13 receptor alpha 1; gene; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 44..1327  
FT /\*tag= a  
FT /product= "Interleukin-13 receptor alpha 1 (IL-13RA1)"  
XX  
PN US2005182007-A1.  
XX  
PD 18-AUG-2005.  
XX  
PF 20-AUG-2004; 2004US-00922675.  
XX  
PR 18-MAY-2001; 2001US-0292217P.  
PR 20-JUL-2001; 2001US-0306883P.

PR 13-AUG-2001; 2001US-0311865P.  
PR 20-FEB-2002; 2002US-0358580P.  
PR 06-MAR-2002; 2002US-0362016P.  
PR 11-MAR-2002; 2002US-0363124P.  
PR 17-MAR-2002; 2002WFO-US015876.  
PR 06-JUN-2002; 2002US-0386782P.  
PR 29-AUG-2002; 2002US-0406784P.  
PR 05-SEP-2002; 2002US-0408378P.  
PR 09-SEP-2002; 2002US-0409293P.  
PR 15-JAN-2003; 2003US-0440129P.  
PR 14-FEB-2003; 2003WFO-US004566.  
PR 20-FEB-2003; 2003WFO-US005028.  
PR 20-FEB-2003; 2003WFO-US005346.  
PR 30-APR-2003; 2003US-0042716P.  
PR 23-MAY-2003; 2003US-00444853.  
PR 23-OCT-2003; 2003US-00693059.  
PR 24-NOV-2003; 2003US-00720448.  
PR 03-DEC-2003; 2003US-00727780.  
PR 14-JAN-2004; 2004US-00757803.  
PR 10-FEB-2004; 2004US-0543480P.  
PR 13-FEB-2004; 2004US-00780447.  
PR 16-APR-2004; 2004US-00826566.  
PR 30-APR-2004; 2004WFO-US013456.  
PR 24-MAY-2004; 2004WFO-US016390.  
PR 09-JUN-2004; 2004US-00863973.  
XX  
PA (SIRN-) SIRNA THERAPEUTICS INC.  
XX  
PI Meswigen J, Beigelman L;  
XX  
DR WPI; 2005-581759/59.  
XX  
DR REFSEQ; NM\_001560.  
XX  
PT New chemically synthesized double stranded siNA molecule that directs  
PT cleavage of an Interleukin-13 receptor (IL-13R) RNA via RNA interference,  
PT useful in preparing a composition for treating e.g., inflammatory  
PT disorders.  
XX  
PS  
XX  
XX  
Claim 32; Page; 127pp; English.  
CC The invention relates to chemically synthesized short interfering nucleic  
CC acids (siNAs) which downregulate expression of receptors for interleukin-  
CC 13 (e.g., IL-13 receptor (IL-13R), IL-4 receptor (IL-4R) and IL-2  
CC receptor gamma (IL-2RG)) by RNA interference. The invention also relates  
CC to similar siNAs which interfere with the expression of the ligands for  
CC these receptors, namely IL-13 and IL-4. The siNAs of the invention may or  
CC may not comprise ribonucleotides, can contain deoxyribonucleotides, can  
CC be chemically modified and may be double or single stranded. They further  
CC comprise sense and antisense regions, or alternatively are assembled from  
CC a sense oligonucleotide and an antisense oligonucleotide. Specifically,  
CC the siNAs include short interfering RNA (siRNA), double-stranded RNA,  
CC micro-RNA (miRNA) and short hairpin RNA (shRNA). The invention also  
CC relates to pharmaceutical compositions comprising an siNA targeted to  
CC human IL-13R (e.g., IL-13R alpha 1 (IL13RA1), see RefSeq accession number  
CC NM\_001560), IL-4R, IL-2RG, IL-4 or IL-13, especially the siRNAs shown in  
CC AECL4082-AECL1592. The invention further discloses expression vectors and  
CC host cells comprising an siNA of the invention. The siNAs exhibit  
CC increased resistance to nuclease degradation compared to the prior art.  
CC The siNAs of the invention can be used to modulate expression of their  
CC target genes in cells, tissue explants or organisms (e.g., by ex vivo  
CC gene therapy), or in grafts and transplants for the treatment of a  
CC variety of interleukin-related conditions. They may be used in the  
CC treatment of cancers and other proliferative conditions, viral infection,  
CC inflammatory conditions, autoimmune diseases, respiratory and pulmonary  
CC diseases (e.g., asthma, chronic obstructive pulmonary disease (COPD),  
CC allergies), cardiovascular diseases, neurological diseases, renal  
CC diseases, ocular diseases, liver diseases, mitochondrial diseases,  
CC endocrine diseases, prion diseases and reproduction-related conditions.  
CC The siNAs may also be used in drug screening, diagnosis, therapeutic  
CC target identification and validation, genetic engineering,  
CC pharmacogenomics, studying gene function, and gene mapping (e.g., of  
CC single nucleotide polymorphisms). The present sequence represents a cDNA  
CC corresponding to human IL-13RA1 mRNA, which is specifically claimed as a

CC target for siRNAs of the invention. Note: The present sequence is not  
 CC shown in the specification, but was obtained from RefSeq accession number  
 CC NM\_001560. Other sequence data for this patent is also available in  
 CC electronic format directly from the US patent office at  
 CC seqdata.uspto.gov/sequence.html?docid=20050182007.

XX  
 SQ Sequence 4006 BP; 1129 A; 827 C; 885 G; 1165 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 14; Length 4006;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACGAACTCAGCCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 194  
 DB 121 CGGCGCTACGAACTCAGCCACTGTGACAAATTGAGTGTCTGTGTAACCTCTG 180  
 QY 195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 254  
 DB 181 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 240  
 QY 255 TTTTAGTCATTTTGGCAGCAAAACAAGATAAAGAAATAGCTCCGAACTGCTGTTCAAT 314  
 DB 241 TTTTAGTCATTTTGGCAGCAAAACAAGATAAAGAAATAGCTCCGAACTGCTGTTCAAT 300  
 QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACCAATGA 374  
 DB 301 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACCAATGA 360  
 QY 375 GAGTGAAGACCTTAGCTTTTGGTTGAAATATGATCTCACCCGAGAGGTGATCCATGA 434  
 DB 361 GAGTGAAGACCTTAGCTTTTGGTTGAAATATGATCTCACCCGAGAGGTGATCCATGA 420  
 QY 435 GTCTGCTGACTGAATCTCAATGCAATGCTTGGCAACACTGAGCTACATGAAGTCTTGTG 494  
 DB 421 GTCTGCTGACTGAATCTCAATGCAATGCTTGGCAACACTGAGCTACATGAAGTCTTGTG 480  
 QY 495 GCTCCCTGGAAGAAATACAGTCCCGACACTAACTATCTCTACTATTGGCAGAGAG 554  
 DB 481 GCTCCCTGGAAGAAATACAGTCCCGACACTAACTATCTCTACTATTGGCAGAGAG 540  
 QY 555 CCTGGAAGAAATATCATATGTAAGAAATCTTTTGAAGAGGCCAATATCTTGGTGTTC 614  
 DB 541 CCTGGAAGAAATATCATATGTAAGAAATCTTTTGAAGAGGCCAATATCTTGGTGTTC 600  
 QY 615 CTTTGATCTGACCAAGAGTGAAGGATTCAGTTTGAACAACAAGTCCCAATTAATGT 674  
 DB 601 CTTTGATCTGACCAAGAGTGAAGGATTCAGTTTGAACAACAAGTCCCAATTAATGT 660  
 QY 675 CAAGATATATGAGAGAAATTAACCATCTTCAATATAGTGCCCTTAATCTCCGCTG 734  
 DB 661 CAAGATATATGAGAGAAATTAACCATCTTCAATATAGTGCCCTTAATCTCCGCTG 720  
 QY 735 GAAACCTGATCTCCACATATTAATAACCTCTCTCTGACAAATGATAGTATGTGA 794  
 DB 721 GAAACCTGATCTCCACATATTAATAACCTCTCTCTGACAAATGATAGTATGTGA 780  
 QY 795 ATGGGGAATCCACAGAAATTTTATAGCAATGCCATTTTATGAAGTGAAGTCAATTA 854  
 DB 781 ATGGGGAATCCACAGAAATTTTATAGCAATGCCATTTTATGAAGTGAAGTCAATTA 840  
 QY 855 CAGCCAAACTGAGACATATATTTTCTAGCTGCTCAAGAGGCTAAATGTGAGATCCAGA 914  
 DB 841 CAGCCAAACTGAGACATATATTTTCTAGCTGCTCAAGAGGCTAAATGTGAGATCCAGA 900  
 QY 915 ATTGGAAGAAATGTGAGAAATACATCTTGTTCATGTCCTGCTGCTTCTCTGATAC 974  
 DB 901 ATTGGAAGAAATGTGAGAAATACATCTTGTTCATGTCCTGCTGCTTCTCTGATAC 960  
 QY 975 TTGGAACACAGTCAAGATATAGAGTCAAAACAATTAAGTATGCTATGAGATGACCAACT 1034  
 DB 961 TTGGAACACAGTCAAGATATAGAGTCAAAACAATTAAGTATGCTATGAGATGACCAACT 1020  
 QY 1035 CTGGAATATTTGAGGCCAAGAAATGAGTATAGTAAAGACGCAATTCACACTTACAT 1094

DB 1021 CTGAGATTAATTGAGCCAAAGAAATAGATATAGTAAGAAGGCAATTCACACTCTACAT 1080  
 QY 1095 AACCATTTCTCACTTTGTCAGATCAATGTCGAGTGGCAATGATAGTCTCTGCTTAA 1154  
 DB 1081 AACCATTTCTCACTTTGTCAGATCAATGTCGAGTGGCAATGATAGTCTCTGCTTAA 1140  
 QY 1155 CCTAAAGAGCTCAAGATTAATTAATTCCTCCAAATTCGATCTCTGCAAGATTTTAA 1214  
 DB 1141 CCTAAAGAGCTCAAGATTAATTAATTCCTCCAAATTCGATCTCTGCAAGATTTTAA 1200  
 QY 1215 AGAAATGTTGAGACCAAGATATGATGATCTGCACTGGAAGAGTACATCTATGA 1274  
 DB 1201 AGAAATGTTGAGACCAAGATATGATGATCTGCACTGGAAGAGTACATCTATGA 1260  
 QY 1275 GAGCAAAACCAAGAGAGAAACCACTCTGTATGCTGATAGAAAACCTGAAAGAACCTC 1334  
 DB 1261 GAGCAAAACCAAGAGAGAAACCACTCTGTATGCTGATAGAAAACCTGAAAGAACCTC 1320  
 QY 1335 TCAGTATGAGATTAATTAATTTTACCTTCACTGTGACCTTGAGAGA 1383  
 DB 1321 TCAGTATGAGATTAATTAATTTTACCTTCACTGTGACCTTGAGAGA 1369

RESULT 8  
 AAT85827  
 ID AAT85827 standard; DNA; 4009 BP.  
 XX  
 AC AAT85827;  
 XX  
 DT 22-JUN-1998 (first entry)  
 XX  
 DE Human interleukin-13 alpha receptor DNA.  
 XX  
 KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 34..1317  
 FT /product= "IL-13\_alpha\_receptor"  
 XX  
 PN WO9720926-A1.  
 XX  
 PD 12-JUN-1997.  
 XX  
 PF 07-NOV-1996; 96MO-FR001756.  
 XX  
 PR 06-DEC-1995; 95FR-00014424.  
 XX  
 PA (SNFI ) SANOFI SA.  
 XX  
 PI Caput D, Ferrara P, Laurent P, Vita N;  
 XX  
 DR WPI: 1997-319773/29.  
 XX  
 PT P-PSDB; AAM24973.  
 XX  
 PS Claim 12; Page 44-45; 83pp; French.  
 XX  
 CC This sequence encodes human interleukin-13 (IL-13) alpha receptor. The  
 CC invention relates to new purified peptides comprising 380 or 427 amino  
 CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
 CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
 CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
 CC affinity, but acquires high affinity when associated with the IL-4  
 CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as  
 CC diagnostic probes to identify aberrant synthesis or genetic anomalies  
 CC such as loss of heterozygosity and rearrangements, or chromosomal  
 CC anomalies. They are also used for production of recombinant IL-13R beta



CC and alpha which can be used as IL-13 antagonists, specifically to  
 CC regulate IL-13-induced responses for treatment of inflammation and  
 CC allergy. IL-13 receptors are also useful as antisense molecules for gene  
 CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard  
 CC immunosays) to diagnose diseases associated with abnormal expression of  
 CC IL-13 receptors; when coupled to a toxin also for treatment of  
 CC overproduction of IL-13R. Cells that express IL-13R at the surface are  
 CC used to identify ligands and modulators of IL-13R

XX Sequence 4009 BP; 1137 A; 826 C; 882 G; 1164 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 2; Length 4009;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 135 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194
DB 111 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 170
QY 195 CACAGTATATGACATGGAATCCACCCGAGGAGCAGCTCAAAATTTGATGCTATAGTA 254
DB 171 CACAGTATATGACATGGAATCCACCCGAGGAGCAGCTCAAAATTTGATGCTATAGTA 230
QY 255 TTTTATGCTATTTGGGACAAACAGATAAATAATGCTCCGGAATCTGCTGCTCAAT 314
DB 231 TTTTATGCTATTTGGGACAAACAGATAAATAATGCTCCGGAATCTGCTGCTCAAT 290
QY 315 AGAAGTACCCCTGATAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTAGCAACATGA 374
DB 291 AGAAGTACCCCTGATAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTAGCAACATGA 350
QY 375 GAGTGAGAAAGCTTAGCATTTTGGTGAATAATCATCTCAACCCCAAGAGTATCCTGA 434
DB 351 GAGTGAGAAAGCTTAGCATTTTGGTGAATAATCATCTCAACCCCAAGAGTATCCTGA 410
QY 435 GTCTGCTGTGACCTGAATCTTAATGCACTTTGGCACAACTGAGTCACTGAAGTCTTG 494
DB 411 GTCTGCTGTGACCTGAATCTTAATGCACTTTGGCACAACTGAGTCACTGAAGTCTTG 470
QY 495 GCTCCCTGGAAGATACCAAGTCCCGACACTAATCTCTACATATGGACAGAG 554
DB 471 GCTCCCTGGAAGATACCAAGTCCCGACACTAATCTCTACATATGGACAGAG 530
QY 555 CCTGGAATAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATCTTGGTGTTC 614
DB 531 CCTGGAATAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATCTTGGTGTTC 590
QY 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTCCAAATTAATGCT 674
DB 591 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTCCAAATTAATGCT 650
QY 675 CAAGATTAATGCAAGAAAAATTAACCAATCTTCAATATGAGCTTTAACTCCGCTG 734
DB 651 CAAGATTAATGCAAGAAAAATTAACCAATCTTCAATATGAGCTTTAACTCCGCTG 710
QY 735 GAAACCTGATCTCCATATTAATAAACTCTCTCTTCCAAATGATGAGCTATATGTA 794
DB 711 GAAACCTGATCTCCATATTAATAAACTCTCTCTTCCAAATGATGAGCTATATGTA 770
QY 795 ATGGGAGATCCCAAGATTTTATAGAGATGCTATTTTATGAGATGAAGTCAATTA 854
DB 771 ATGGGAGATCCCAAGATTTTATAGAGATGCTATTTTATGAGATGAAGTCAATTA 830
QY 855 CAGCCAAACTGAGACATTAATGTTTCTAGCTCAAGAGGCTAAATGAGATCCAGA 914
DB 831 CAGCCAAACTGAGACATTAATGTTTCTAGCTCAAGAGGCTAAATGAGATCCAGA 890
QY 915 ATTTGAGAGAAATGTGAGAAATCAATCTTGTTCATGAGTCCCTGTTGTTCTCTGATAC 974
DB 891 ATTTGAGAGAAATGTGAGAAATCAATCTTGTTCATGAGTCCCTGTTGTTCTCTGATAC 950
QY 975 TTTGAAACACAGTACGAATTAAGAGTCAAAACAAATTAAGTTTGTCTATGAGATGACAACT 1034
DB 951 TTTGAAACACAGTACGAATTAAGAGTCAAAACAAATTAAGTTTGTCTATGAGATGACAACT 1010

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DB 951 TTTGAAACACAGTACGAATTAAGAGTCAAAACAAATTAAGTTTGTCTATGAGATGACAACT 1010
QY 1035 CTGAGATTAATTTGAGGCAAGAAATGATATAGTAAAGCCCAATTTCCACACTTACAT 1094
DB 1011 CTGAGATTAATTTGAGGCAAGAAATGATATAGTAAAGCCCAATTTCCACACTTACAT 1070
QY 1095 AACCATGTTTACATATTTTCCAGTCACTGCTGCGAGGTGCAATCATATGTACTCTGCTTAA 1154
DB 1071 AACCATGTTTACATATTTTCCAGTCACTGCTGCGAGGTGCAATCATATGTACTCTGCTTAA 1130
QY 1155 CCTAAAGAGCTCAAGATTAATTAATTTCCCTCAATTCCTGATCCGCGAAGTTTTPAA 1214
DB 1131 CCTAAAGAGCTCAAGATTAATTAATTTCCCTCAATTCCTGATCCGCGAAGTTTTPAA 1190
QY 1215 AGAATATTTTGGAGACCAAGATGATATCTGTGACCTGGAAGAAATGACATCTATGA 1274
DB 1191 AGAATATTTTGGAGACCAAGATGATATCTGTGACCTGGAAGAAATGACATCTATGA 1250
QY 1275 GAAACCAACCAAGAGGAAACCGACTCTGTAGTCTGATAGAAAACCTGAGAAAGCTTC 1334
DB 1251 GAAACCAACCAAGAGGAAACCGACTCTGTAGTCTGATAGAAAACCTGAGAAAGCTTC 1310
QY 1335 TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383
DB 1311 TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1359

RESULT 9
AAA88907
ID AAA88907 standard; cDNA; 4038 BP.
XX
AC AAA88907;
XX
DT 05-MAR-2001 (first entry)
XX
DE Human interleukin-13 receptor alpha-1 cDNA.
XX
XX Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
XX atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
XX dermatological; antiasthmatic; antiallergic; therapy; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 43..1326
FT FT /*tag= a
FT sig_peptide 43..120
FT FT /*tag= b
FT mat_peptide 121..1323
FT FT /*tag= c
XX
XX US6143871-A.
XX
XX PD 07-NOV-2000.
XX
XX PF 12-NOV-1997; 97US-00969125.
XX
XX PR 13-DEC-1996; 96GB-00025899.
XX
XX PA (GAUC/) GAUCHAT J.
XX PA (BONN/) BONNEFOY J.
XX
XX PI Gauchat J, Bonnefoy J;
XX
XX DR WPI: 2001-006445/01.
XX DR P-PSDB; AABI9807.
XX
XX PT Novel polypeptide capable of binding interleukin-13 or interleukin-4
XX useful for treating atopy, atopic dermatitis, allergies, rhinitis,
XX eczema, asthma or AIDS.
XX
XX PS Example 1; Fig 1A-B; 26pp; English.
XX

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CC The present sequence is that of cDNA encoding a protein (see AAB19807)  
CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-  
CC 4 (IL-4) in the presence of IL-4 receptor alpha. To isolate the cDNA, PCR  
CC primers (see AAB8908-10) were designed from expressed sequence tags  
CC isolated from a database using mouse IL-13 receptor alpha. The primers  
CC were used to amplify human IL-13 receptor cDNA from activated tonsillar B  
CC cell cDNA. The resulting cDNA fragment was used to screen a lambda gt10  
CC library of activated tonsillar B cell cDNA and sequencing of the largest  
CC cDNA insert provided the present sequence. This IL-13 receptor alpha-1  
CC can be used to inhibit IL-13 or IL-4 induced IgE synthesis in B cells,  
CC useful in the treatment of diseases where IgE or Th2 differentiation  
CC plays a role, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema,  
CC asthma or AIDS. Antibodies raised against the polypeptide are useful for  
CC detecting IL-13 and IL-4 receptor or parts of them which have been shed  
CC from cells as a result of disease, e.g. cancer, leukemia, atopy, atopic  
CC dermatitis, allergies, rhinitis, eczema, asthma, AIDS, lupus  
CC erythematosus, thyroiditis, diabetes, uveitis, dermatitis, psoriasis,  
CC urticaria, nephrotic syndrome, glomerulonephritis, inflammatory bowel  
CC disease, ulcerative colitis, Crohn's disease, Sjogren's syndrome and  
CC toxoplasmosis

XX Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 4; Length 4038;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGGCCCTACGGAACTCAGCCACTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTG 194  
DB 120 CGGGCCCTACGGAACTCAGCCACTGTGACAAATTTAGTGTCTCTGTTGAAAACCTCTG 179  
QY 195 CACAGTAATATGACATGAAATCCACCGAGGAGCCAGCTCAAAATTTAGTGTCTATGATA 254  
DB 180 CACAGTAATATGACATGAAATCCACCGAGGAGCCAGCTCAAAATTTAGTGTCTATGATA 239  
QY 255 TTTTACGATTTTGGCACAACAGATTAAGAAATAGCTCCGGAACCTGCTGTCAT 314  
DB 240 TTTTACGATTTTGGGACAACAAGATAAGAAATAGCTCCGGAACCTGCTGTCAT 299  
QY 315 AGAAGTAACCCCTGATAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGCACCAATGA 374  
DB 300 AGAAGTAACCCCTGATAGAGATTTGTCTGCAAGTGGGCTCCAGTGTAGCACCAATGA 359  
QY 375 GAGTGAAGAGCTTGAATTTGTTGAAATAGATCTACCCCAAGGTATCTCTGA 434  
DB 360 GAGTGAAGAGCTTGAATTTGTTGAAATAGATCTACCCCAAGGTATCTCTGA 419  
QY 435 GTCTGCTGTGACCTGAACTTCAATGATTTGGACAACCTGAGTACATGAAGTCTTGG 494  
DB 420 GTCTGCTGTGACCTGAGCTTCAATGATTTGGACAACCTGAGTACATGAAGTCTTGG 479  
QY 495 GCTCCCTGGAAGATATCCAGTCCGACACTAACTATAGTCTCTACTATTGGACAGAG 554  
DB 480 GCTCCCTGGAAGATATCCAGTCCGACACTAACTATAGTCTCTACTATTGGACAGAG 539  
QY 555 CCTGGAAGAAATTCATCAATGTGAAAATCTTTAGGAAGGCCAATCTTTGGTCTTC 614  
DB 540 CCTGGAAGAAATTCATCAATGTGAAAATCTTTAGGAAGGCCAATCTTTGGTCTTC 599  
QY 615 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAAATTAATGT 674  
DB 600 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAAATTAATGT 659  
QY 675 CAAGGATATATGCGAAAAATTTAAACCATCTCTCAATATATGTGCTTTAACTCCGTGT 734  
DB 660 CAAGGATATATGCGAAAAATTTAAACCATCTCTCAATATATGTGCTTTAACTCCGTGT 719  
QY 735 GAAACCTGATCTCCACATATTAATAAACTCTCTTCCACATGATGACCTATATGATGA 794  
DB 720 GAAACCTGATCTCCACATATTAATAAACTCTCTTCCACATGATGACCTATATGATGA 779  
QY 795 ATGGAGAAATCCACAGATTTTATTTAGAGATGCTTATTTATGAAGTAGAAGCAATAA 854  
DB 780 ATGGAGAAATCCACAGATTTTATTTAGAGATGCTTATTTATGAAGTAGAAGCAATAA 839  
QY 855 CAGCAAACTGAGACATATATGTTTCTGCTCCAGAGGCTTAATGTGAATTCAGA 914  
DB 840 CAGCAAACTGAGACATATATGTTTCTGCTCCAGAGGCTTAATGTGAATTCAGA 899  
QY 915 ATTTGAGAGAAATGTGAGATATCATCTTTTCATGATGCTCCGTGTTCTCTGATAC 974  
DB 900 ATTTGAGAGAAATGTGAGATATCATCTTTTCATGATGCTCCGTGTTCTCTGATAC 959  
QY 975 TTGGAACACAGTCAGATTAAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAACT 1034  
DB 960 TTGGAACACAGTCAGATTAAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAACT 1019  
QY 1035 CTGAGATTAATTTGAGCCCAAAATTAAGTATGATTAAGAGGCAATTCACATCTTACAT 1094  
DB 1020 CTGAGATTAATTTGAGCCCAAAATTAAGTATGATTAAGAGGCAATTCACATCTTACAT 1079  
QY 1095 AACCATGTAATCTATTTGTCAGTCAATGTCGACAGTGCATCATAGTACCTGCTTTA 1154  
DB 1080 AACCATGTAATCTATTTGTCAGTCAATGTCGACAGTGCATCATAGTACCTGCTTTA 1139  
QY 1155 CTTAAAAAGCTCAAGATTAATTAATTCCTCCATTCATGATCTGCGCAAGATTTTAA 1214  
DB 1140 CTTAAAAAGCTCAAGATTAATTAATTCCTCCATTCATGATCTGCGCAAGATTTTAA 1199  
QY 1215 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAGTACATCTATGA 1274  
DB 1200 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAGTACATCTATGA 1259  
QY 1275 GAAGCAAAACCAAGAGAGAAACCGACTCTGATGCTGATTAAGAAAACCTGAAGAAAGCTC 1334  
DB 1260 GAAGCAAAACCAAGAGAGAAACCGACTCTGATGCTGATTAAGAAAACCTGAAGAAAGCTC 1319  
QY 1335 TCAGTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
DB 1320 TCAGTGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1368

RESULT 10  
ADL71811  
ID ADL71811 standard; cDNA; 4038 BP.  
XX  
AC ADL71811;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human interleukin-13 receptor alpha (IL-13 Ra1pha) cDNA.  
XX  
KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;  
KW eczema; asthma; AIDS; gene therapy; gene; ss; interleukin.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 43..1326  
FT FT /\*tag= b  
FT FT /product= "Human IL-13 protein"  
FT FT sig\_peptide 43..120  
FT FT /\*tag= a  
FT FT CDS 121..1323  
FT FT /\*tag= c  
FT FT /product= "Human mature IL-13 protein"  
FT FT misc\_feature 1321..1380  
FT FT /\*tag= d  
FT FT /note= "GC rich region"  
XX  
PN US2004043921-A1.  
XX  
PD 04-MAR-2004.  
XX  
XX 29-SEP-2003; 2003US-00671697.  
XX

PR 13-DEC-1996; 96GB-00025899.  
PR 12-NOV-1997; 97US-00969125.  
PR 06-APR-2000; 2000US-00545002.  
XX  
XX (BONN/) BONNEFOY J.  
PA (GAUC/) GAUCHAT J.  
XX  
XX Bonnefoy J, Gauchat J;  
PI WPI; 2004-225726/21.  
DR P-PSDB; ADL1812.  
XX  
XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse  
PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma  
PT or AIDS, comprises administering a polypeptide or soluble polypeptide.  
XX  
XX Example 1; SEQ ID NO 8; 27pp; English.  
XX  
XX The invention relates to polypeptides capable of binding human  
CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The  
CC invention also relates to a method of treatment of a disease in which  
CC IL13 and IL4 cause adverse effects. The method is useful for treating a  
CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic  
CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides  
CC of the invention are useful in raising antibodies. It is also useful in  
CC gene therapy. The present sequence is human interleukin-13 receptor alpha  
CC (IL-13 Ralpha) cDNA.  
SQ Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;  
Query Match 86.6%; Score 1198; DB 12; Length 4038;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CCGGCTTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194  
DB 120 CCGGCTTACGGAACCTCAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 179  
QY 195 CACAGTAATATGACATGGAATCACCCGAGGAGCCAGCTCAATTTGATCTATGTA 254  
DB 180 CACAGTAATATGACATGGAATCACCCGAGGAGCCAGCTCAATTTGATCTATGTA 239  
QY 255 TTTTATGTCATTTTGGGACAAACAAAGATTAAGAAATAGCTCCGGAAACCTGTGTTCAAT 314  
DB 240 TTTTATGTCATTTTGGGACAAACAAAGATTAAGAAATAGCTCCGGAAACCTGTGTTCAAT 299  
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGAGTATGACCAATGA 374  
DB 300 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGAGTATGACCAATGA 359  
QY 375 GAGTGGAAGACCTAGCATTTTGGTGAATAATGATCTCACCCCAGAAAGTGATCTCTGA 434  
DB 360 GAGTGGAAGACCTAGCATTTTGGTGAATAATGATCTCACCCCAGAAAGTGATCTCTGA 419  
QY 435 GTCTGTGTGACTGAACTTCAATGATGCTTTGGCAACCTGAGTACATGAAGTCTTGG 494  
DB 420 GTCTGTGTGACTGAACTTCAATGATGCTTTGGCAACCTGAGTACATGAAGTCTTGG 479  
QY 495 GCTCCCTGGAAGAAATACCAAGTCCCGACACTAATCTCTACATGTTGGACAGAG 554  
DB 480 GCTCCCTGGAAGAAATACCAAGTCCCGACACTAATCTCTACATGTTGGACAGAG 539  
QY 555 CCTGGAATAATTCATCAATGTGAAACATCTTTAGAGAGGCCAATTAATCTTGGTGTTC 614  
DB 540 CCTGGAATAATTCATCAATGTGAAACATCTTTAGAGAGGCCAATTAATCTTGGTGTTC 599  
QY 615 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAATTAATGT 674  
DB 600 CTTTGTATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAATTAATGT 659  
QY 675 CAAGGTAATGACAGAAAAATTAAACATCTTCAATATATAGTGTCTTAACTCCGTGT 734  
DB 660 CAAGGTAATGACAGAAAAATTAAACATCTTCAATATATAGTGTCTTAACTCCGTGT 719

QY 735 GAAACCTGATCTCCACATATTAACAACTCTCTTCCACAAATGATGACCTATATGTGA 794  
DB 720 GAAACCTGATCTCCACATATTAACAACTCTCTTCCACAAATGATGACCTATATGTGA 779  
QY 795 ATGGAGAAATCCACAAATTTTATAGAGATGCGATCTTTATGAAGTGAACATTA 854  
DB 780 ATGGAGAAATCCACAAATTTTATAGAGATGCGATCTTTATGAAGTGAACATTA 839  
QY 855 CAGCCAACTGAGACATATGTTTCTACGTCGAAGAGGCTAAATGTGAGAAATCCAGA 914  
DB 840 CAGCCAACTGAGACATATGTTTCTACGTCGAAGAGGCTAAATGTGAGAAATCCAGA 899  
QY 915 ATTTGAGAAATGTGAGAAATATCATCTTGTTCATGTCCTCTGTTCTTCTGATAC 974  
DB 900 ATTTGAGAAATGTGAGAAATATCATCTTGTTCATGTCCTCTGTTCTTCTGATAC 959  
QY 975 TTTGAACACAGTCAGAAATTAAGATCAAACTAAATTAAGTATGAGAGATCAAACT 1034  
DB 960 TTTGAACACAGTCAGAAATTAAGATCAAACTAAATTAAGTATGAGAGATCAAACT 1019  
QY 1035 CTGAGTAATTTGAGCCCAAGAAATGATAGTAAAGCCGAATTCACACTTACAT 1094  
DB 1020 CTGAGTAATTTGAGCCCAAGAAATGATAGTAAAGCCGAATTCACACTTACAT 1079  
QY 1095 AACCATGTTACTCATTTGTCAGTCATCTGTGAGGTCATATCATCTCTGCTTTA 1154  
DB 1080 AACCATGTTACTCATTTGTCAGTCATCTGTGAGGTCATATCATCTCTGCTTTA 1139  
QY 1155 CCTAAAGAGCTCAATATTAATATTCCTCCCAATTCCTGATCCGCGAAGTTTAA 1214  
DB 1140 CCTAAAGAGCTCAATATTAATATTCCTCCCAATTCCTGATCCGCGAAGTTTAA 1199  
QY 1215 AGAATGTTTGGAGACCAAGATGATATCTGTCACTGGAGAAATACACATCTATGA 1274  
DB 1200 AGAATGTTTGGAGACCAAGATGATATCTGTCACTGGAGAAATACACATCTATGA 1259  
QY 1275 GAAACCAACAGAGAGAAACCGACTCTGTAGTCTGATAGAAACCTGAGAAAGCTTC 1334  
DB 1260 GAAACCAACAGAGAGAAACCGACTCTGTAGTCTGATAGAAACCTGAGAAAGCTTC 1319  
QY 1335 TCAGTATGAGATTAATTTTACCTTCACTGACCTGAGAGAA 1383  
DB 1320 TCAGTATGAGATTAATTTTACCTTCACTGACCTGAGAGAA 1368  
RESULT 11  
ADN62574  
ID ADN62574 standard; cDNA; 4038 BP.  
XX  
XX ADN62574;  
AC XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human cDNA encoding interleukin 13 (IL-13) receptor alpha 1 chain.  
XX  
XX Human; ss; gene; interleukin 13 receptor alpha 1 chain; IL-13; IL-4;  
KW atopy; atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;  
KW cancer; inflammatory disease; rheumatoid arthritis;  
KW inflammatory bowel disease; multiple sclerosis; Alzheimer's disease;  
KW lupus erythematosus; chyloditis; diabetes; uveitis; psoriasis;  
KW urticaria; nephrotic syndrome; glomerulonephritis; ulcerative colitis;  
KW Crohn's disease; Sjogren's syndrome; toxoplasmosis; listeriosis; leprosy;  
KW Lyme disease; tuberculosis; malaria; leishmaniasis.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 43..1326  
FT CDS /tag= b  
FT /product= "IL-13 receptor alpha 1 chain"  
FT 43..120  
FT sig\_peptide /tag= a

FT mat\_peptide 121..1323  
FT /\*tag= C  
FT /note= "Mature IL-13 receptor alpha 1 chain"  
XX US6743604-B1.  
XX  
XX 01-JUN-2004.  
XX  
XX 06-APR-2000; 2000US-00545002.  
XX  
XX 13-DEC-1996; 96GB-00025899.  
XX 12-NOV-1997; 97US-00969125.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX Bonnefoy J, Gauchat J;  
XX WPI; 2004-409324/38.  
XX P-PSDB; ADN62575.  
XX  
XX New isolated nucleic acid molecule encoding a polypeptide capable of  
PT binding human IL-13 and/or binding human IL-4, useful in medicine, in  
PT diagnostics or for producing antibodies.  
XX  
XX Claim 1; SEQ ID NO 8; 24bp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (ADN62574),  
CC which encodes the mature form of a polypeptide capable of binding human  
CC IL-13 (interleukin 13) and/or binding human IL-4 (designated IL-13  
CC receptor alpha 1 subunit) appearing as ADN62575. Also included are a  
CC vector comprising the nucleic acid molecule and a host cell comprising  
CC the vector. The nucleic acids are useful as probes or primers or in the  
CC analysis of allelic variation. The polypeptides are useful for binding  
CC human IL-13 and/or binding human IL-4 and act as inhibitors by  
CC interfering with the interaction between human IL-13 or IL-4 and their  
CC natural receptors. They can also be used in medicine, e.g. for treatment  
CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,  
CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and  
CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,  
CC lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,  
CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,  
CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,  
CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be  
CC used for producing antibodies, which can be used for diagnosing diseases.  
CC The present sequence encodes IL-13 receptor alpha 1 subunit.  
XX  
XX Sequence 4038 BP; 1135 A; 839 C; 896 G; 1168 T; 0 U; 0 Other;  
SQ  
Query Match 86.6%; Score 1198; DB 12; Length 4038;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CGGCGCTACGAACTCAGCCACCTGTGACAAATTGAGTGTCTCTGTTGAAAACCTCTG 194  
DB 120 CGGCGCTACGAACTCAGCCACCTGTGACAAATTGAGTGTCTCTGTTGAAAACCTCTG 179  
QY 195 CAGAGTAATTGACATGGAATCCACCCGAGGAGCCAGTCAAAATTGTTGTTATGTA 254  
DB 180 CAGAGTAATTGACATGGAATCCACCCGAGGAGCCAGTCAAAATTGTTGTTATGTA 239  
QY 255 TTTTAACTATTGGCGACAAACAGATAAGAAAATAGTCCGGAATCTGTGTTCAAT 314  
DB 240 TTTTAACTATTGGCGACAAACAGATAAGAAAATAGTCCGGAATCTGTGTTCAAT 299  
QY 315 AGAAGTAACCTCTGAATGAGAGATTTGTCTGCAAGTGGGTTCCAGTGTAGCAACCAATGA 374  
DB 300 AGAAGTAACCTCTGAATGAGAGATTTGTCTGCAAGTGGGTTCCAGTGTAGCAACCAATGA 359  
QY 375 GAGTGAAGAGCTTAGCATTTTGGTTGAAAATGATCTACCCCGAGAAAGTATCTCTGA 434  
DB 360 GAGTGAAGAGCTTAGCATTTTGGTTGAAAATGATCTACCCCGAGAAAGTATCTCTGA 419  
QY 435 GTCTGTGTGACTGAATCTTCAATGATCTTGGCAACACCTGAGTACTGATGAAGTGTCTTG 494

DB 420 GTCTGTGTGACTGAGCTTCAATGATCTTGGCAACACCTGAGTACTGATGAAGTGTCTTG 479  
QY 495 GCTTCCCTGGAAGGAATCCAGTCCCGACATTAATATCTCTCAATATTGGCACAAG 554  
DB 480 GCTTCCCTGGAAGGAATCCAGTCCCGACATTAATATCTCTCAATATTGGCACAAG 539  
QY 555 CTTGGAATAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATACCTTGTGTTTC 614  
DB 540 CTTGGAATAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATACCTTGTGTTTC 599  
QY 615 CTTGATCTGACCAAAATGAGATTCAGTTTGAACACACAGTGTCCAAATATGTT 674  
DB 600 CTTGATCTGACCAAAATGAGATTCAGTTTGAACACACAGTGTCCAAATATGTT 659  
QY 675 CAAGATTAATGCAAGAAAATTAACCATCTCTCAATATATAGTCTTAACTTCCGTGT 734  
DB 660 CAAGATTAATGCAAGAAAATTAACCATCTCTCAATATATAGTCTTAACTTCCGTGT 719  
QY 735 GAAACCTGATCTTCCACATATTAATAAAGCTCTCTCCACAAATGATGACCTATATGCA 794  
DB 720 GAAACCTGATCTTCCACATATTAATAAAGCTCTCTCCACAAATGATGACCTATATGCA 779  
QY 795 ATGGAGAAATCCACAGAAATTTTATGACATGCTTATTTATGAAATGATGAAATCAAT 854  
DB 780 ATGGAGAAATCCACAGAAATTTTATGACATGCTTATTTATGAAATGATGAAATCAAT 839  
QY 855 CAGCCAAATGAGACATATATGTTTCTACAGTCCAAAGAGCTTAATATGTAATCCAGA 914  
DB 840 CAGCCAAATGAGACATATATGTTTCTACAGTCCAAAGAGCTTAATATGTAATCCAGA 899  
QY 915 ATTTGAGAAATGAGAAATATCATCTTCTTCAATGCTCCGAGTCTCTCTGATAC 974  
DB 900 ATTTGAGAAATGAGAAATATCATCTTCTTCAATGCTCCGAGTCTCTCTGATAC 959  
QY 975 TTTGAACACAGTCAATATGATGTAAGTCAAAACAAATATGTTATGATGATGATCAACT 1034  
DB 960 TTTGAACACAGTCAATATGATGTAAGTCAAAACAAATATGTTATGATGATGATCAACT 1019  
QY 1035 CTGAGTAATTGAGACCAAGAAATGATATAGTAAAGCCCAATTCACACTCTACAT 1094  
DB 1020 CTGAGTAATTGAGACCAAGAAATGATATAGTAAAGCCCAATTCACACTCTACAT 1079  
QY 1095 AACCATGTTACATGATGTTCCAGTCAATGCTGAGGAGCAATGATCTCCGCTTAA 1154  
DB 1080 AACCATGTTACATGATGTTCCAGTCAATGCTGAGGAGCAATGATCTCCGCTTAA 1139  
QY 1155 CCTAAAAAGGCTCAAGTTATTTATTTCTCTCCCAATTCCTGATCTGGAAGATTTTAA 1214  
DB 1140 CCTAAAAAGGCTCAAGTTATTTATTTCTCTCCCAATTCCTGATCTGGAAGATTTTAA 1199  
QY 1215 AGAATGTTTGAACCAAGATGATATCTGCACTGGAAGATGACATCTATGA 1274  
DB 1200 AGAATGTTTGAACCAAGATGATATCTGCACTGGAAGATGACATCTATGA 1259  
QY 1275 GAAGCAAAACCAAGAGAAAACGACCTGTGATGCTGATGAAAACCTGAAAGAAAGCCTC 1334  
DB 1260 GAAGCAAAACCAAGAGAAAACGACCTGTGATGCTGATGAAAACCTGAAAGAAAGCCTC 1319  
QY 1335 TCAGTATGAGATATTTATTTTACCTTCACTGTGACCTTGAGAA 1363  
DB 1320 TCAGTATGAGATATTTATTTTACCTTCACTGTGACCTTGAGAA 1368  
RESULT 12  
AAA35214  
ID AAA35214 standard; DNA; 4039 BP.  
XX  
XX AAA35214;  
AC  
XX 28-JUL-2000 (first entry)  
DT  
XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:88.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO200009525-A2.  
XX  
XX 24-FEB-2000.  
XX  
XX 03-AUG-1999; 99WO-US017712.  
XX  
XX 03-AUG-1998; 98US-0095212P.  
XX  
XX (UYEC-) UNITV EAST CAROLINA.  
XX  
XX Myce JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
XX cancers.  
XX  
XX Disclosure; Page 1253-1254; 1343p; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antialsthmatic, cyostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA3312 represent the  
CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
XX listing  
XX  
XX Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;  
SQ  
Query Match 86.6%; Score 1198; DB 3; Length 4039;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CGGGCTAGGAAACACGACACCTGTGACAAATTTGAGTCTCTGTTGAAAACCTCTG 194  
DB 121 CGGGCTAGGAAACACGACACCTGTGACAAATTTGAGTCTCTGTTGAAAACCTCTG 180  
QY 195 CACAGTAATATGACATGATCCACCCGAGGAGGACGCTCAATTTGATGTTATGTA 254  
DB 181 CACAGTAATATGACATGATCCACCCGAGGAGGACGCTCAATTTGATGTTATGTA 240

QY 255 TTTTATGTCATTTTGGCGACAAAACAAGATTAAGAAAATAGCTCCGGAAACCTGCTTCAAT 314  
DB 241 TTTTATGTCATTTTGGCGACAAAACAAGATTAAGAAAATAGCTCCGGAAACCTGCTTCAAT 300  
QY 315 AGAAGTACCCCGAATGAGAGATTTGTCTGAAAGGGGGTCCAGTGTAGACCAATGA 374  
DB 301 AGAAGTACCCCGAATGAGAGATTTGTCTGAAAGGGGGTCCAGTGTAGACCAATGA 360  
QY 375 GAGTGAAAGCCCTAGCATTTTGGTTGAAAATATGATCTTCACCCCGAAGAGTGATCTTA 434  
DB 361 GAGTGAAAGCCCTAGCATTTTGGTTGAAAATATGATCTTCACCCCGAAGAGTGATCTTA 420  
QY 435 GTCTGCTGTGACTGAACTTCAATGCAATTTGGCAACCTGAGCTACATGAATGTTCTTG 494  
DB 421 GTCTGCTGTGACTGAGCTTCAATGCAATTTGGCAACCTGAGCTACATGAATGTTCTTG 480  
QY 495 GCTCCCTGGAAGAAATACCAAGTCCGACCTAATATATCTCTATATTTGGACAGAG 554  
DB 481 GCTCCCTGGAAGAAATACCAAGTCCGACCTAATATATCTCTATATTTGGACAGAG 540  
QY 555 CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAAGCCAAATCTTTGGTTGTC 614  
DB 541 CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAAGCCAAATCTTTGGTTGTC 600  
QY 615 CTTTGATCTGACCAAAAGTGAAGATTTCCAGTTTGAACAACACAGTGTCCAATATATGAT 674  
DB 601 CTTTGATCTGACCAAAAGTGAAGATTTCCAGTTTGAACAACAGTGTCCAATATATGAT 660  
QY 675 CAAGATTAATGAGAGAAAAATTAACCATCTTCAATATAGAGCCCTTAATCTCCGCTGT 734  
DB 661 CAAGATTAATGAGAGAAAAATTAACCATCTTCAATATAGAGCCCTTAATCTCCGCTGT 720  
QY 735 GAAACCTGATCTCCACATATTTAAAAACCTCTCTTCCAAATGATGACCTATATGTGCA 794  
DB 721 GAAACCTGATCTCCACATATTTAAAAACCTCTCTTCCAAATGATGACCTATATGTGCA 780  
QY 795 ATGGAGAAATCCACAGAAATTTATTTAGCAGATGCTTATTTATGAAATGAAATCAATA 854  
DB 781 ATGGAGAAATCCACAGAAATTTATTTAGCAGATGCTTATTTATGAAATGAAATCAATA 840  
QY 855 CAGCCAAATGAGACACATATATGTTTCTACGTCGAAGGCTTAATGTGAAATCCAGA 914  
DB 841 CAGCCAAATGAGACACATATATGTTTCTACGTCGAAGGCTTAATGTGAAATCCAGA 900  
QY 915 ATTTGAGAAATGTGAGAAATACATCTTTTCAATGCTCCCTGTGTTCTTCTGTATAC 974  
DB 901 ATTTGAGAAATGTGAGAAATACATCTTTTCAATGCTCCCTGTGTTCTTCTGTATAC 960  
QY 975 TTTGAAACACATGACATATAGAGTCAAAAACAATTAATGTTATGTATGAGATGACAAACT 1034  
DB 961 TTTGAAACACATGACATATAGAGTCAAAAACAATTAATGTTATGTATGAGATGACAAACT 1020  
QY 1035 CTGGAGTAATTTGAGGCAAGAAATGATATGATTAAGAGCCAAATTCACACTACAT 1094  
DB 1021 CTGGAGTAATTTGAGGCAAGAAATGATATGATTAAGAGCCAAATTCACACTACAT 1080  
QY 1095 AACCATGTTACTCATTTGTTCCAGTCATGTCGAGGTGCAATCATATGATCTCTGCTTTA 1154  
DB 1081 AACCATGTTACTCATTTGTTCCAGTCATGTCGAGGTGCAATCATATGATCTCTGCTTTA 1140  
QY 1155 CCTAAAAAGGCTCAAGATTTATATTTCCCTCCATTTCTGTATCTCTGCAAGATTTTAA 1214  
DB 1141 CCTAAAAAGGCTCAAGATTTATATTTCCCTCCATTTCTGTATCTCTGCAAGATTTTAA 1200  
QY 1215 AGAATATGTTTGGAGACCAAGATGATATCTCTGCACTGGAAGAGTACGACATCTATGA 1274  
DB 1201 AGAATATGTTTGGAGACCAAGATGATATCTCTGCACTGGAAGAGTACGACATCTATGA 1260  
QY 1275 GAAGCAAAACCAAGAGAAACCGACTGTGTAGTCTGATAGAAAACCTGAAGAAAGCTTC 1334  
DB 1261 GAAGCAAAACCAAGAGAAACCGACTGTGTAGTCTGATAGAAAACCTGAAGAAAGCTTC 1320  
QY 1335 TCAATGATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383

Db 1321 TCAGTGTAGAGATTAATTTTACCTCAGTGTGAGAGAGA 1369

## RESULT\_13

AAF21336 ID AAF21336 standard; DNA; 4039 BP.

XX AAF21336;

DT 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2903.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
XX human; airway disorder; bronchoconstriction; lung inflammation;  
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
XX immunosuppressive; antiaesthetic; analgesic; hypotensive; cytotactic;  
XX respiratory obstruction; pulmonary obstruction; impeded respiration;  
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
XX cancer; ss.

XX Homo sapiens.

PN W0200062736-A2.

XX 26-OCT-2000.

PF 24-MAR-2000; 2000WO-US008020.

XX 06-APR-1999; 99US-0127958P.

PA (UYEC-) UNIV EAST CAROLINA.

XX (NYCE/) NYCE J W.

PI NYCE JW;

XX WPI; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not trigger  
PT adenosine receptors during metabolism, useful e.g. for treating cancers  
PT and respiratory obstructions.

PS Disclosure; Page 1337-1338; 1592p; English.

XX The present invention describes low adenosine (A) content antisense  
CC oligonucleotides and compositions (I) comprising them. In the antisense  
CC oligonucleotides the A is replaced by a 'universal' or alternative base.  
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
CC immunosuppressive, antiaesthetic, hypotensive and cytotactic activities.  
CC The antisense oligonucleotides and (I) can be used to down-regulate the  
CC expression and/or activity of target polypeptides associated with  
CC lung/respiratory disorders and malignancies, such as stimulating and  
CC activating peptide factors and transmitters, transcription factors,  
CC immunoglobulins and antibodies, antibody receptors, cytokines and  
CC chemokines, endogenously produced specific and non-specific enzymes,  
CC binding proteins, adhesion molecules and their receptors, cytokine and  
CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
CC nervous system (CNS) and peripheral nervous and non-nervous system  
CC receptors, CNS and peripheral nervous and non-nervous system peptide  
CC transmitters, defensins, growth factors, vasoactive peptides and  
CC receptors, binding proteins and malignancy associated proteins. The  
CC antisense oligonucleotides may be used in this way to treat disorders  
CC including respiratory obstruction (especially pulmonary obstruction  
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
CC surfactant hypoproduction which are associated with a disease or  
CC condition selected from pulmonary vasoconstriction, inflammation,  
CC allergies, asthma, impeded respiration, respiratory distress syndrome  
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
CC hyperinflation, emphysema, chronic obstructive pulmonary disease (COPD),

CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
CC and/or cancer. AAF21336 to AAF21543 represent human polynucleotide  
CC fragments and antisense oligonucleotides used in the exemplification of  
CC the present invention

XX Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;

Query Match 86.6%; Score 1198; DB 3; Length 4039;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGCGCTACGGAACCTGAGCCACCTGTGACAAATTTGAGTCTCTGTTGAAAACCTGTG 194  
Db 121 CGGCGCTACGGAACCTGAGCCACCTGTGACAAATTTGAGTCTCTGTTGAAAACCTGTG 180  
QY 195 CACGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTTAGTCTATGTA 254  
Db 181 CACGTAATATGACATGGAATCCACCGAGGAGCCAGCTCAATTTAGTCTATGTA 240  
QY 255 TTTTAGCATTTTGGCGCAAAAGATTAAGAAATAGCTCCGGAACCTGCTGTTCAAT 314  
Db 241 TTTTAGCATTTTGGCGCAAAAGATTAAGAAATAGCTCCGGAACCTGCTGTTCAAT 300  
QY 315 AGAAGTACCCCTGAATGAGAGATTTGCTGCAAGTGGGTCCAGTGTACACCAATGA 374  
Db 301 AGAAGTACCCCTGAATGAGAGATTTGCTGCAAGTGGGTCCAGTGTACACCAATGA 360  
QY 375 GAGTGAAGAGCTTACGATTTTGGTTGAAAATGATCTACCCCCAGAGGTATCTCTGA 434  
Db 361 GAGTGAAGAGCTTACGATTTTGGTTGAAAATGATCTACCCCCAGAGGTATCTCTGA 420  
QY 435 GTCTGCTGTGCTGAATGATGATGATTTGGCAACACCTGAGTACATGAAGTGTCTTG 494  
Db 421 GTCTGCTGTGCTGAATGATGATGATTTGGCAACACCTGAGTACATGAAGTGTCTTG 480  
QY 495 GCTCCCTGGAAGAAATCCAGTCCCGACACTTAATCTCTACTATTGGCAGAGAG 554  
Db 481 GCTCCCTGGAAGAAATCCAGTCCCGACACTTAATCTCTACTATTGGCAGAGAG 540  
QY 555 CTTGGAAGAAATTTGATGATGATGATTTGAGAGAGGCAATATCTTGGTGTTC 614  
Db 541 CTTGGAAGAAATTTGATGATGATGATTTGAGAGAGGCAATATCTTGGTGTTC 600  
QY 615 CTTGATCTGACCAAGATGGAAGATTCAGTTTGAACAACAGTGTCCAAATATGAT 674  
Db 601 CTTGATCTGACCAAGATGGAAGATTCAGTTTGAACAACAGTGTCCAAATATGAT 660  
QY 675 CAAGGATATGACAGGAAATTTAAACCATCTTCAATATAGTGCCTTAACTCCCGGT 734  
Db 661 CAAGGATATGACAGGAAATTTAAACCATCTTCAATATAGTGCCTTAACTCCCGGT 720  
QY 735 GAAACCTGATCTTCAATATTTAAACCTCTCTCCACAAATGATGATGATGATGCA 794  
Db 721 GAAACCTGATCTTCAATATTTAAACCTCTCTCCACAAATGATGATGATGATGCA 780  
QY 795 ATGGGAATTCACAGAAATTTTATTTAGCAATGCTTATTTTAAAGTGAAGCAATTA 854  
Db 781 ATGGGAATTCACAGAAATTTTATTTAGCAATGCTTATTTTAAAGTGAAGCAATTA 840  
QY 855 CAGGCAATGACAGACATATGTTTCTAGTCCAGAGGCTAAATGTGGAATTCAGA 914  
Db 841 CAGGCAATGACAGACATATGTTTCTAGTCCAGAGGCTAAATGTGGAATTCAGA 900  
QY 915 ATTTGAGAAATGTGGAATATACATTTGTTTCATGCTCTCTGTTCTCTGATAC 974  
Db 901 ATTTGAGAAATGTGGAATATACATTTGTTTCATGCTCTCTGTTCTCTGATAC 960  
QY 975 TTTGAACACGTGCAATTAAGATCAAAACAAATTAATGATGATGATGATGCAACT 1034  
Db 961 TTTGAACACGTGCAATTAAGATCAAAACAAATTAATGATGATGATGATGCAACT 1020  
QY 1035 CTGAGATTAATTTGAGCCAAAGAAATGATATATGATGATGATGATGATGATGATGAT 1094

|    |      |  |      |
|----|------|--|------|
| Db | 102  | CTGGAGTAATTGGAGCCAGAGAAATGAGTATAGTAAAGAGGCCAATTCACACTCTACAT  | 1080 |
| Qy | 1095 | AACCATGTTACTCATTTGTTCCAGTCATGTCGCAGGTGCAATCATAGTACTCTGCTTTA  | 1154 |
| Db | 1081 | AACCATGTTACTCATTTGTTCCAGTCATGTCGCAGGTGCAATCATAGTACTCTGCTTTA  | 1140 |
| Qy | 1155 | CCTAAAAAGGCTCAAGATTATTATATTCCTCCACATTCCTGATCTGGCAAGATTTTAA   | 1214 |
| Db | 1141 | CCTAAAAAGGCTCAAGATTATTATATTCCTCCACATTCCTGATCTGGCAAGATTTTAA   | 1200 |
| Qy | 1215 | AGAAATGTTTGGAGACCAGAAATGATGATCTCTGCATCGAAGAAAGTACGACATCTATGA | 1274 |
| Db | 1201 | AGAAATGTTTGGAGACCAGAAATGATGATCTCTGCATCGAAGAAAGTACGACATCTATGA | 1260 |
| Qy | 1275 | GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTCTGTATAAAAACCTGGAAGAAGCTC  | 1334 |
| Db | 1261 | GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTCTGTATAAAAACCTGGAAGAAGCTC  | 1320 |
| Qy | 1335 | TCAGTGATGAGATATTTATTTTACCTTCACTGTGACCTTGAGAGA                | 1383 |
| Db | 1321 | TCAGTGATGAGATATTTATTTTACCTTCACTGTGACCTTGAGAGA                | 1369 |

|          |  |
|----------|--|
| RESULT   | 14   |
| ABL67709 |  |
| ID       | ABL67709 standard; DNA; 4039 BP.   |
| XX       |  |
| AC       |  |
| XX       | ABL67709;  |
| DT       | 15-MAY-2002 (first entry)  |
| XX       |  |
| DE       | Oesophagus cancer related gene sequence SEQ ID NO:6046.                  |
| KW       | Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;        |
| KW       | stomach; lung; prostate; pancreas; carcinoma; antitumour; carcinos;      |
| KW       | cyclosatic; gene therapy; antineoplastic; Wiln's tumour; adenocarcinoma, |
| XX       | gene; ds.  |
| XX       |  |
| OS       | Homo sapiens.  |
| XX       |  |
| PN       | MO200194629-A2.  |
| PD       |  |
| XX       | 13-DEC-2001.   |
| PF       |  |
| XX       | 30-MAY-2001; 2001WO-US010838.  |
| PR       |  |
| PR       | 05-JUN-2000; 2000US-0209473P.  |
| PR       | 05-JUN-2000; 2000US-0209531P.  |
| PR       | 18-SEP-2000; 2000US-0233133P.  |
| PR       | 18-SEP-2000; 2000US-0233617P.  |
| PR       | 20-SEP-2000; 2000US-0234009P.  |
| PR       | 20-SEP-2000; 2000US-0234034P.  |
| PR       | 20-SEP-2000; 2000US-0234052P.  |
| PR       | 22-SEP-2000; 2000US-0234509P.  |
| PR       | 22-SEP-2000; 2000US-0234567P.  |
| PR       | 25-SEP-2000; 2000US-0234923P.  |
| PR       | 25-SEP-2000; 2000US-0234924P.  |
| PR       | 25-SEP-2000; 2000US-0235077P.  |
| PR       | 25-SEP-2000; 2000US-0235082P.  |
| PR       | 25-SEP-2000; 2000US-0235134P.  |
| PR       | 25-SEP-2000; 2000US-0235280P.  |
| PR       | 26-SEP-2000; 2000US-0235637P.  |
| PR       | 26-SEP-2000; 2000US-0235638P.  |
| PR       | 27-SEP-2000; 2000US-0235711P.  |
| PR       | 27-SEP-2000; 2000US-0235720P.  |
| PR       | 27-SEP-2000; 2000US-0235840P.  |
| PR       | 27-SEP-2000; 2000US-0235863P.  |
| PR       | 28-SEP-2000; 2000US-0236028P.  |
| PR       | 28-SEP-2000; 2000US-0236032P.  |
| PR       | 28-SEP-2000; 2000US-0236033P.  |
| PR       | 28-SEP-2000; 2000US-0236034P.  |
| PR       | 28-SEP-2000; 2000US-0236109P.  |
| PR       | 28-SEP-2000; 2000US-0236111P.  |

|    |                       |  |
|----|-----------------------|--|
| XX | 29-SEP-2000;          | 2000US-0236842P.                           |
| RR | 29-SEP-2000;          | 2000US-0236891P.                           |
| RR | 02-OCT-2000;          | 2000US-0237172P.                           |
| RR | 02-OCT-2000;          | 2000US-0237173P.                           |
| PR | 02-OCT-2000;          | 2000US-0237278P.                           |
| PR | 02-OCT-2000;          | 2000US-0237294P.                           |
| PR | 02-OCT-2000;          | 2000US-0237295P.                           |
| PR | 02-OCT-2000;          | 2000US-0237316P.                           |
| RR | 03-OCT-2000;          | 2000US-0237425P.                           |
| RR | 03-OCT-2000;          | 2000US-0237598P.                           |
| PR | 03-OCT-2000;          | 2000US-0237604P.                           |
| PR | 03-OCT-2000;          | 2000US-0237606P.                           |
| PR | 03-OCT-2000;          | 2000US-0237608P.                           |
| RR | 01-NOV-2000;          | 2000US-0244867P.                           |
| RR | 01-NOV-2000;          | 2000US-0245084P.                           |
| XX |                       |  |
| PA | (AVAL-) AVALON PHARM. |  |
| XX |                       |  |
| P1 | Young PE, Augustus M, | Carter KC, Ebner R, Endress G, Horrigan S; |
| P1 | Soppet DR, Weaver Z;  |  |
| XX |                       |  |
| DR | WPI; 2002-188264/24.  |  |

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 6046; 44pp; English.

CC The present invention describes method (M1) for screening for an anti  
CC neoplastic agent. The method involves exposing cells to a chemical agent  
CC to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (1) of a signature gene set, where (1)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664  
CC to ABU70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (1) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening  
CC anti-neoplastic agent, and can be used for producing a product which is  
CC the data collected with respect to the anti-neoplastic agent as a result  
CC of M1, and the data is sufficient to convey the chemical structure and/or  
CC properties of the agent. M1 can be used in the treatment of cancer such  
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's  
CC tumour  
XX  
XX Sequence 4039 BP; 1135 A; 839 C; 896 G; 1169 T; 0 U; 0 Other;  
XQ

|             |        |             |       |              |
|-------------|--------|-------------|-------|--------------|
| every Match | 86.6%; | Score 1198; | DB 6; | Length 4039; |
|-------------|--------|-------------|-------|--------------|

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st Local Similarity 99.9%; Pred. No. 0;
tches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0

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|    |     |  |     |
|----|-----|--|-----|
| Qy | 13  | CGGCGCTACGGAAACCTCAGCCACCCCTGTACAAATTAGAGTCTCTGTGGAAACCTCTG    | 194 |
| Db | 121 | CGGCGCTACGGAAACCTCAGCCACCTGTACAAATTAGAGTCTCTGTGGAAACCTCTG      | 180 |
| Qy | 195 | CACAGTATATGACATGGAATCCACCCGAGGAGCCAGCTCAAAATTGTAGTCTATGTA      | 254 |
| Db | 181 | CACAGTATATGGAATGGAATCCACCCGAGGAGCCAGCTCAAAATTGTAGTCTATGTA      | 240 |
| Qy | 255 | TTTTTACTCATTTTGGCGACAAACAAGATTAAGAAAAATAGCTCCGGAAACTGTCGTTCAAT | 314 |
| Db | 241 | TTTTTACTCATTTTGGCGACAAACAAGATTAAGAAAAATAGCTCCGGAAACTGTCGTTCAAT | 300 |
| Qy | 315 | AGAGATACCCCTGAATGAGAGGATTTGTCTCAAGTGGGGTCCAGATGACACCAATGA      | 374 |
| Db | 301 | AGAGATACCCCTGAATGAGAGGATTTGTCTCAAGTGGGGTCCAGATGACACCAATGA      | 360 |
| Qy | 375 | GAGTGAAGACCTAGACATTTTGGTTGAAAAATGCATCTCACCCGAGAGGTGATCTGA      | 434 |
| Db | 361 | GAGTGAAGACCTAGACATTTTGGTTGAAAAATGCATCTCACCCGAGAGGTGATCTGA      | 420 |







| Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |      |  |      |
|---|------|--|------|
| QY  | 135  | CGGCGCTACGGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTGTAACCTCTG         | 194  |
| Db  | 121  | CGGCGCTACGGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTGTAACCTCTG         | 180  |
| QY  | 195  | CACAGTAATATGGAATGCAATCCCGAGGAGCCAGTCAATTTGATGCTATGTA           | 254  |
| Db  | 181  | CACAGTAATATGGAATGCAATCCCGAGGAGCCAGTCAATTTGATGCTATGTA           | 240  |
| QY  | 255  | TTTTTACTGATTTGGGGACAAACAAGATAGAAAATAGCTCCGGAAACTGTGTCAT        | 314  |
| Db  | 241  | TTTTTACTGATTTGGGGACAAACAAGATAGAAAATAGCTCCGGAAACTGTGTCAT        | 300  |
| QY  | 315  | AGAAATGACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACA       | 374  |
| Db  | 301  | AGAAATGACCCCTGGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACA       | 360  |
| QY  | 375  | GAGTGAAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCGAAGGTGATCTGA       | 434  |
| Db  | 361  | GAGTGAAAGCCTAGCATTTTGGTTGAAAAATGCATCTCACCCCGAAGGTGATCTGA       | 420  |
| QY  | 435  | GTCTGCTGACGTGAACCTTCAATGCAATTTGGGCAACACCTGACATGAAGTTCCTG       | 494  |
| Db  | 421  | GTCTGCTGACGTGAACCTTCAATGCAATTTGGGCAACACCTGACATGAAGTTCCTG       | 480  |
| QY  | 495  | GCTCCCTGGAAGGAATACAGTCCCGACACTAACTACTCTCTACTATTGGCACAAG        | 554  |
| Db  | 481  | GCTCCCTGGAAGGAATACAGTCCCGACACTAACTACTCTCTACTATTGGCACAAG        | 540  |
| QY  | 555  | CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGGAAGGCCAATACTTTGGTGTTC     | 614  |
| Db  | 541  | CCTGGAAAAAATTCATCAATGTGAAAACATCTTTAGGAAGGCCAATACTTTGGTGTTC     | 600  |
| QY  | 615  | CTTTGATCGAACCAAGTGAAGATCCAGTTTGAACAACAGTGTCCAAATAATGTG         | 674  |
| Db  | 601  | CTTTGATCGAACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAATGTG         | 660  |
| QY  | 675  | CAAGATAATGCAAGAAAAATTTAAACCATCTTCAATATAGTCCCTTAACCTCCGCTG      | 734  |
| Db  | 661  | CAAGATAATGCAAGAAAAATTTAAACCATCTTCAATATAGTCCCTTAACCTCCGCTG      | 720  |
| QY  | 735  | GAAACCTGATCTCCCATATTTAAAACTCTCTCTTCACATGATGACCTATATGTGCA       | 794  |
| Db  | 721  | GAAACCTGATCTCCCATATTTAAAACTCTCTCTTCACATGATGACCTATATGTGCA       | 780  |
| QY  | 795  | ATGGGAGAAATCCACAGAAATTTTATAGAGATGACCTATTTATAGAGTAGAAGTCAATTA   | 854  |
| Db  | 781  | ATGGGAGAAATCCACAGAAATTTTATAGAGATGACCTATTTATAGAGTAGAAGTCAATTA   | 840  |
| QY  | 855  | CAGCCAAACTGAGACATATATGTTTCTACGTCCAAGAGCTAAATGTGAGATCCAGA       | 914  |
| Db  | 841  | CAGCCAAACTGAGACATATATGTTTCTACGTCCAAGAGCTAAATGTGAGATCCAGA       | 900  |
| QY  | 915  | ATTGAGAGAAATGTGAGAAATACATCTGTGTTTCATGTGCTCCGTGTCTTCTCGATAC     | 974  |
| Db  | 901  | ATTGAGAGAAATGTGAGAAATACATCTGTGTTTCATGTGCTCCGTGTCTTCTCGATAC     | 960  |
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Job time : 955 secs

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

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Searched: 6366136 seqs, 31973710525 residues

Word size : 1  
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Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

Database : GenEmbl:\*

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- 2: gb\_pat:\*
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- 12: gb\_hcg:\*
- 13: gb\_in:\*
- 14: gb\_om:\*
- 15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ACCESSION AR691934  
VERSION AR691934.1 GI:74480011  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1383)  
AUTHORS Willson,T., Nicola,N.A., Hilton,D.J., Metcalf,D. and Zhang,J.G.  
TITLE Haemopoietin receptor and genetic sequences encoding same  
JOURNAL Patent: US 6911530-A 3 28-JUN-2005;  
Amrad Operations, Pty., Ltd.; Richmond;  
AUX;

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VERSION U81379.3 GI:5870850  
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REFERENCE 1 (bases 1 to 1708)  
AUTHORS Wada, M., Hisano, T. and Kuwano, M.  
TITLES Direct Submission  
JOURNAL Submitted (07-DEC-1996) Biochemistry, Kyushu University School of  
Medicine, Maidashi, Fukuoka 812-82, Japan  
REFERENCE 2 (bases 1 to 1708)  
AUTHORS Wada, M., Hisano, T. and Kuwano, M.  
TITLES Direct Submission  
JOURNAL Submitted (24-JUN-1999) Biochemistry, Kyushu University School of  
Medicine, Maidashi, Fukuoka 812-82, Japan  
REFERENCE 3 (bases 1 to 1708)  
AUTHORS Wada, M., Hisano, T. and Kuwano, M.  
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DEFINITION

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DEFINITION
Homo sapiens interleukin 13 receptor, alpha 1, mRNA (cDNA clone
MGC:23204 IMAGE:4868206), complete cds.
ACCESSION
BC015768
VERSION
BC015768.1 GI:16041774
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 2153)
REFERENCE
1 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
2 (bases 1 to 2153)  
Strausberg, R.  
Direct Submission  
Submitted (09-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@cgsc.bc.ca](mailto:info@cgsc.bc.ca)  
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lisa Priddy, Parvaneh Saeedi, JR Santos, Angelique Scherch, Ursula Skalska, Duane Smalls, Jeff Stolt, Miranda Tsai, George Yang, Jacques Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 34 Row: k Column: 19  
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

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Location/Qualifiers

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## ORIGIN

Query Match 86.6%; Score 1198; DB 5; Length 2153;  
Best Local Similarity 99.9%; Pred. No. 0;

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LOCUS HSL13RA1 3999 bp mRNA linear PRI 26-FEB-1997  
DEFINITION H.sapiens mRNA for IL13 receptor alpha-1 chain.  
ACCESSION Y09328  
VERSION Y09328.1 GI:1885307  
KEYWORDS alpha 1 chain; IL13RA1 gene; interleukin-13 receptor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE 1  
AUTHORS Miloux,B., Laurent,P., Bonnin,O., Lupker,J., Caput,D., Vitea,N. and  
Ferrara,P.  
TITLE Cloning of the human IL-13R alpha chain and reconstruction with  
the IL4R alpha of a functional IL-4/IL-13 receptor complex  
JOURNAL FEBS Lett. 401 (2-3), 163-166 (1997)  
PUBMED 9013879  
REFERENCE 2 (bases 1 to 3999)  
AUTHORS Caput,D.  
TITLE Direct Submission  
JOURNAL Submitted (08-NOV-1996) D. Caput, SANOFI Recherche, BP 137, F-  
31676 Labège Cedex, FRANCE

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ACCESSION A63257  
VERSION A63257.1 GI:3717098  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified sequences.

REFERENCE 1  
AUTHORS Caput, D., Ferrara, P., Laurent, P., Vita and Natalio.  
TITLE IL-13 RECEPTOR POLYPEPTIDE  
JOURNAL Patent: WO 9720926-A 3 12-JUN-1997;  
SANOFI SA (FR)  
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Other publication FR 2742156 19970613.  
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Qy 135 CGGCGCCACGGAACCTGAGCACTGTGACAAATTTGAGTGTCTCTGTGAAACCTGTG 194  
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Qy 795 ATGGGAGAAATCCAGAAATTTTATAGAGATGCTATTTATGAAGAGAGCAATTA 854  
Db 771 ATGGGAGAAATCCAGAAATTTTATAGAGATGCTATTTATGAAGAGAGCAATTA 830  
Qy 855 CAGCCAACTGAGACACATATATTTTCTACGCTCCAGAGGCTAATATGAGATCCAGA 914  
Db 831 CAGCCAACTGAGACACATATATTTTCTACGCTCCAGAGGCTAATATGAGATCCAGA 890  
Qy 915 ATTTGAGAAATGTGAGAAATATACATCTTTGTCATGCTGCTGCTGTCTCTGATAC 974  
Db 891 ATTTGAGAAATGTGAGAAATATACATCTTTGTCATGCTGCTGCTGTCTCTGATAC 950  
Qy 975 TTGGAACACGTCGATTAATTAAGATCAAAACAAATTAATGATGATGATGACAACT 1034  
Db 951 TTGGAACACGTCGATTAATTAAGATCAAAACAAATTAATGATGATGATGACAACT 1010  
Qy 1035 CTGAGATTAATTTGAGCAAGAAATGATATGATGATGATGATGATGATGATGATGAT 1094  
Db 1011 CTGAGATTAATTTGAGCAAGAAATGATATGATGATGATGATGATGATGATGATGAT 1070  
Qy 1095 AACCATGTTACTATTTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1154  
Db 1071 AACCATGTTACTATTTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1130  
Qy 1155 CCTTAAAGAGCTCAAGATTTATATTTCCCTCCCAATTTCTGATCTCTGCAAGATTTTAA 1214  
Db 1131 CCTTAAAGAGCTCAAGATTTATATTTCCCTCCCAATTTCTGATCTCTGCAAGATTTTAA 1190  
Qy 1215 AGAAATGTTTGGAGACAGATGATGATCTGTCATGTCATGTCATGTCATGTCATGTCAT 1274  
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Qy 1275 GAAGCAACCAAGAGAGAAACCGACTGTGATGTCATGTCATGTCATGTCATGTCATGTCAT 1334  
Db 1251 GAAGCAACCAAGAGAGAAACCGACTGTGATGTCATGTCATGTCATGTCATGTCATGTCAT 1310  
Qy 1335 TCAGTGTAGGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGAA 1383  
Db 1311 TCAGTGTAGGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGAA 1359

RESULT 7  
AR541611 4038 bp DNA linear PAT 08-OCT-2004  
LOCUS AR541611  
DEFINITION Sequence 8 from patent US 6743604.  
ACCESSION AR541611  
VERSION AR541611.1 GI:53933625  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
unclassified.

REFERENCE 1 (bases 1 to 4038)  
AUTHORS Bonnefoy, J.-Y. and Gauchat, J.-F.  
TITLE Substances and their uses  
JOURNAL Patent: US 6743604-A 8 01-JUN-2004;  
Smithline Beecham Corporation; Philadelphia, PA;  
WOX;

FEATURES  
source 1..4038  
location/Qualifiers  
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## ORIGIN

Query Match 86.6%; Score 1198; DB 2; Length 4038;  
Best Local Similarity 99.9%; Pred. No. 0;

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| QY  | 135  | CGGCGCTACGGAACTCAGCCACCTGTGCACAAATTTGAGTGTCTGTGTAACCACTCTG   | 194  |  |
| Db  | 120  | CGGCGCTACGGAACTCAGCCACCTGTGCACAAATTTGAGTGTCTGTGTAACCACTCTG   | 179  |  |
| QY  | 195  | CACAGTAATATGACATGTGAATCCACCGAGGAGCCAGCTCAAAATTTGATGTCTATGTGA | 254  |  |
| Db  | 180  | CACAGTAATATGACATGTGAATCCACCGAGGAGCCAGCTCAAAATTTGATGTCTATGTGA | 239  |  |
| QY  | 255  | TTTATGCTATTTTGGGACAAACAGATAAGAAAATAGCTCCGGAAAATGTCGTGTTCAAT  | 314  |  |
| Db  | 240  | TTTATGCTATTTTGGGACAAACAGATAAGAAAATAGCTCCGGAAAATGTCGTGTTCAAT  | 299  |  |
| QY  | 315  | AGAAGTACCCCTGTAATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACACCAATGA | 374  |  |
| Db  | 300  | AGAAGTACCCCTGTAATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACACCAATGA | 359  |  |
| QY  | 375  | GAGTGAAAGCCTTAGCATTTTGGTTGAAAAATGCATCTCACCCGAGAGGTGATCTCTGA  | 434  |  |
| Db  | 360  | GAGTGAAAGCCTTAGCATTTTGGTTGAAAAATGCATCTCACCCGAGAGGTGATCTCTGA  | 419  |  |
| QY  | 435  | GTCTGCTGTGACTGAACCTTCAATGACATTTGGGCAACCTGAGCTACATGAAAGTCTTG  | 494  |  |
| Db  | 420  | GTCTGCTGTGACTGAACCTTCAATGACATTTGGGCAACCTGAGCTACATGAAAGTCTTG  | 479  |  |
| QY  | 495  | GCTCCCTGGAGGAATACAGTCCCGACACTAACTACTCTCTACTATTGGACAGAG       | 554  |  |
| Db  | 480  | GCTCCCTGGAGGAATACAGTCCCGACACTAACTACTCTCTACTATTGGACAGAG       | 539  |  |
| QY  | 555  | CCTGGAATAATTCATCATGTGTAATAACATCTTTAGAGAGGCCAATATCTTTGGTGTTC  | 614  |  |
| Db  | 540  | CCTGGAATAATTCATCATGTGTAATAACATCTTTAGAGAGGCCAATATCTTTGGTGTTC  | 599  |  |
| QY  | 615  | CTTTGATCTGACCAAGGTGAAGGATTCAGTCTTTTGAACAACAGAGTCCAAATATATGT  | 674  |  |
| Db  | 600  | CTTTGATCTGACCAAGGTGAAGGATTCAGTCTTTTGAACAACAGAGTCCAAATATATGT  | 659  |  |
| QY  | 675  | CAAGATAATGACAGAAAAATTAACCATCTTCAATATATAGTCCCTTTAACTCCGGTGT   | 734  |  |
| Db  | 660  | CAAGATAATGACAGAAAAATTAACCATCTTCAATATATAGTCCCTTTAACTCCGGTGT   | 719  |  |
| QY  | 735  | GAAACCTGATCTCCCATATTTAAAACTCTCTCCACAAATGATGACCTATATGTGCA     | 794  |  |
| Db  | 720  | GAAACCTGATCTCCCATATTTAAAACTCTCTCTCCACAAATGATGACCTATATGTGCA   | 779  |  |
| QY  | 795  | ATGGGGAATCCACAGATTTTATTTAGCAGATGCCATTTTATGAGATAGAACTCAATA    | 854  |  |
| Db  | 780  | ATGGGGAATCCACAGATTTTATTTAGCAGATGCCATTTTATGAGATAGAACTCAATA    | 839  |  |
| QY  | 855  | CAGCCAACTGAGACATATATGTTTCTACGTCACAAAGAGCTAAATGTGAGATCCAGA    | 914  |  |
| Db  | 840  | CAGCCAACTGAGACATATATGTTTCTACGTCACAAAGAGCTAAATGTGAGATCCAGA    | 899  |  |
| QY  | 915  | ATTGGAAGAATGTGAGAAATCATCTTGTTCATGTCCTCGTGTTCTTCTCTGATAC      | 974  |  |
| Db  | 900  | ATTGGAAGAATGTGAGAAATCATCTTGTTCATGTCCTCGTGTTCTTCTCTGATAC      | 959  |  |
| QY  | 975  | TTTGAACACAGTCAGATAAGAGTCAAAACAATAATGTTATGCTATGAGATGACAAATC   | 1034 |  |
| Db  | 960  | TTTGAACACAGTCAGATAAGAGTCAAAACAATAATGTTATGCTATGAGATGACAAATC   | 1019 |  |
| QY  | 1035 | CTGAGTAATTTGGAGCCAAAGAAATGAGTATAGTAAGAACGCAATTTCCACTATACAT   | 1094 |  |
| Db  | 1020 | CTGAGTAATTTGGAGCCAAAGAAATGAGTATAGTAAGAACGCAATTTCCACTATACAT   | 1079 |  |
| QY  | 1095 | AACCATGTACTCATTTGTCAGTCAATCGTGCAGGTGCAATCATAGTACTCTCTGCTTAA  | 1154 |  |
| Db  | 1080 | AACCATGTACTCATTTGTCAGTCAATCGTGCAGGTGCAATCATAGTACTCTCTGCTTAA  | 1139 |  |
| QY  | 1155 | CCTAATAAGGCTCAAGATTTATTTATTTCCCTCCAAATTCCTGATCCGCGAAAGTTTAA  | 1214 |  |
| Db  | 1140 | CCTAATAAGGCTCAAGATTTATTTATTTCCCTCCAAATTCCTGATCCGCGAAAGTTTAA  | 1199 |  |

|    |      |   |      |  |
|----|------|---|------|--|
| QY | 1215 | AGAAATGTTTGGAGACAGAAATGATATCTGTGCACTGGAAGACTACGACTATATGA    | 1274 |  |
| Db | 1200 | AGAAATGTTTGGAGACAGAAATGATATCTGTGCACTGGAAGACTACGACTATATGA    | 1259 |  |
| QY | 1275 | GAGCAAAACCAAGAGAGAAAACGACTCTGTAGTGTGATATGAAAACCTGAAGAAACCTC | 1334 |  |
| Db | 1260 | GAGCAAAACCAAGAGAGAAAACGACTCTGTAGTGTGATATGAAAACCTGAAGAAACCTC | 1319 |  |
| QY | 1335 | TCAGTATGAGATATATTTATTTTACCTTCACTGTGACCTTGAGAGA              | 1383 |  |
| Db | 1320 | TCAGTATGAGATATATTTATTTTACCTTCACTGTGACCTTGAGAGA              | 1368 |  |

|            |  |             |     |        |
|------------|--|-------------|-----|--------|
| RESULT 8   |  |             |     |        |
| CO894698   |  |             |     |        |
| LOCUS      | CO894698   | 4039 bp     | DNA | linear |
| DEFINITION | Sequence 8 from Patent EP1471075.                                |             |     |        |
| ACCESSION  | CO894698   |             |     |        |
| VERSION    | CO894698.1   | GI:55467447 |     |        |
| KEYWORDS   |  |             |     |        |
| SOURCE     |  |             |     |        |
| ORGANISM   | Homo sapiens (human)   |             |     |        |
| REFERENCE  |  |             |     |        |
| AUTHORS    | Rosenthal,A.D., Pilarsky,C., Dahl,E., Specht,T., Bruemendorf,T., |             |     |        |
| TITLE      | Lichtner,R., Straub,E., Roepcke,S. and Li,X.I.                   |             |     |        |
| JOURNAL    | Human nucleic acid sequences expressed in pancreatic carcinomas  |             |     |        |
|            | Patent: EP 1471075-A 8 27-OCT-2004;                              |             |     |        |
|            | Hinzmann, Bernd (DE); Rosenthal, Andre (DE); Pilarsky, Christian |             |     |        |
|            | (DE); Dahl, Edgar (DE); Specht, Thomas (DE); Lichtner, Rosemarie |             |     |        |
|            | (DE)   |             |     |        |
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|            | /mol_type="unassigned DNA"                                       |             |     |        |
|            | /db_xref="taxon:9606"  |             |     |        |
| ORIGIN     |  |             |     |        |

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| Best Local Similarity      | 99.9%; | Pred. No. 0;   |           |              |
| Matches 1248; Conservative | 0;     | Mismatches 1;  | Indels 0; | Gaps 0;      |
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| Db                         | 121    | CGGCGCTACGGAACTCAGCCACCTGTGCACAAATTTGAGTGTCTGTGTAACCACTCTG   | 180       |              |
| QY                         | 195    | CACAGTAATATGACATGTGAATCCACCGAGGAGCCAGCTCAAAATTTGATGTCTATGTGA | 254       |              |
| Db                         | 181    | CACAGTAATATGACATGTGAATCCACCGAGGAGCCAGCTCAAAATTTGATGTCTATGTGA | 240       |              |
| QY                         | 255    | TTTATGCTATTTTGGGACAAACAGATAAGAAAATAGCTCCGGAAAATGTCGTGTTCAAT  | 314       |              |
| Db                         | 241    | TTTATGCTATTTTGGGACAAACAGATAAGAAAATAGCTCCGGAAAATGTCGTGTTCAAT  | 300       |              |
| QY                         | 315    | AGAAGTACCCCTGTAATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGA   | 374       |              |
| Db                         | 301    | AGAAGTACCCCTGTAATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGA   | 360       |              |
| QY                         | 375    | GAGTGAAAGCCTTAGCATTTTGGTTGAAAAATGCACTCACCCGAGAGGTGATCTCTGA   | 434       |              |
| Db                         | 361    | GAGTGAAAGCCTTAGCATTTTGGTTGAAAAATGCACTCACCCGAGAGGTGATCTCTGA   | 420       |              |
| QY                         | 435    | GTCTGCTGTGACTGAACCTTCAATGCAATTTGGCAAACTGAGCTACATGAAGTGTCTTG  | 494       |              |
| Db                         | 421    | GTCTGCTGTGACTGAACCTTCAATGCAATTTGGCAAACTGAGCTACATGAAGTGTCTTG  | 480       |              |
| QY                         | 495    | GCTCCCTGGAAGGAATACAGAGTCCGAGCACTAATCTACTACTATTGGACAGAG       | 554       |              |
| Db                         | 481    | GCTCCCTGGAAGGAATACAGAGTCCGAGCACTAATCTACTACTATTGGACAGAG       | 540       |              |

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QY 615 CTTGATCTGACCAAGTAGAGATTCAGTTTGAACAACAGTCCCAATAATAGT 674  
DB 601 CTTGATCTGACCAAGTAGAGATTCAGTTTGAACAACAGTCCCAATAATAGT 660  
QY 675 CAAGATATATGCAAGAAAAATTAACATCTTCAATATAGTGCCTTAACTTCCGT 734  
DB 661 CAAGATATATGCAAGAAAAATTAACATCTTCAATATAGTGCCTTAACTTCCGT 720  
QY 735 GAAACCTGATCTTCAATATTAACCTTCTTCCCAATATAGTACCTATATGTGA 794  
DB 721 GAAACCTGATCTTCAATATTAACCTTCTTCCCAATATAGTACCTATATGTGA 780  
QY 795 ATGGAGAAATCCACAGAAATTTATAGAGATGCTATTTATAGAGAGAGCAATTA 854  
DB 781 ATGGAGAAATCCACAGAAATTTATAGAGATGCTATTTATAGAGAGAGCAATTA 840  
QY 855 CAGCAAACTGAGACATATATGTTTCTACGTCAGAGGCTAAATGTGAGATCCAGA 914  
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DB 1201 AGAATGTTTGGAGACAGATGATGATCTGCACTGGAAGAATAGCAATCTATGA 1260  
QY 1275 GAAACCAACCAAGAGAGAAACGATCTGTATGTGCTGATAGAAAACCTGAGAAAGCTC 1334  
DB 1261 GAAACCAACCAAGAGAGAAACGATCTGTATGTGCTGATAGAAAACCTGAGAAAGCTC 1320  
QY 1335 TCAGTATGAGATATATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
DB 1321 TCAGTATGAGATATATTTATTTTACCTTCACTGTGACCTTGAGAGA 1369

RESULT 9  
AX335537 4039 bp DNA linear PAT 09-JAN-2002  
LOCUS AX335537  
DEFINITION Sequence 6046 from Patent WO194629.  
ACCESSION AX335537  
VERSION AX335537.1 GI:18126256  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,  
Horigan, S., Soppet, D. R. and Weaver, Z.  
TITLE Cancer gene determination and therapeutic screening using signature

JOURNAL gene sets  
Patent: WO 0194629-A 6046 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
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source location/Qualifiers  
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Query Match 86.6%; Score 1198; DB 2; Length 4039;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DB 121 CGGCGCTACGGAATCTGAGCACTGTGACAAATTTAGTGTCTGTGAAACCTCTG 180  
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QY 315 AGAAGTACCCCTGAATAGAGAAATTTGTCTGCAAGTGGGTCCAGGTAGACCAATGA 374  
DB 301 AGAAGTACCCCTGAATAGAGAAATTTGTCTGCAAGTGGGTCCAGGTAGACCAATGA 360  
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QY 555 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGCCCAATACCTTGGTGTTC 614  
DB 541 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGCCCAATACCTTGGTGTTC 600  
QY 615 CTTGATCTGACCAAGTAGAGATTCAGTTTGAACAACAGTCCCAATAATAGT 674  
DB 601 CTTGATCTGACCAAGTAGAGATTCAGTTTGAACAACAGTCCCAATAATAGT 660  
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DB 661 CAAGATATATGCAAGAAAAATTAACATCTTCAATATAGTGCCTTAACTTCCGT 720  
QY 735 GAAACCTGATCTTCAATATTAACCTTCTTCCCAATATAGTACCTATATGTGA 794  
DB 721 GAAACCTGATCTTCAATATTAACCTTCTTCCCAATATAGTACCTATATGTGA 780  
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QY 855 CAGCAAACTGAGACATATATGTTTCTACGTCAGAGGCTAAATGTGAGATCCAGA 914  
DB 841 CAGCAAACTGAGACATATATGTTTCTACGTCAGAGGCTAAATGTGAGATCCAGA 900  
QY 915 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGCTCCGTGTTCTTCTGATAC 974  
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QY 975 TTTGAGACAGTCAATAGATCAAAACAAATAGTATGCTATGAGAGATGCAAACT 1034  
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|    |      |   |      |
|----|------|---|------|
| QY | 1035 | CTGGAGTATTTGGAGCCCAAGAAATAGATATAGTAAAGAGGCCAATTCACACTCTACAT   | 1094 |
| Db | 1021 | CTGGAGTATTTGGAGCCCAAGAAATAGATATAGTAAAGAGGCCAATTCACACTCTACAT   | 1080 |
| QY | 1095 | AACCATGTATCATTTGTTCCAGTCATGTGCGAGTCACATTCATAGTACTCTCGCTTTA    | 1154 |
| Db | 1081 | AACCATGTATCTCATTTGTTCCAGTCATGTGCGAGTCACATTCATAGTACTCTCGCTTTA  | 1140 |
| QY | 1155 | CCTAAAAAGGCTCAAGATTATTTATTTCCCTCCCAATTCCTGATCTGGCAAGATTTTAA   | 1214 |
| Db | 1141 | CCTAAAAAGGCTCAAGATTATTTATTTCCCTCCCAATTCCTGATCTGGCAAGATTTTAA   | 1200 |
| QY | 1215 | AGAAATGTTTSGAGACCAAGATGATGATACTCTGCATCGAAGAAAGTACGACATCTATGA  | 1274 |
| Db | 1201 | AGAAATGTTTSGAAGACCAAGATGATGATACTCTGCATCGAAGAAAGTACGACATCTATGA | 1260 |
| QY | 1275 | GAAGCAAAACCAAGAGGAAACCGACTCTGTAGTGTCTGATAGAAAACCTGAAGAAAGCCTC | 1334 |
| Db | 1261 | GAAGCAAAACCAAGAGGAAACCGACTCTGTAGTGTCTGATAGAAAACCTGAAGAAAGCCTC | 1320 |
| QY | 1335 | TCAGTGATGAGATTAATTTATTTTAACTTCACTGTGACCTTGAGAA                | 1383 |
| Db | 1321 | TCAGTGATGAGATTAATTTATTTTAACTTCACTGTGACCTTGAGAA                | 1369 |

|            |                                      |             |     |        |                 |
|------------|--------------------------------------|-------------|-----|--------|-----------------|
| RESULT 10  |                                      |             |     |        |                 |
| AX411212   | AX411212                             | 4039 bp     | DNA | linear | PAT 14-JUN-2002 |
| LOCUS      | Sequence 3859 from Patent WO0229103. |             |     |        |                 |
| DEFINITION |                                      |             |     |        |                 |
| ACCESSION  | AX411212                             |             |     |        |                 |
| VERSION    | AX411212.1                           | GI:21443917 |     |        |                 |

|          |                      |
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| SOURCE   | Homo sapiens (human) |
| ORGANISM | Homo sapiens         |

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

| REFERENCE | AUTHORS  | TITLE                                    | JOURNAL                                |
|-----------|--|--|--|
| 1         | Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G. | Gene expression profiles in liver cancer | Patent: WO 0229103-A 3859 11-APR-2002; |

| FEATURES | Location/Qualifiers |
|----------|---------------------|
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| Query Match           | 86.6%        | Score     | 1198       | DB 2 | Length | 4039 |
| Best Local Similarity | 99.98%       | Pred. No. | 0          |      |        |      |
| Matches 1248          | Conservative | 0         | Mismatches | 1    | Indels | 0    |
|                       |              |           |            |      | Gaps   | 0    |

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Db 301 AGAGTACCCCTGATGAGAGATTGTCTTCGCAAGTGGGGTCCCAGTGTAGCACCAATGA 360

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 675 CAAAGGATAAAGCAGGAAAAATTAAACCATCTCTTCAATATAGTGCCTTAACTTCCGGTGT 734  
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109

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Db 1321 TCAGTCATGGAGATATTATTATTTTACCTTCACTGACCTTGAGAGAGA 1369

## RESULT 11

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| LOCUS      | HS1L13RA               | 4039 bp | mRNA | linear | PRI 22-JAN-199 |
| DEFINITION | H sapiens IT-13Pa mRNA |         |      |        |                |

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|-----------|------------|
| ACCESSION | Y10659     |
| VERSION   | Y10659.1   |
|           | GI:1806035 |



REFERENCE 1 (bases 1 to 11927)  
AUTHORS Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.  
TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property  
JOURNAL Patent: US 6524792-A 5-25-FEB-2003;  
Cytos Biotechnology; Zurich-Schlieren;  
CHX;  
FEATURES  
source Location/Qualifiers  
1..11927  
/organism="unknown"  
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Query Match 86.6%; Score 1198; DB 2; Length 11927;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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DEFINITION Synthetic construct Homo sapiens clone FHL141766.01L inter-leukin 13  
ACCESSION AY892945  
VERSION AY892945.1 GI:60654342  
KEYWORDS Human ORF project.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1284)  
AUTHORS Hines, L., Rolfe, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.  
TITLE Cloning of human full-length cDNAs in Creator (TM) recombinational vector system  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1284)  
AUTHORS Hines, L., Rolfe, A., Jepson, D., Moreira, D., Raphael, J., Kelley, F., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D., Taycher, E., Williamson, J. and Labaer, J.  
TITLE Direct Substitution  
JOURNAL Submitted (05-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA  
COMMENT This cDNA clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). The cDNA has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Each clone is clonally isolated and full-length sequence-verified.  
FEATURES  
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## ORIGIN

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Query Match      83.4%; Score 1154; DB 8; Length 1284;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1204; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 378 GTCTGCTGACTGAGCTTCAATGCTATTTGGCAACCTGAGCTACATGAAGTGTCTTG 437
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QY 615 CTTTGAATCTGACCAAGAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAAGT 674
DB 558 CTTTGAATCTGACCAAGAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAAGT 617
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DEFINITION Homo sapiens mRNA for interleukin 13 receptor, alpha 1 precursor
variant protein.
ACCESSION AB209849
VERSION AB209849.1 GI:62089283
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S.,
Ohara, O., Nagase, T., and F. Kikuno, R.
TITLE None Title
JOURNAL Published Only in Database (2005)
AUTHORS 2 (bases 1 to 3960)
TITLE T Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S.,
Ohara, O., Nagase, T., and F. Kikuno, R.
JOURNAL Direct Submission
Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute,
Department of Human Gene Research; 2-6-7 Kazusa-Kamatari, Kisarazu,
Chiba, 292-0818, Japan (E-mail: cdnainfo@kazusa.or.jp,
URL: http://protein.gsc.riken.go.jp/, Tel: 81-438-52-3930,
Fax: 81-438-52-3931)
COMMENT This work was supported in part by the National Project on Protein
Structural and Functional Analysis, Ministry of Education, Culture
Sports, Science and Technology of Japan. Totoki Y, Toyoda A,
Takeda T, Sakaki Y, Tanaka A, Yokoyama S. RIKEN Genomic Sciences
Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan.
e-mail: aktenaka@postman.riken.go.jp
URL: http://protein.gsc.riken.go.jp/.
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## ORIGIN

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QY 195 CACAGTAATATGACATGTAATCAACCGAGGAGCCAGCTCAATTTGATGCTATGTA 254  
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DEFINITION Sequence 32 from Patent WO0119988.  
ACCESSION AX099392  
VERSION AX099392.1 GI:13538519  
KEYWORDS  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
1 Jacobs, K., McCoy, J.M., Lavallie, E.R., Collins-Racie, L.A., Evans, C.,  
Merberg, D., Treacy, M., Bowman, M.R., Spaulding, V., and Agostino, M.J.  
Secreted proteins and polynucleotides encoding them  
Patent: WO 0119988-A 32 22-MAR-2001;  
JOURNAL Genetics Institute, Inc. (US)  
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Query Match      82.3%; Score 1138; DB 2; Length 3906;  
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QY 504 AAGGAATCCAGTCCGACACTAACTATCTCTACTATTGGCAAGAAAGCTGAAAA 563  
Db 361 AAGGAATCCAGTCCGACACTAACTATCTCTACTATTGGCAAGAAAGCTGAAAA 420  
QY 564 AATTCAATATGTAATAAATCTTTAGAAAGGCCAATCTTGGTGTCTTGAATCT 623  
Db 421 AATTCAATATGTAATAAATCTTTAGAAAGGCCAATCTTGGTGTCTTGAATCT 480  
QY 624 GACCAAGTGAAGATTCAGTTTGAACAAACAGTGTCCAAATATGTCAGAGATTA 683  
Db 481 GACCAAGTGAAGATTCAGTTTGAACAAACAGTGTCCAAATATGTCAGAGATTA 540  
QY 684 TGAGAGAAAAATTAACCATCTTCAATATAGTCTTAACTTCCGTGAAAACTGA 743  
Db 541 TGAGAGAAAAATTAACCATCTTCAATATAGTCTTAACTTCCGTGAAAACTGA 600  
QY 744 TCTTCCCATATTAATAAATCTCTCTCCACATGATGACCTATATGTGCAATGGAGAA 803  
Db 601 TCTTCCCATATTAATAAATCTCTCTCCACATGATGACCTATATGTGCAATGGAGAA 660  
QY 804 TCCACAGATTTTATGAGATGCTATTTTATGAAGTGAAGTCAATTAACGCCAAAC 863  
Db 661 TCCACAGATTTTATGAGATGCTATTTTATGAAGTGAAGTCAATTAACGCCAAAC 720  
QY 864 TGAGACATATATGTTTCTACGTCGAAGAGCTAAATGAGAAATCCAGAAATTTGAGAG 923  
Db 721 TGAGACATATATGTTTCTACGTCGAAGAGCTAAATGAGAAATCCAGAAATTTGAGAG 780  
QY 924 AAATGTGAGAAATACATCTTGTTCATGTCTCTGATCTTCTGATATCTTTGAAAC 983  
Db 781 AAATGTGAGAAATACATCTTGTTCATGTCTCTGATCTTCTGATATCTTTGAAAC 840  
QY 984 AGTCAAGATTAAGTCAAAACAAATTAAGTATGCTATGAGATGACAACTCTGAGATTA 1043  
Db 841 AGTCAAGATTAAGTCAAAACAAATTAAGTATGCTATGAGATGACAACTCTGAGATTA 900  
QY 1044 TTGAGGCAAGAAATAGTATAGTAAAGCCGAATTCACACTTACATTAACCATGTT 1103  
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QY 1104 ACTCATTTTTCAGTCACTGCTCGAGGTGCAATCATAGTACTCTGCTTTAACCCTAAAG 1163  
Db 961 ACTCATTTTTCAGTCACTGCTCGAGGTGCAATCATAGTACTCTGCTTTAACCCTAAAG 1020  
QY 1164 GCTCAAGATTAATATATCTCTCCCAATTCCTGATCCCTGGCAAGATTTTAAAGAAATGTT 1223  
Db 1021 GCTCAAGATTAATATATCTCTCCCAATTCCTGATCCCTGGCAAGATTTTAAAGAAATGTT 1080  
QY 1224 TGAGAGCCAGATGATGATCTCTGCACTGGAAGAGTACGACATCTATGAGAAAGCAAC 1283

Db 1081 TGAGAGCCAGATGATGATGATCTCTGCACTGGAAGAGTACGACATCTATGAGAAAGCAAC 1140  
QY 1284 CAAGGAGAAACCGACTCTGTAGTGTGATAGAAAACTGAAAGAAAGCTCTGATGATG 1343  
Db 1141 CAAGGAGAAACCGACTCTGTAGTGTGATAGAAAACTGAAAGAAAGCTCTGATGATG 1200  
QY 1344 GAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
Db 1201 GAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1240

Search completed: July 8, 2006, 01:14:16  
Job time : 7832 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 22:39:11 ; Search time 7196 Seconds  
(without alignments)  
10747.142 Million cell updates/sec

Title: US-09-051-843D-3

Perfect score: 1383

Sequence: 1 gagctcaacacgagaccag.....tcactgtgacctgagaaga 1383

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

EST:  
1: gb\_est1:  
2: gb\_est3:  
3: gb\_est4:  
4: gb\_est5:  
5: gb\_est6:  
6: gb\_est7:  
7: gb\_est8:  
8: gb\_est9:  
9: gb\_est10:  
10: gb\_est11:  
11: gb\_est12:  
12: gb\_est13:  
13: gb\_est14:  
14: gb\_est15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 1063  | 76.9        | 1756   | 6     | CR603161 full-length |
| 2          | 846   | 61.2        | 1016   | 1     | AL543336             |
| 3          | 728   | 52.6        | 951    | 3     | BM905033             |
| 4          | 689   | 49.8        | 866    | 14    | DQ034842             |
| 5          | 655   | 47.4        | 842    | 5     | CK000442             |
| 6          | 600   | 43.4        | 799    | 4     | CB956372             |
| 7          | 587   | 42.1        | 792    | 4     | CA488843             |
| 8          | 582   | 42.1        | 633    | 4     | CA391344             |
| 9          | 577   | 41.7        | 580    | 3     | CA102323             |
| 10         | 573   | 41.4        | 573    | 9     | DB150552             |
| 11         | 567   | 41.0        | 567    | 9     | DB150552             |
| 12         | 565   | 40.1        | 570    | 9     | DA757245             |
| 13         | 552   | 39.9        | 552    | 9     | DA707381             |
| 14         | 543   | 39.3        | 543    | 9     | DA992396             |
| 15         | 541   | 39.1        | 541    | 2     | DA990183             |
| 16         | 515   | 37.2        | 754    | 4     | CB161269             |
| 17         | 505   | 36.5        | 556    | 2     | BG699187             |
| 18         | 496   | 35.9        | 547    | 9     | DB148485             |
| 19         | 487   | 35.2        | 621    | 8     | DA340823             |

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|----|-----|------|------|----|----------|
| 20 | 477 | 34.5 | 533  | 1  | AA41323  |
| 21 | 451 | 32.6 | 502  | 9  | DA195272 |
| 22 | 442 | 32.0 | 978  | 3  | BO678245 |
| 23 | 435 | 31.5 | 531  | 9  | DB218269 |
| 24 | 427 | 30.9 | 636  | 4  | CB134112 |
| 25 | 420 | 30.4 | 724  | 2  | BF969803 |
| 26 | 418 | 30.2 | 578  | 3  | BP267255 |
| 27 | 413 | 29.9 | 581  | 9  | DA549879 |
| 28 | 408 | 29.5 | 551  | 9  | DB061920 |
| 29 | 403 | 29.1 | 599  | 3  | BM788541 |
| 30 | 399 | 28.9 | 560  | 9  | DA325930 |
| 31 | 394 | 28.5 | 553  | 3  | DA839608 |
| 32 | 391 | 28.3 | 552  | 9  | DA294933 |
| 33 | 389 | 28.1 | 578  | 9  | DA685427 |
| 34 | 382 | 27.6 | 580  | 2  | DA845286 |
| 35 | 381 | 27.5 | 580  | 3  | BP268026 |
| 36 | 380 | 27.5 | 380  | 1  | AA127509 |
| 37 | 379 | 27.4 | 729  | 14 | DQ034843 |
| 38 | 374 | 27.0 | 571  | 9  | DB261081 |
| 39 | 372 | 26.9 | 532  | 9  | DA990941 |
| 40 | 368 | 26.6 | 419  | 4  | CA389226 |
| 41 | 355 | 25.7 | 595  | 3  | BM763177 |
| 42 | 345 | 24.9 | 624  | 1  | A1768613 |
| 43 | 338 | 24.4 | 561  | 4  | CA398074 |
| 44 | 324 | 23.4 | 1009 | 2  | BI464939 |
| 45 | 322 | 23.3 | 634  | 7  | BE971462 |

#### ALIGNMENTS

RESULT 1  
CR603161  
LOCUS  
DEFINITION  
full-length cDNA clone CSOD1001YN10 of Placenta Cot 25-normalized  
of Homo sapiens (human).  
ACCESSION  
CR603161  
VERSION  
CR603161.1 GI:50483968  
KEYWORDS  
HTC; CNSLT; CDNA.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1756)  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished  
Contact: Peng Liang Email: [liang@lifetech.com](mailto:liang@lifetech.com) URL:  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Paradise Avenue  
2 (bases 1 to 1756)  
Genoscope.  
REFERENCE  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BF191 91006 EVRY cedex - FRANCE (E-mail: [seque@genoscope.cns.fr](mailto:seque@genoscope.cns.fr))  
- Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
Location/Qualifiers  
1..1756  
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/db\_xref="taxon:9606"  
/clone="CSOD1001YN10"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"  
ORIGIN  
Query Match 76.9%; Score 1063; DB 6; Length 1756;

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|---|------|--|------|
| Best Local Similarity 99.9%; Pred. No. 0;                     |      |  |      |
| Matches 1113; Conservative 0; Mismatches 1; Indels 0; Gaps 0; |      |  |      |
| QY  | 135  | CCGCGCTACGAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAACTCTG | 194  |
| DB  | 78   | CGCGCTACGAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAACTCTG  | 137  |
| QY  | 195  | CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATGTA | 254  |
| DB  | 138  | CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATGTA | 197  |
| QY  | 255  | TTTTTACTCAATTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAACTCGTGTTCAT | 314  |
| DB  | 198  | TTTTTACTCAATTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAACTCGTGTTCAT | 257  |
| QY  | 315  | AGAAATACCTCGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA  | 374  |
| DB  | 258  | AGAAATACCTCGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA  | 317  |
| QY  | 375  | GAGTGAGAAAGCTGAGATTTGGTGAATAATGATCTCACTCCCAAGAGTATCTGA   | 434  |
| DB  | 318  | GAGTGAGAAAGCTGAGATTTGGTGAATAATGATCTCACTCCCAAGAGTATCTGA   | 377  |
| QY  | 435  | GTCTGTGAGTGAATCTTCAATGATTTGGGCAACCTGAGTACATGAAGTGTCTTG   | 494  |
| DB  | 378  | GTCTGTGAGTGAATCTTCAATGATTTGGGCAACCTGAGTACATGAAGTGTCTTG   | 437  |
| QY  | 495  | GCTCCCTGAGAAAGATACGAGTCCGACACTAATCTCTCACTATGAGCACAAG     | 554  |
| DB  | 438  | GCTCCCTGAGAAAGATACGAGTCCGACACTAATCTCTCTATGTTGGACAGAG     | 497  |
| QY  | 555  | CCTGAGAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATCTTGTGTTC    | 614  |
| DB  | 498  | CCTGAGAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATCTTGTGTTC    | 557  |
| QY  | 615  | CTTTGATCTGACCAAGTGAAGATTTCCAGTTTGAACAACAGTGTCCAATATGT    | 674  |
| DB  | 558  | CTTTGATCTGACCAAGTGAAGATTTCCAGTTTGAACAACAGTGTCCAATATGT    | 617  |
| QY  | 675  | CAAGATTAATGACGAAAAATTAACCATCTTCAATATGATGCTTTAACTCCGCT    | 734  |
| DB  | 618  | CAAGATTAATGACGAAAAATTAACCATCTTCAATATGATGCTTTAACTCCGCT    | 677  |
| QY  | 735  | GAAACCTGATCTCTCAATTTAAAAAATCTCTCTTCCACAAATGATGACCTATATG  | 794  |
| DB  | 678  | GAAACCTGATCTCTCAATTTAAAAAATCTCTCTTCCACAAATGATGACCTATATG  | 737  |
| QY  | 795  | ATGGAGATTCACACAAATTTTATAGCAGATGCCATTTTATGAAGTAAAGTCAATA  | 854  |
| DB  | 738  | ATGGAGATTCACACAAATTTTATAGCAGATGCCATTTTATGAAGTAAAGTCAATA  | 797  |
| QY  | 855  | CAGCCAACTGAGACATATGTTTCTACGTCGAAGAGGCTAAATGTGAAATCCAGA   | 914  |
| DB  | 798  | CAGCCAACTGAGACATATGTTTCTACGTCGAAGAGGCTAAATGTGAAATCCAGA   | 857  |
| QY  | 915  | ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTCGTGTCTCTGATAC    | 974  |
| DB  | 858  | ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTCGTGTCTCTGATAC    | 917  |
| QY  | 975  | TTTTGAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTATGCTATGAGATGACA | 1034 |
| DB  | 918  | TTTTGAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTATGCTATGAGATGACA | 977  |
| QY  | 1035 | CTGAGTAATTTGGAGCAAGAAATGATATAGGTAAGAGCGCAATTCACAGCTACAT  | 1094 |
| DB  | 978  | CTGAGTAATTTGGAGCAAGAAATGATATAGGTAAGAGCGCAATTCACAGCTACAT  | 1037 |
| QY  | 1095 | AACCATGTTACTCATTTGTCACATCTGTGAGAGTGCATCATAGTACTCTGCTTAA  | 1154 |
| DB  | 1038 | AACCATGTTACTCATTTGTCACATCTGTGAGAGTGCATCATAGTACTCTGCTTAA  | 1097 |
| QY  | 1155 | CCTAAAAAGGCTCAAGATTATATTTCTCCATTTCTGATCTCGGCAAGTTTTTAA   | 1214 |

|  |      |  |      |
|--|------|--|------|
| DB   | 1098 | CCTAAAAAGGCTCAAGATTATATATCCCTCCAAATCTGATCTGGCAAGTTTTTAA  | 1157 |
| QY   | 1215 | AGAAATGTTTGGAGACCAAGATGATGATCTCTG                        | 1248 |
| DB   | 1158 | AGAAATGTTTGGAGACCAAGATGATGATCTCTG                        | 1191 |
| RESULT 2   |      |  |      |
| AL543336 1016 bp mRNA linear EST 24-MAR-2004   |      |  |      |
| LOCUS  |      |  |      |
| DEFINITION   |      |  |      |
| AL543336 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA                       |      |  |      |
| Accession  |      |  |      |
| Version  |      |  |      |
| Keywords   |      |  |      |
| Source   |      |  |      |
| Organism   |      |  |      |
| Reference  |      |  |      |
| Authors  |      |  |      |
| Title  |      |  |      |
| Journal  |      |  |      |
| Comment  |      |  |      |
| FEATURES   |      |  |      |
| source   |      |  |      |
| 1..1016  |      |  |      |
| /organism="Homo sapiens"   |      |  |      |
| /mol_type="mRNA"   |      |  |      |
| /db_xref="taxon:9606"  |      |  |      |
| /clone="CS01001YN10"   |      |  |      |
| /cissue_type="PLACENTA COT 25-NORMALIZED"  |      |  |      |
| /clone_1lb="Homo sapiens PLACENTA COT 25-NORMALIZED"                                     |      |  |      |
| /note="1st strand cDNA was primed with a NotI-oligo(dT)                                  |      |  |      |
| primer. Five prime end enriched, double-strand cDNA was                                  |      |  |      |
| digested with Not I and EcoR V sites of the pcwvSPORT 6 vector. Library was normalized." |      |  |      |
| sites of the pcwvSPORT 6 vector. Library was normalized."                                |      |  |      |
| ORIGIN   |      |  |      |
| Query Match 61.2%; Score 846; DB 1; Length 1016;   |      |  |      |
| Best Local Similarity 99.9%; Pred. No. 0;  |      |  |      |
| Matches 896; Conservative 0; Mismatches 1; Indels 0; Gaps 0;                             |      |  |      |
| QY   | 135  | CGCGCTACGAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAACTCTG  | 194  |
| DB   | 79   | CGCGCTACGAGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTTGAAAACTCTG  | 138  |
| QY   | 195  | CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATGTA | 254  |
| DB   | 139  | CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATGTA | 198  |
| QY   | 255  | TTTTTACTCAATTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAACTCGTGTTCAT | 314  |
| DB   | 199  | TTTTTACTCAATTTGGGAGCAAAAGATTAAGAAATAGCTCCGGAACTCGTGTTCAT | 258  |
| QY   | 315  | AGAAATACCTCGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA  | 374  |
| DB   | 259  | AGAAATACCTCGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA  | 318  |
| QY   | 375  | GAGTGAGAAAGCTGAGATTTGGTGAATAATGATCTCACTCCCAAGAGTATCTGA   | 434  |

Db 319 GAGTGAAGAGCTGACATTTTGGTTGAAATGATCTACCCCCAGAGGTGATCTCGA 378  
Qy 435 GTCTGCTGTAAGTGAATGATGATTTGGACAACTGAGTACATGAGAGTGTCTTG 494  
Db 379 GTCTGCTGTAAGTGAATGATGATTTGGACAACTGAGTACATGAGAGTGTCTTG 438  
Qy 495 GCTCCCTGGAAGAAATACAGTCCGACACTACTATATCTCTTACTATTTGGACAGAG 554  
Db 439 GCTCCCTGGAAGAAATACAGTCCGACACTACTATATCTCTTACTATTTGGACAGAG 498  
Qy 555 CTTGGAAAAAATTCATCATATGTGAAAACATCTTTAGAGAGGCCAATACCTTGGTGTTC 614  
Db 499 CTTGGAAAAAATTCATCATATGTGAAAACATCTTTAGAGAGGCCAATACCTTGGTGTTC 558  
Qy 615 CTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGCCTTAAATAGT 674  
Db 559 CTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGCCTTAAATAGT 618  
Qy 675 CAAGATATGACAGAAAAATTAACCATCTTCAATATAGTGCCTTAACTCCGTGT 734  
Db 619 CAAGATATGACAGAAAAATTAACCATCTTCAATATAGTGCCTTAACTCCGTGT 678  
Qy 735 GAAACCTGATCTTCAATATTAATAAAGCTCTCTTCCACATATGACCTATATGTGCA 794  
Db 679 GAAACCTGATCTTCAATATTAATAAAGCTCTCTTCCACATATGACCTATATGTGCA 738  
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LOCUS BM905033  
DEFINITION AGENCOURT\_6699542 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:5557892  
5', mRNA sequence.  
ACCESSION BM905033  
VERSION BM905033.1 GI:19355424  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1 (bases 1 to 951)  
REFERENCE NIH-MGC http://mgc.ncbi.nlm.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: csabbs-remail.nih.gov  
Tissue Procurement: ATCC/DCMP/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
CDNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM12279 row: p column: 21  
High quality sequence stop: 719.  
Location/Qualifiers  
1..951

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5557892"  
/issue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_id="NIH MGC 72"  
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

ORIGIN

Query Match 52.6%; Score 728; DB 3; Length 951;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 778; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 166 AATTGAGTGTCTGTGTTGAAACCTCTGACAGTAATATGACATGGAATCCACCGAG 225  
Db 13 AATTGAGTGTCTGTGTTGAAACCTCTGACAGTAATATGACATGGAATCCACCGAG 72  
Qy 226 GGAGCCAGCTCAAAATGTAGTCTATGTTATTTAGTCAATTTGGCCGACAAAGATTAAG 285  
Db 73 GGAGCCAGCTCAAAATGTAGTCTATGTTATTTAGTCAATTTGGCCGACAAAGATTAAG 132  
Qy 286 AAAATAGCTCCGGAACCTCGTCTCAATAGAAATACCCCTGATGAGAGATTTGCTG 345  
Db 133 AAAATAGCTCCGGAACCTCGTCTCAATAGAAATACCCCTGATGAGAGATTTGCTG 192  
Qy 346 CAAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGAGCTTACATTTTGGTTGAAAAA 405  
Db 193 CAAAGTGGGGTCCAGTGTAGACCAATGAGAGTGAAGAGCTTACATTTTGGTTGAAAAA 252  
Qy 406 TGCATCTACCCCGAAGAGTATCTGAGTCTGCTGTGACTGAACTTCAATGCAATTTGG 465  
Db 253 TGCATCTACCCCGAAGAGTATCTGAGTCTGCTGTGACTGAACTTCAATGCAATTTGG 312  
Qy 466 CACAACTGAGTCAATGAAAGTGTCTTGGTCTCCCTGGAAAGATTAACAGTCCGACACT 525  
Db 313 CACAACTGAGTCAATGAAAGTGTCTTGGTCTCCCTGGAAAGATTAACAGTCCGACACT 372  
Qy 526 AACTATCTCTCTACTATTGGGACAGAGAGCTGGAAAAAATTCATCATATGGAACATC 585  
Db 373 AACTATCTCTCTACTATTGGGACAGAGAGCTGGAAAAAATTCATCATATGGAACATC 432  
Qy 586 TTTAGAGAGGCCAATATCTTGGTGTCTCTTGTATGACCAAGTGAAGATTCAGT 645  
Db 433 TTTAGAGAGGCCAATATCTTGGTGTCTCTTGTATGACCAAGTGAAGATTCAGT 492  
Qy 646 TTTGAACACACAGTGTCCAAATATATGTGTCAAGATATGACAGAAAAATTAACCATCC 705  
Db 493 TTTGAACACACAGTGTCCAAATATATGTGTCAAGATATGACAGAAAAATTAACCATCC 552  
Qy 706 TTTCAATATATGATGATCTTAACTTCCCGTGTGAAACCTGATCTCCACATATTAACATC 765  
Db 553 TTTCAATATATGATGATCTTAACTTCCCGTGTGAAACCTGATCTCCACATATTAACATC 612  
Qy 766 TCTTTCACAAATGATGATCTTAACTTCCCGTGTGAAACCTGATCTCCACATATTAACATC 825  
Db 613 TCTTTCACAAATGATGATCTTAACTTCCCGTGTGAAACCTGATCTCCACATATTAACATC 672  
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Qy 886 GTCCAGAGAGCTAAATGTGAGATTCAGAAATTTGAGAGAAATGTGAGAAATATCATCTTG 944  
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RESULT 4  
DQ034842  
LOCUS DQ034842 866 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens IL13RA1 gene, VIRUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION DQ034842  
VERSION DQ034842.1 GI:66886051  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,  
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.  
A Scan for Positively Selected Genes in the Genomes of Humans and  
Chimpanzees  
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)  
PUBMED 15869325  
REFERENCE  
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,  
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.  
Direct Submission  
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering of  
them based on alignment. Translating starts at the beginning of  
alignment.  
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Best Local Similarity 99.9%; Pred. No. 0;  
Matches 739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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1 AAACAGCCACCTGTGACAAATTTGAGTGTCTCTGTGAAAACTCTGCACAGTAATAT 60  
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Db 481 CCAAGTGAAGATTCAGTTTGAACAACAACAGTGTCCAAATTAATGATCAAGATTAAG 540  
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Db 721 AGACACATTAATGTTTCTAC 740  
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DEFINITION AGENCOURT 1636365 NIH MGC 221 Homo sapiens cDNA clone  
IMAGE:30708826 5', mRNA sequence.  
ACCESSION CK000442  
VERSION CK000442.1 GI:38526476  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: James Martin, University of Iowa  
cDNA Library Preparation: M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
http://image.llnl.gov  
plate: NDAM1075 row: k column: 11  
High quality sequence stop: 681.  
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Site 2: NotI; Library is oligo-dT primed and directionally  
cloned. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated with  
EcoR I adaptor, digested with Not I and then cloned  
directionally into pYX-Asc vector. Average insert size  
4-5kb. Adaptors 5' (AATTGGCAGAGG) 3' and 5' d  
(CCTGCTGCCG) 3'. 3' linker sequence - GGGCGGCTGAGAGCC T18.  
Sequencing primers 3' end: T3 promoter primer 5' d



(ATTAACTCCCTCAAGGA)3'. 5' End: T7 promoter primer 5'd  
(TAATAGACTACTATAGG)3'. Library was constructed in the  
laboratory of M. Bento Soares. Note: this is a NIH\_MGC  
Library"

## ORIGIN

Query Match 47.4%; Score 655; DB 5; Length 842;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 655; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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IMAGE:3053391 5', mRNA sequence.  
ACCESSION  
CB956372  
VERSION  
CB956372.1 GI:30212489  
KEYWORDS  
EST.  
SOURCE  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
REFERENCE  
1 (bases 1 to 799)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.

Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
CDNA Library Preparation: Clontech Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNLI at:  
<http://image.llnl.gov>  
Plate: NDCM154 row: a column: 16  
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Location/Qualifiers  
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Library is oligo-dT primed and directionally cloned. cDNA  
was prepared from a glandular pool of tissues from thyroid,  
parathyroid, adrenal, cortex and pineal gland. 5' and 3'  
adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATATGAGC-3' and 3' adaptor sequence:  
5'-ATTCTAGGCGCGAGGCGCGCATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.38  
kb (range 0.60-3.5 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

## FEATURES

source

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QY 258 TAGCATTTTGGGCAACAAAGATTAAGAAATAGCTCCGGAACCTGCTCAATATGA 317
DB 3 TAGCATTTTGGGCAACAAAGATTAAGAAATAGCTCCGGAACCTGCTCAATATGA 62
QY 318 AGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGAACCAATGAGAG 377
DB 63 AGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGTCCAGTGAACCAATGAGAG 122
QY 378 TGAGAGCTTAGCATTTTGGTGAAGAAATGATCTCACCCCGAAGGTATCTGAGTC 437
DB 123 TGAGAGCTTAGCATTTTGGTGAAGAAATGATCTCACCCCGAAGGTATCTGAGTC 182
QY 438 TGCTGTGACGAACTTCAATGCAATTTGGGCAACCTGAGTACATGAAAGTCTTGAGCT 497
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DEFINITION mRNA sequence.  
ACCESSION CA488843 GI:24951634  
VERSION CA488843  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 902)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Kristi A. Eglund, Ira Pastan  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLAM4281 row: 1 column: 09  
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Location/Qualifiers

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Directionally cloned. Priming method: oligo-dT. Average  
insert size: 1800 bp. Library amplification: 26,000 fold.  
Kristi A. Eglund, James J. Vincent, Robert Strausberg,  
Bungkok Lee & Ira Pastan: Discovery of new breast  
cancer genes encoding membrane and secreted proteins.  
Manuscript submitted."

## ORIGIN

Query Match 42.4%; Score 587; DB 4; Length 902;  
Best Local Similarity 100.0%; Pred. No. 1.1e-307;  
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 GGGAGAAATCCACAGATTTTATAGCAGATCCCTATTATTTATGAAAGTAGAAGTCAATAACAG 856  
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QY 857 GCGAAACTGAGACCAATTAATGTTTCTACAGTCCCAAGAGGCTTAATGAGAAATCCAGAAAT 916  
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5', mRNA sequence.  
ACCESSION CA391344  
VERSION CA391344  
KEYWORDS EST.  
SOURCE CA391344.1 GI:24723148  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 633)  
REFERENCE Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NIHBank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
JOURNAL PUBLISHED  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 14 row: a column: 05  
Seq primer: M13Rpl reverse primer (ABI).  
Location/Qualifiers

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(note="Organ: Eye; Vector: PCWSPOR6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD; now part of Invitrogen Corp), essentially following the protocols of the Superscript Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>". The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/Mui sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 42.1%; Score 582; DB 4; Length 633;  
Best Local Similarity 99.8%; Pred. No. 5.9e-305; Mismatches 1; Indels 0; Gaps 0;  
Matches 633; Conservative 0;

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QY 738 ACCGTATCTCCCATATTAATAAACCCTCTCCTT 770  
601 ACCGTATCTCCCATATTAATAAACCCTCTCCTT 633  
Db

RESULT 9  
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LOCUS DA102323 BRACE3 Homo sapiens cDNA clone BRACE3014879 5', mRNA  
DEFINITION  
Sequence.  
ACCESSION DA102323  
VERSION DA102323.1 GI:78564889

## KEYWORDS

EST.

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 580)

## AUTHORS

Yamashita, R., Yamamoto, J., Sekine, M., Tsutsumi, K., Makaguri, H., Iehi, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushiida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi, Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

## TITLE

Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

## JOURNAL

Genome Res. 16 (1), 55-65 (2006)

## PUBMED

16344560

## COMMENT

Contact: Takao Isogai  
FLJ Project (HRI Team)

## Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com

NEO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute for Biotechnology (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

## FEATURES

Location/Qualifiers

## ORIGIN

Query Match 41.7%; Score 577; DB 9; Length 580;  
Best Local Similarity 100.0%; Pred. No. 3.1e-302; Mismatches 0; Indels 0; Gaps 0;  
Matches 577; Conservative 0;

QY 678 GATTAATGACGAGAAAAATTAAACCATCTTCAATATAGTGCCTTTAACTTCCGTGGA 737  
Db 4 GATTAATGACGAGAAAAATTAAACCATCTTCAATATAGTGCCTTTAACTTCCGTGGA 63  
QY 738 ACCGTATCTCCCATATTAATAAACCCTCTTCCACAAATGATGATGATGATG 797  
64 ACCGTATCTCCCATATTAATAAACCCTCTTCCACAAATGATGATGATGATGATG 123  
Db 798 GGAATTCACAGAAATTTTATGACAGATGCTATTTATGAAGTAGAAGCATTAACAG 857  
124 GGAATTCACAGAAATTTTATGACAGATGCTATTTATGAAGTAGAAGCATTAACAG 183  
QY 184 CCAATGACACATATATGTTTCTACGTCGCAAGAGGCTTAATATGATGATGATG 243  
Db 918 TGAGAGAAATGTGAGAAATCATCTTGTTCATAGTCCCTGGGTCTTCTGTAATCTT 977  
244 TGAGAGAAATGTGAGAAATCATCTTGTTCATAGTCCCTGGGTCTTCTGTAATCTT 303  
QY 978 GAAACAGTCAGATTAAGATCAAAACAATTAATGATGATGATGATGATGATGATG 1037  
304 GAAACAGTCAGATTAAGATCAAAACAATTAATGATGATGATGATGATGATGATG 363  
QY 1038 GAGTAATTTGAGCCCAAGAAATGATATGATGATGATGATGATGATGATGATG 1097  
364 GAGTAATTTGAGCCCAAGAAATGATATGATGATGATGATGATGATGATGATGATG 423  
Db

|                       |  |   |                        |
|-----------------------|--|---|------------------------|
| Oy                    | 1098   | CATGTTACTCATTTGGTCCAGTCATCGTCGAGGTCGCAATCATATAGATCCCGCTTTACT  | 1157                   |
| Db                    | 424  | CATGTTACTCATTTGGTCCAGTCATCGTCGAGGTCGCAATCATATAGATCCCGCTTTACT  | 483                    |
| Oy                    | 1158   | AAAAAGCTCAGATTATTTATATTTCCCTCCCAATTCCTGATCCGTCGCAAGATTTTAAAGA | 1217                   |
| Db                    | 484  | AAAAAGCTCAGATTATTTATATTTCCCTCCCAATTCCTGATCCGTCGCAAGATTTTAAAGA | 543                    |
| Oy                    | 1218   | AATGTTTGAGACCCAGATGATGATCTCTGCATCGG                           | 1254                   |
| Db                    | 544  | AATGTTTGAGACCCAGATGATGATCTCTGCATCGG                           | 580                    |
| RESULT 10             |  |   |                        |
| DB150552              |  |   |                        |
| LOCUS                 | DB150552   | 573 bp  | linear EST 11-DEC-2005 |
| DEFINITION            | DB150552 THYMU3 Homo sapiens cDNA clone THYMU3027195 5', mRNA  |   |                        |
| ACCESSION             | DB150552   |   |                        |
| VERSION               | DB150552.1   | GI:83538764   |                        |
| KEYWORDS              | EST.   |   |                        |
| SOURCE                | Homo sapiens (human)   |   |                        |
| ORGANISM              | Homo sapiens   |   |                        |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euheteria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo  |   |                        |
| AUTHORS               | 1 (bases 1 to 573)   |   |                        |
|                       | Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Megatsuna,M., Murakawa,K., Ishida,S., Ieshibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.   |   |                        |
| TITLE                 | Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes  |   |                        |
| JOURNAL               | Genome Res. 16 (1), 55-65 (2006)   |   |                        |
| PUBMED                | 16344560   |   |                        |
| COMMENT               | Contact: Takao Isogai<br>FlJ Project (HRI Team)<br>Helix Research Institute<br>2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan<br>Tel.: 81-438-52-3975<br>Fax: 81-438-52-3986<br>Email: flj-cdna@hri.fujitsu.com<br>NEBO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB. |   |                        |
| FEATURES              |  |   |                        |
| source                | Location/Qualifiers  |   |                        |
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|                       | /organism="Homo sapiens"   |   |                        |
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|                       | /db_xref="taxon:9606"  |   |                        |
|                       | /clone="THYMU3027195"  |   |                        |
|                       | /tissue_type="thymus"  |   |                        |
|                       | /clone_id="THYMU3"   |   |                        |
|                       | /note="Vector: pME18SFL3"  |   |                        |
| ORIGIN                |  |   |                        |
| Query Match           | 41.4%;   | Score 573;  | DB 9; Length 573;      |
| Best Local Similarity | 100.0%;  | Pred. No. 4,7e-300;   |                        |
| Matches               | 573; Conservative  | 0; Mismatches   | 0; Indels 0; Gaps 0;   |
| Oy                    | 755  | TTAAAAAAGCTCTCCCTCCACAAATGATGACCTATATGTGCAATGGAGATCCACAGATT   | 814                    |
| Db                    | 1  | TTAAAAAAGCTCTCTCCACAAATGATGACCTATATGTGCAATGGAGATCCACAGATT     | 60                     |
| Oy                    | 815  | TTAATTAGAGATGCTATTTTATGAAAGTAGAAGTCATTAACAGCCAACTGAGACACATA   | 874                    |

|                        |  |   |  |                             |
|------------------------|--|---|--|-----------------------------|
| Df                     |  | 61  | TTATTACAGATGGCTATTTTTATGAAAGTAGAATCATTAACGCCAAACTGAGACAATA     | 120                         |
| OY                     |  | 875   | ATGTTTTTCVACGTCGCAAGAGCGCTAAATGTGGAATCCAGAATTTTGAGAAAATGTGAGA  | 934                         |
| Df                     |  | 121   | ATGTTTTTCVACGTCGCAAGAGCGCTAAATGTGGAATCCAGAATTTTGAGAAAATGTGAGA  | 180                         |
| OY                     |  | 935   | ATACATCTGTTTCATATGTCCTCCGAGCTTCTCCTGATACCTTTGAACACAGTCGAATAA   | 994                         |
| Df                     |  | 181   | ATACATCTGTTTCATATGTCCTCCGAGCTTCTCCTGATACCTTTGAACACAGTCGAATAA   | 240                         |
| OY                     |  | 995   | GAGTCMAAACCAATAGTTATGTCTATGAGATGACAAACTCTGGAGTAATTTGAGCCCAAG   | 1054                        |
| Df                     |  | 241   | GAGTCMAAACCAATAGTTATGTCTATGAGATGACAAACTCTGGAGTAATTTGAGCCCAAG   | 300                         |
| OY                     |  | 1055  | AAATGAGTATAGGTAAAGAGCGCAATTCACACTCTACATPACCATGTTACTCATTTGTC    | 1114                        |
| Df                     |  | 301   | AAATGAGTATAGGTAAAGAGCGCAATTCACACTCTACATPACCATGTTACTCATTTGTC    | 360                         |
| OY                     |  | 1115  | CAGTCATCTGTCGACGAGTGCAATCATTAATCTCCTGCCTTTACCTTAAAGAGTCGAAGTTA | 1174                        |
| Df                     |  | 361   | CAGTCATCTGTCGACGAGTGCAATCATTAATCTCCTGCCTTTACCTTAAAGAGTCGAAGTTA | 420                         |
| OY                     |  | 1175  | TTATATTCCTCCCAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGAGACACAGA    | 1234                        |
| Df                     |  | 421   | TTATATTCCTCCCAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGAGACACAGA    | 480                         |
| OY                     |  | 1235  | ATGATGATCTCTGTCGACCTGGAAGAGTACGACATCTATGAGAAAGCAACCAAGAGAGAA   | 1294                        |
| Df                     |  | 481   | ATGATGATCTCTGTCGACCTGGAAGAGTACGACATCTATGAGAAAGCAACCAAGAGAGAA   | 540                         |
| OY                     |  | 1295  | CCGACTCTGTAAGTCTGATAGAAAACTGGAAGA                              | 1327                        |
| Df                     |  | 541   | CCGACTCTGTAAGTCTGATAGAAAACTGGAAGA                              | 573                         |
| RESULT 11              |  |   |  |                             |
| Df/57245               |  |   |  |                             |
| LOCUS                  |  | DA757245  | 567 bp   | mRNA linear EST 03-DEC-2005 |
| DEFINITION             |  | DA757245 NT2RP8 Homo sapiens cDNA clone NT2RP8004310 5', mRNA sequence.   |  |                             |
| ACCESSION              |  | DA757245  |  |                             |
| VERSION                |  | DA757245.1  | GI:83067459  |                             |
| KEYWORDS               |  | EST.  |  |                             |
| SOURCE                 |  | Homo sapiens (human)  |  |                             |
| ORGANISM               |  | Homo sapiens  |  |                             |
|                        |  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |  |                             |
|                        |  | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;   |  |                             |
|                        |  | Homnidae; Homo.   |  |                             |
| REFERENCE              |  | 1 (bases 1 to 567)  |  |                             |
| AUTHORS                |  | Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagsatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.   |  |                             |
| TITLE                  |  | Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes   |  |                             |
| JOURNAL PUBMED COMMENT |  | Genome Res. 16 (1), 55-65 (2006)<br>16344560<br>Contact: Takao Isogai<br>FLJ Project (HRI Team)<br>Helix Research Institute<br>2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan<br>Tel.: 81-438-52-3975<br>Fax: 81-438-52-3986<br>Email: flj-chna@nifty.com<br>NEO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI), 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB. |  |                             |

FEATURES  
Source  
Location/Qualifiers  
1. 567  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="NT2RP804310"  
/cell\_type="teratocarcinoma"  
/cell\_line="NT2"  
/clone\_lib="NT2RP8"  
/note="Vector: pME18SFU3; mRNA from NT2 neuronal precursor cells after 5-weeks retinoic acid (RA) induction"

ORIGIN  
Query Match 41.0%; Score 567; DB 9; Length 567;  
Best Local Similarity 100.0%; Pred. No. 8.8e-297;  
Matches 567; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 652 CAACACAGTGTCCAAATATATGTCAGATATGCGAGAAATTTAAACATCTTCAT 711  
DB 1 CAACACAGTGTCCAAATATATGTCAGATATGCGAGAAATTTAAACATCTTCAT 60  
QY 712 ATAGTGCCTTAATCTCCGTTGAACCTGATCTCCATATTTAAACCTCTCTC 771  
DB 61 ATAGTGCCTTAATCTCCGTTGAACCTGATCTCCATATTTAAACCTCTCTC 120  
QY 772 CACATATGATGACCTATATGTCAGATGAGAAATCCAGATTTTATAGAGATGCTTA 831  
DB 121 CACATATGATGACCTATATGTCAGATGAGAAATCCAGATTTTATAGAGATGCTTA 180  
QY 832 TTTTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 891  
DB 181 TTTTATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
QY 892 GAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 951  
DB 241 GAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
QY 952 GTCCCTGCTGTTCTCTGATGATCTTTGAACACAGTCAAGATPAGAGTCAAAATAG 1011  
DB 301 GTCCCTGCTGTTCTCTGATGATCTTTGAACACAGTCAAGATPAGAGTCAAAATAG 360  
QY 1012 TTATGCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1071  
DB 361 TTATGCTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
QY 1072 AAGGCGAATTCACACTCTACATACATGATGATGATGATGATGATGATGATGATG 1131  
DB 421 AAGGCGAATTCACACTCTACATACATGATGATGATGATGATGATGATGATGATG 480  
QY 1132 GCAATCATAGTACTCCGCTTTTACCTAAGGCTCAAGATTTATATTCCTCCCAAT 1191  
DB 481 GCAATCATAGTACTCCGCTTTTACCTAAGGCTCAAGATTTATATTCCTCCCAAT 540  
QY 1192 CCGATCCTGGCAAGATTTTAAAGAA 1218  
DB 541 CCGATCCTGGCAAGATTTTAAAGAA 567

RESULT 12  
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LOCUS DA707381 NT2R12 Homo sapiens cDNA clone NT2R12011802 5', mRNA  
DEFINITION  
sequence.  
ACCESSION DA707381  
VERSION DA707381.1 GI:82349574  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo  
1 (bases 1 to 570)  
REFERENCE  
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,

TITLE  
JOURNAL  
PUBMED  
COMMENT  
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,  
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushiida,N.,  
Yonekawa,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Magatsuma,M.,  
Murakawa,K., Ishida,S., Ishihashi,T., Takahashi-Fujii,A.,  
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T., and Sugano,S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
16344560  
Contact: Takao Isogai  
Fid Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: filj-cdna@nifty.com  
NEDO human cDNA project (New Energy and Industrial Technology  
Developmental Organization, Japan); cDNA library construction:  
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,  
Research Association for Biotechnology (RAB) and Biotechnology  
Center, National Institute of Technology and Evaluation; 3'-end one  
pass sequencing: RAB.  
Location/Qualifiers  
1. 570  
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/cell\_line="NT2"  
/clone\_lib="NT2R12"  
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NT2 neuronal precursor cells treated 2-weeks mitotic  
inhibitor after 5-weeks retinoic acid (RA) induction."

ORIGIN  
Query Match 40.1%; Score 555; DB 9; Length 570;  
Best Local Similarity 100.0%; Pred. No. 3.1e-290;  
Matches 555; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 829 CTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 888  
DB 1 CTATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60  
QY 889 CAAGAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 948  
DB 61 CAAGAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120  
QY 949 ATGTCCTGCTGTTCTCTGATGATCTTTGAACACAGTCAAGATPAGAGTCAAAAT 1008  
DB 121 ATGTCCTGCTGTTCTCTGATGATCTTTGAACACAGTCAAGATPAGAGTCAAAAT 180  
QY 1009 AAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1068  
DB 181 AAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240  
QY 1069 AAGAGGCAATTCACACTCTACATACATGATGATGATGATGATGATGATGATG 1128  
DB 241 AAGAGGCAATTCACACTCTACATACATGATGATGATGATGATGATGATGATG 300  
QY 1129 GGTGCAATCATAGTACTCCGCTTTTACCTAAGGCTCAAGATTTATATTCCTCCCA 1188  
DB 301 GGTGCAATCATAGTACTCCGCTTTTACCTAAGGCTCAAGATTTATATTCCTCCCA 360  
QY 1189 ATTCTGATCCTGGCAAGATTTTAAAGAAATGTTTGAAGCCAGATGATGATCTGTG 1248  
DB 361 ATTCTGATCCTGGCAAGATTTTAAAGAAATGTTTGAAGCCAGATGATGATCTGTG 420  
QY 1249 CACTGGAAGAGTACGATCTATGAGAGCAAAACCAAGAGAAACCGACTCTGTAGTG 1308  
DB 421 CACTGGAAGAGTACGATCTATGAGAGCAAAACCAAGAGAAACCGACTCTGTAGTG 480

QY 1309 CTGATGAAAACCTGAGAAAGCCTCTCACTGATGAGATTAATTTTACCTTCACT 1368  
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Db 481 CTGATGAAAACCTGAGAAAGCCTCTCACTGATGAGATTAATTTTACCTTCACT 540  
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QY 1369 GTGACCTTGAGAGA 1383  
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Db 541 GTGACCTTGAGAGA 555  
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RESULT 13  
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LOCUS DA992396 SYN04 Homo sapiens cDNA clone SYN04004609 5', mRNA  
DEFINITION DA992396 Homo sapiens cDNA clone SYN04004609 5', mRNA  
sequence.  
ACCESSION DA992396  
VERSION DA992396.1 GI:83066687  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 552)  
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,  
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,  
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,  
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,  
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,  
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
JOURNAL PUBLISHED 16344560  
COMMENT Contact: Takao Isogai  
FLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com

FEATURES  
source  
location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="SYNOV4004609"  
/rissue\_type="synovial membrane tissue from rheumatoid  
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/note="Vector: PME18SFL3"

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Matches 552; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 535 CTCTACTATTGGCAGCAGAGCCTGAGAAAATTCATCAATGTGAAAACATCTTAGAGAA 594  
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Db 1 CTCTACTATTGGCAGCAGAGCCTGAGAAAATTCATCAATGTGAAAACATCTTAGAGAA 60  
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QY 595 GGGCAATACCTTGGTGGTTCCTTTGATCTGACCAAGAGGATTCAGTTTGAACA 654  
|||||  
Db 61 GGGCAATACCTTGGTGGTTCCTTTGATCTGACCAAGAGGATTCAGTTTGAACA 120  
|||||  
QY 655 CACAGTGTCCAATTAATGTGCAAGATTAATGCAGGAAAAATTAACCATCTTCAATATA 714  
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Db 121 CACAGTGTCCAATTAATGTGCAAGATTAATGCAGGAAAAATTAACCATCTTCAATATA 180  
|||||  
QY 715 GTGCCCTTTAACTCCCGTGGAACCTGATCCGCATATTTAAAAACCTCTTCAC 774  
|||||  
Db 181 GTGCCCTTTAACTCCCGTGGAACCTGATCCGCATATTTAAAAACCTCTTCAC 240  
|||||  
QY 775 AATGATGACCTTATATGTGCAATGGGGAATCCACAGATTTTATTGCGAGTCCATTT 834  
|||||  
Db 241 AATGATGACCTTATATGTGCAATGGGGAATCCACAGATTTTATTGCGAGTCCATTT 300  
|||||  
QY 835 TATGAAGTGAAGTCAATTAACAGCCCAACTGAGACCATTAAGTTTTCACGCAAG 894  
|||||  
Db 301 TATGAAGTGAAGTCAATTAACAGCCCAACTGAGACCATTAAGTTTTCACGCAAG 360  
|||||  
QY 895 GCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTGAGAAATACATCTGTTTCATGTC 954  
|||||  
Db 361 GCTAAATGTGAGAAATCCAGAAATTTGAGAGAAATGTGAGAAATACATCTGTTTCATGTC 420  
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QY 955 CCTGCTGTTCTTCTGATACCTTTGAAACACAGTCAGATTAAGTCAAAACAATAAGTTA 1014  
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Db 421 CCTGCTGTTCTTCTGATACCTTTGAAACACAGTCAGATTAAGTCAAAACAATAAGTTA 480  
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RESULT 14  
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LOCUS DA990183 SYN04 Homo sapiens cDNA clone SYN04001683 5', mRNA  
DEFINITION DA990183 SYN04 Homo sapiens cDNA clone SYN04001683 5', mRNA  
sequence.  
ACCESSION DA990183  
VERSION DA990183.1 GI:82428308  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 543)  
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,  
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,  
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,  
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,  
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,  
Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
JOURNAL PUBLISHED 16344560  
COMMENT Contact: Takao Isogai  
FLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com

FEATURES  
source  
location/Qualifiers  
1..543  
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/mol\_type="mRNA"

/db xref="taxon:9606"  
/clone="SYNOV4001683"  
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arthritis"  
/clone\_id="SYNOV4"  
/note="Vector: PME18SFL3"

## ORIGIN

Query Match 39.3%; Score 543; DB 9; Length 543;  
Best Local Similarity 100.0%; Pred. No. 1.1e-283; Indels 0; Gaps 0;  
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 835 TATGAGTAGAGTCAATAACAGCCAACTGAGACACATATGTTTCTAGCTCCAGAG 894  
DB 1 TATGAGTAGAGTCAATAACAGCCAACTGAGACACATATGTTTCTAGCTCCAGAG 60  
QY 895 GCTTAATGTGAATCCAGAAATTTGAGAAATGTGAGAAATACATCTGTTTCATGTC 954  
DB 61 GCTAAATGTGAATCCAGAAATTTGAGAAATGTGAGAAATACATCTGTTTCATGTC 120  
QY 955 CCTGAGTCTCTCTGATCTTGAACACAGTCAGATTAAGATCAAAACAAATTAATTA 1014  
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DB 541 TTG 543

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DEFINITION U7N670205n1-20-D03 5', mRNA sequence.  
ACCESSION CBI61269  
VERSION CBI61269.1 GI:28147395  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 541)  
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
Kim, Y.S.  
TITLE 21C Frontier Korean EST Project 2001  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kim YS

Genome Research Center  
Korea Research Institute of Bioscience & Biotechnology  
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Tel: +82-42-860-4470  
Fax: +82-42-860-4409  
Email: yongseung@mail.kribb.re.kr  
Plate: 20 row: D column: 03  
High quality sequence stop: 541.  
Location/Qualifiers  
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/clone="U7N670205n1-20-D03"  
/sex="F"  
/lab\_host="Top10P"  
/clone\_id="U7N670205n1"  
/note="Organ: Liver; Vector: pTZ19-PacI; Site 1: EcoRI;  
Site 2: NotI; The library was contributed by the Soares  
laboratory and it was constructed as described by Bonaldo,  
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research  
6(9): 791-806. RNA was prepared from harvested cell  
culture."

## FEATURES

source

## ORIGIN

Query Match 39.1%; Score 541; DB 4; Length 541;  
Best Local Similarity 100.0%; Pred. No. 1.3e-282; Indels 0; Gaps 0;  
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.9  
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Searched: 1403666 seqs, 935554401 residues

Word size : 1

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Minimum DB seq length: 0  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2          | 1198  | 86.6        | 3999   | US-09-543-679A-2902 | Sequence 2902, Ap  |
| 3          | 1198  | 86.6        | 4038   | US-08-969-125-8     | Sequence 8, Appl1  |
| 4          | 1198  | 86.6        | 4038   | US-09-545-002-8     | Sequence 8, Appl1  |
| 5          | 1198  | 86.6        | 4039   | US-09-949-016-223   | Sequence 223, App  |
| 6          | 1198  | 86.6        | 4039   | US-09-880-107-3856  | Sequence 3856, Ap  |
| 7          | 1198  | 86.6        | 4039   | US-09-543-679A-2903 | Sequence 2903, Ap  |
| 8          | 1198  | 86.6        | 11927  | US-09-193-707-5     | Sequence 5, Appl1  |
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| C 43 | 22 | 1.6 | 702   | US-10-305-770B-1    | Sequence 1, Appl1  |
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## ALIGNMENTS

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Sequence 3, Application US/09688286D  
Patent No. 6911530  
GENERAL INFORMATION:  
APPLICANT: Willson, Tracey  
APPLICANT: Nicola, Nicos  
APPLICANT: Hilton, Douglas  
APPLICANT: Metcalf, Donald  
APPLICANT: Zhang, Jian  
TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding sam  
FILE REFERENCE: 23199-215  
CURRENT APPLICATION NUMBER: US/09/688, 286D  
CURRENT FILING DATE: 2003-07-10  
PRIOR APPLICATION NUMBER: AU PM6135  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: AU PM7276  
PRIOR FILING DATE: 1995-12-22  
PRIOR APPLICATION NUMBER: AU PM2208  
PRIOR FILING DATE: 1996-09-09  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 1383  
TYPE: DNA  
ORGANISM: human  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (61)..(1338)  
OTHER INFORMATION:  
US-09-688-286D-3  
Query Match 100.0%; Score 1383; DB 3; Length 1383;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1383; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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| OY | 241  | TGTAGTCATAGGTATTTTATAGTCATTTTGGCCGACAACAAGATATGAAAAATAGCTCCGGAA    | 300  |
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| OY | 301  | ACTGTCGTTCAATGAGAATACCCCTGATGAGAGATTTTGTCTGCAAGTGGGGTCCAG          | 360  |
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| Db | 901  | TGTGGAATCCAGAAATTTGAGGAATGTGAGAAATACATCTTGTTCATAGTCCCTGCT          | 960  |
| OY | 961  | GTTCTTCTGTATCTTTGAAACAGTCAAGATTAAGATGTCAAAACCAATTAAGTTATGCTAT      | 1020 |
| Db | 961  | GTTCTTCTGTATCTTTGAAACAGTCAAGATTAAGATGTCAAAACCAATTAAGTTATGCTAT      | 1020 |
| OY | 1021 | GAGAGTGAACAACCTGTGAGATTAATGGAGCCAAAGAAATGAGATATGTAAGAAAGGCAAT      | 1080 |
| Db | 1021 | GAGAGTGAACAACCTGTGAGATTAATGGAGCCAAAGAAATGAGATATGTAAGAAAGGCAAT      | 1080 |
| OY | 1081 | TCCAACTCTATCAATACCATGTTACTCATTTGTTCCAGTCATCTGTGCAAGTGGCAATCATA     | 1140 |
| Db | 1081 | TCCAACTCTATCAATACCATGTTACTCATTTGTTCCAGTCATCTGTGCAAGTGGCAATCATA     | 1140 |
| OY | 1141 | GTACTCTGTGCTTAAACCAAGCTCAAGATTAATATTCCTTCCAAATTCGTATCTT            | 1200 |
| Db | 1141 | GTACTCTGTGCTTAAACCAAGCTCAAGATTAATATTCCTTCCAAATTCGTATCTT            | 1200 |
| OY | 1201 | GGCAAGATTTTAAAGAAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAG          | 1260 |
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| Oy | 1261 | TAGACACATCATATGAGAGCAAA       | CCAGAGAGAAACCGA              | CTCTTAGGCTGATAGAAAC | 1320 |
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| Oy | 1381 | AGA                           | 1383                         |                     |      |
| Db | 1381 | AGA                           | 1383                         |                     |      |

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RESULT 2
US-09-543-679A-2902
/ Sequence 2902, Application US/09543679A
/ Patent No. 7034007
/ GENERAL INFORMATION:
/ APPLICANT: NYCE, Jonathan W.
/ TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
/ COMPOSITIONS, KIT & METHOD FOR TREATMENT
/ OF AIRWAY DISORDERS ASSOCIATED WITH
/ BRONCHOCONSTRICTION, LUNG INFLAMMATION,
/ NUMBER OF SEQUENCES: 3111
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
/ STREET: 7 Clarke Drive
/ CITY: Cranbury
/ STATE: NJ
/ COUNTRY: USA
/ ZIP: 08512
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: CD-R
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: N/A
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/543,679A
/ FILING DATE: 13-Apr-2000
/ CLASSIFICATION: UNKNOWN
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/127,958
/ FILING DATE: 1998-08-03
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Amzel, Viviana
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: EPI-0067191b
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 609-409-3035
/ TELEFAX: 413-254-9245
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 2902:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3999 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2902:
US-09-543-679A-2902

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1035 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1094  
1011 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1070  
1095 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1154  
1071 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1130  
1155 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1214  
1131 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1190  
1215 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1274  
1191 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1250  
1275 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1334  
1251 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1310  
1335 GAGTGAAGTGAAGTGAAGATTTTGTGTAAGAAATGATCTCAACCCGAGAGGATCTCTGA 1383

1311 TCAGTGAATGAGATTAATTTTATTTTACCTTCACTGATGACCTTGAGAGGA 1359  
RESULT 3  
US-08-969-125-8  
Sequence 8, Application US/08969125B  
Patent No. 6143871  
GENERAL INFORMATION:  
APPLICANT: BONNEFOY, JEAN-YVES  
GAUCHAT, JEAN-FRANCOIS  
TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHAYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/969,125B  
FILING DATE: 12-NO. 6143871-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9625899.1  
FILING DATE: 13-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1430-179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 8  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4038 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FRAGMENT TYPE: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..1323  
SEQUENCE DESCRIPTION: SEQ ID NO: 8  
US-08-969-125-8  
Query Match 86.6%; Score 1198; DB 3; Length 4038;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
135 CCGGCTACGGAAGTCAAGCACTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 194  
120 CCGGCTACGGAAGTCAAGCACTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 179  
195 CAGATGAATATGACATGGAATTCACCCGAGAGGACGATCAAAATTTGATGTTAGTGA 254  
180 CAGATGAATATGACATGGAATTCACCCGAGAGGACGATCAAAATTTGATGTTAGTGA 239  
255 TTTTATGATTTTGGGCAAAAGATTAAGAAAAATAGCTCCGAAAATCTGCTGTTCAAT 314  
240 TTTTATGATTTTGGGCAAAAGATTAAGAAAAATAGCTCCGAAAATCTGCTGTTCAAT 299  
315 AGAAGTACCCCTGAAATGAGAGATTTTGTCTGCAAGTGGGCTCCAGTGTACCAAAATGA 374  
300 AGAAGTACCCCTGAAATGAGAGATTTTGTCTGCAAGTGGGCTCCAGTGTACCAAAATGA 359

QY 375 GAGTGAAGACCTAGCATTTTGGTGAAGAAATGATCTCAACCCCGAGAGGTATCTCTGA 434  
DB 360 GAGTGAAGACCTAGCATTTTGGTGAAGAAATGATCTCAACCCCGAGAGGTATCTCTGA 419  
QY 435 GTCTGCTGAGACCTGCAATGCAATTTGGGCAACCTGAGCTACATGAAAGTCTTG 494  
DB 420 GTCTGCTGAGACCTGCAATGCAATTTGGGCAACCTGAGCTACATGAAAGTCTTG 479  
QY 495 GCTCCCTGGAGAGATACAGTCCCGACACTAACTACTCTCTACTATTTGGGCAAG 554  
DB 480 GCTCCCTGGAGAGATACAGTCCCGACACTAACTACTCTCTACTATTTGGGCAAG 539  
QY 555 CCTGGAAAAATTCATCATCTGTAAGAAAATCTTTAGAGAGCCATCTTTGGTGTTC 614  
DB 540 CCTGGAAAAATTCATCATCTGTAAGAAAATCTTTAGAGAGCCATCTTTGGTGTTC 599  
QY 615 CTTTGAATCGAACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATATATGTGT 674  
DB 600 CTTTGAATCGAACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATATATGTGT 659  
QY 675 CAAGATTAATGACAGAAAAATTTAAACATCTTCAATATAGTCCCTTAACTCCGCTGT 734  
DB 660 CAAGATTAATGACAGAAAAATTTAAACATCTTCAATATAGTCCCTTAACTCCGCTGT 719  
QY 735 GAAACCTGATCTCCCATATTTAAAAAATCTTCTCCCTCCCAATGATGACCTATATGTGA 794  
DB 720 GAAACCTGATCTCCCATATTTAAAAAATCTTCTCCCTCCCAATGATGACCTATATGTGA 779  
QY 795 ATGGAGATTCACAGAAATTTTATGACAGATGCTTATTTAGAGATTAAGTCAATTA 854  
DB 780 ATGGAGATTCACAGAAATTTTATGACAGATGCTTATTTAGAGATTAAGTCAATTA 839  
QY 855 CAGCCAACTGACACATTAATTTTCTCAAGTCCAGAGAGCTAAATGAGATCCAGA 914  
DB 840 CAGCCAACTGACACATTAATTTTCTCAAGTCCAGAGAGCTAAATGAGATCCAGA 899  
QY 915 ATTTGAGAGAAATGAGAGATTCATCTTTGATGAGTCCCTGAGTCTTCTCTGATAC 974  
DB 900 ATTTGAGAGAAATGAGAGATTCATCTTTGATGAGTCCCTGAGTCTTCTCTGATAC 959  
QY 975 TTTGAACACAGTGAAGATTAAGTCAAAATTAATGATTTGATGAGATTAAGTCAAACT 1034  
DB 960 TTTGAACACAGTGAAGATTAAGTCAAAATTAATGATTTGATGAGATTAAGTCAAACT 1019  
QY 1035 CTGAGATTAATGAGAGCAAGAAATGAGTAAAGAGCCGAATTCACACTCTACAT 1094  
DB 1020 CTGAGATTAATGAGAGCAAGAAATGAGTAAAGAGCCGAATTCACACTCTACAT 1079  
QY 1095 AACCATGTTACTCATTTGTCAGTCAATGTCGAGGTGCAATCATAGTACTCTCCGCTTTA 1154  
DB 1080 AACCATGTTACTCATTTGTCAGTCAATGTCGAGGTGCAATCATAGTACTCTCCGCTTTA 1139  
QY 1155 CCTAAAGAGCTCAAGATTAATTTTCCCTCCCAATTCCTGAGAGAGATTTTAA 1214  
DB 1140 CCTAAAGAGCTCAAGATTAATTTTCCCTCCCAATTCCTGAGAGAGATTTTAA 1199  
QY 1215 AGAAATGTTTGGAGACAGAGATGATGATCTGCACTGAGAGAGATGACATCTATGA 1274  
DB 1200 AGAAATGTTTGGAGACAGAGATGATGATCTGCACTGAGAGAGATGACATCTATGA 1259  
QY 1275 GAAAGCAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGAGAAAGCTTC 1334  
DB 1260 GAAAGCAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGAGAAAGCTTC 1319  
QY 1335 TCAGTATGAGATTAATTTTATCTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1383  
DB 1320 TCAGTATGAGATTAATTTTATCTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1368

RESULT 4  
US-09-545-002-8  
; Sequence 8, Application US/09545002  
; Patent No. 6743604

GENERAL INFORMATION:  
APPLICANT: BONNEFOY, JEAN-YVES  
GAUCHAT, JEAN-FRANCOIS  
TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHIVE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/545,002  
FILING DATE: 12-NO. 6743604-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/969,125  
FILING DATE: 12-NO. 6743604-1997  
APPLICATION NUMBER: GB 9625899.1  
FILING DATE: 13-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1430-179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 8  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4038 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FRAGMENT TYPE: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..1323  
SEQUENCE DESCRIPTION: SEQ ID NO: 8  
US-09-545-002-8  
Query Match 86.6%; Score 1198; DB 3; Length 4038;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CGGCGCTACGGAACCTCAGCGACCTGTGACAAATTTGAGTGTCTGTGAAAACCTCTG 194  
DB 120 CGGCGCTACGGAACCTCAGCGACCTGTGACAAATTTGAGTGTCTGTGAAAACCTCTG 179  
QY 195 CACAGTAAATATGACATGGAATCCACCGAGAGGAGCCAGCTCAAAATTTAGTATAGTA 254  
DB 180 CACAGTAAATATGACATGGAATCCACCGAGAGGAGCCAGCTCAAAATTTAGTATAGTA 239  
QY 255 TTTTATGCTATTTTGGGCAACCAAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 314  
DB 240 TTTTATGCTATTTTGGGCAACCAAGATTAAGAAATAGCTCCGGAATCTGTGTTCAAT 299  
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGA 374  
DB 300 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGA 359  
QY 375 GAGTGAAGACCTAGCATTTTGGTGAAGAAATGATCTCAACCCCGAGAGGTATCTCTGA 434  
DB 360 GAGTGAAGACCTAGCATTTTGGTGAAGAAATGATCTCAACCCCGAGAGGTATCTCTGA 419  
QY 435 GTCTGCTGAGACCTGCAATGCAATTTGGGCAACCTGAGCTACATGAAAGTCTTG 494

Db 420 GTCTGCTGACGAGCTTCAATGCAATTTGGCACAACCTGAGCTAATGAAGTGTCTTG 479  
Qy 495 GCTCCCTGGAAGAAATCAAGTCCCGACACATATCTCTACTATTGGACAGAG 554  
Db 480 GCTCCCTGGAAGAAATCAAGTCCCGACACATATCTCTACTATTGGACAGAG 539  
Qy 555 CTTGGAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATATCTTGGTGTTC 614  
Db 540 CTTGGAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATATCTTGGTGTTC 599  
Qy 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAAAGT 674  
Db 600 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATAAAGT 659  
Qy 675 CAAGATATATGCAAGGAAAAATTAACATCTTCAATATATGTGCTTAACTTCCCGGT 734  
Db 660 CAAGATATATGCAAGGAAAAATTAACATCTTCAATATATGTGCTTAACTTCCCGGT 719  
Qy 735 GAAACCTGATCTTCACATATTAATAAACTCTCTCCCTCACAATGATGACCTATATGTGA 794  
Db 720 GAAACCTGATCTTCACATATTAATAAACTCTCTCCCTCACAATGATGACCTATATGTGA 779  
Qy 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTATTTATGAGTAGAAGTCAATAA 854  
Db 780 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTATTTATGAGTAGAAGTCAATAA 839  
Qy 855 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAAGTCAAT 914  
Db 840 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAAGTCAAT 899  
Qy 915 ATTTGAGAAATGTGGAGAAATCATCTTGTTCATGAGTCCCTGGTGTCTCTGATAC 974  
Db 900 ATTTGAGAAATGTGGAGAAATCATCTTGTTCATGAGTCCCTGGTGTCTCTGATAC 959  
Qy 975 TTTGAAACACAGTCAAGTAAGAGTCAAAACAATTAAGTATGCTATGAGTAGAAGTCA 1034  
Db 960 TTTGAAACACAGTCAAGTAAGAGTCAAAACAATTAAGTATGCTATGAGTAGAAGTCA 1019  
Qy 1035 CTGAGTAATTTGGAGCCAAAGAAATGATATAGGTAAGAGGCAATCCACACTCTAT 1094  
Db 1020 CTGAGTAATTTGGAGCCAAAGAAATGATATAGGTAAGAGGCAATCCACACTCTAT 1079  
Qy 1095 AACCATGTTACTCATTTGTCAGATCATCTGCGAGGTGCAATCATATGATCTCTGCTTAA 1154  
Db 1080 AACCATGTTACTCATTTGTCAGATCATCTGCGAGGTGCAATCATATGATCTCTGCTTAA 1139  
Qy 1155 CCTAAAAAGGCTCAAGATTTATATATTCCTCAATTCCTGATCTGGCAAGATTTTAA 1214  
Db 1140 CCTAAAAAGGCTCAAGATTTATATATTCCTCAATTCCTGATCTGGCAAGATTTTAA 1199  
Qy 1215 AGAAATGTTTGGAGCCAGAAATGATATCTCTGCACTGGAAGAGTACGACATCTATGA 1274  
Db 1200 AGAAATGTTTGGAGCCAGAAATGATATCTCTGCACTGGAAGAGTACGACATCTATGA 1259  
Qy 1275 GAAGCAAAACCAAGAGAAAACGAGCTGTAGTGTGCTGATAGAAAACCTGAAGAAAGCTC 1334  
Db 1260 GAAGCAAAACCAAGAGAAAACGAGCTGTAGTGTGCTGATAGAAAACCTGAAGAAAGCTC 1319  
Qy 1335 TCAGTATGAGATATATTTATTTTATCTTCACTGTGACCTTGAGAGA 1383  
Db 1320 TCAGTATGAGATATATTTATTTTATCTTCACTGTGACCTTGAGAGA 1368

RESULT 5  
US-09-949-016-223  
; Sequence 223, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

Qy 135 CGGCGCTAGGAAACCTGAGCACTGTGACAAATTTGAGTGTCTGTGAAAACCTCTG 194  
Db 121 CGGCGCTAGGAAACCTGAGCACTGTGACAAATTTGAGTGTCTGTGAAAACCTCTG 180  
Qy 195 CACAGTAATATGACATGAGATCCACCGAGGAGCCAGCTCAATTTGATGATGATGTA 254  
Db 181 CACAGTAATATGACATGAGATCCACCGAGGAGCCAGCTCAATTTGATGATGATGTA 240  
Qy 255 TTTTATGATTTTGGCGACAACAGATTAAGAAAATGCTCCGGAATCTGCTGTCAT 314  
Db 241 TTTTATGATTTTGGCGACAACAGATTAAGAAAATGCTCCGGAATCTGCTGTCAT 300  
Qy 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 374  
Db 301 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTGACCAATGA 360  
Qy 375 GAGTGAAGAACCTAGCATTTTGTGTTGAAAATGATCTCACCCCAAGAGTGTCTGA 434  
Db 361 GAGTGAAGAACCTAGCATTTTGTGTTGAAAATGATCTCACCCCAAGAGTGTCTGA 420  
Qy 435 GTCTGCTGTAAGTGAATCTTCAATGATTTGGCAACCTAGCTACATGAAGTGTCTTG 494  
Db 421 GTCTGCTGTAAGTGAATCTTCAATGATTTGGCAACCTAGCTACATGAAGTGTCTTG 480  
Qy 495 GCTCCCTGGAAGAAATCCAGTCCCGACATTAATCTCTACATATGAGTGGCAAGAG 554  
Db 481 GCTCCCTGGAAGAAATCCAGTCCCGACATTAATCTCTACATATGAGTGGCAAGAG 540  
Qy 555 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATATTTGGTGTTC 614  
Db 541 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAGGCCAATATTTGGTGTTC 600  
Qy 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGAT 674  
Db 601 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGAT 660  
Qy 675 CAAGATATATGCAAGGAAAAATTAACATCTTCAATATATGTGCTTAACTTCCCGGT 734  
Db 661 CAAGATATATGCAAGGAAAAATTAACATCTTCAATATATGTGCTTAACTTCCCGGT 720  
Qy 735 GAAACCTGATCTTCACATATTAATAAACTCTCTCCCTCACAATGATGACCTATATGTGA 794  
Db 721 GAAACCTGATCTTCACATATTAATAAACTCTCTCCCTCACAATGATGACCTATATGTGA 780  
Qy 795 ATGGAGAAATCCACAGAAATTTATAGCAGATGCTTATTTATGAGTAGAAGTCAATAA 854  
Db 781 ATGGAGAAATCCACAGAAATTTATAGCAGATGCTTATTTATGAGTAGAAGTCAATAA 840  
Qy 855 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAAGTCAAT 914  
Db 841 CAGCCAACTGAGACATATATGTTTCTAGCTCAGAGGCTTAATGAGTAGAAGTCAAT 900  
Qy 915 ATTTGAGAAATGTGAGAAATCATCTTGTTCATGAGTCCCTGAGTGTCTCTGATAC 974

Db 901 ATTGAGAAATGTGAGAAATACATCTGTTCATGTCCTGGTGTCTTCCTGATAC 960  
QY 975 TTGGAACAGAGTCAGATAAGTCAAAACAATAATTATGCTATGAGATGACAAACT 1034  
Db 961 TTGGAACAGAGTCAGATAAGTCAAAACAATAATTATGCTATGAGATGACAAACT 1020  
QY 1035 CTGAGATATTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1094  
Db 1021 CTGAGATATTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1080  
QY 1095 AACCATGTTACTGATTTGTCACATCGTCGAGGTCGACATCATAGTACTCCGCTTTA 1154  
Db 1081 AACCATGTTACTGATTTGTCACATCGTCGAGGTCGACATCATAGTACTCCGCTTTA 1140  
QY 1155 CCTAAAAGGCTCAAGATTTATTTATTTCTCCATTCCTGATCTCGGCAAGATTTTAA 1214  
Db 1141 CCTAAAAGGCTCAAGATTTATTTATTTCTCCATTCCTGATCTCGGCAAGATTTTAA 1200  
QY 1215 AGAAATGTTTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1274  
Db 1201 AGAAATGTTTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1260  
QY 1275 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1334  
Db 1261 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1320  
QY 1335 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
Db 1321 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1369

## RESULT 6

US-09-880-107-3856  
Sequence 3856, Application US/09880107  
Patent No. 6974667  
GENERAL INFORMATION:  
APPLICANT: Horne, Darci T.  
APPLICANT: Vockley, Joseph G.  
APPLICANT: Scherf, Uwe  
APPLICANT: Gene Logic, Inc.  
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
FILE REFERENCE: 44921-5028-WO  
CURRENT APPLICATION NUMBER: US/09/880.107  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/211.379  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: US 60/237,054  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 3950  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3856  
LENGTH: 4039  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. 6974667 Y10659  
US-09-880-107-3856

Query Match 86.6%; Score 1198; DB 4; Length 4039;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTGTAACCACTCTG 194  
Db 121 CGGCGCTACGAACTCAGCCACTGTGACAAATTTGAGTGTCTGTGTAACCACTCTG 180  
QY 195 CACAGTAATATGACATGGAATCACCCGAGGAGCCAGCTCAATTTGATGCTATGTA 254  
Db 181 CACAGTAATATGACATGGAATCACCCGAGGAGCCAGCTCAATTTGATGCTATGTA 240  
QY 255 TTTTACTGATTTTGGGAGCAAAACAAGTAAAGAAATAGCTCCGGAATCTGCTCAAT 314  
Db 241 TTTTACTGATTTTGGGAGCAAAACAAGTAAAGAAATAGCTCCGGAATCTGCTCAAT 300

QY 315 AGAAGTACCCCTGATGATGAGGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374  
Db 301 AGAAGTACCCCTGATGATGAGGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 360  
QY 375 GAGTGAAGAGCTTACGATTTTGGTTGAAAAATGCAATCTCAACCCCGAAGGATATCTGA 434  
Db 361 GAGTGAAGAGCTTACGATTTTGGTTGAAAAATGCAATCTCAACCCCGAAGGATATCTGA 420  
QY 435 GTCTGCTGATGATGAACTTCAATGATTTGGCAACAACCTGAGCTATGAAAGTGTCTTG 494  
Db 421 GTCTGCTGATGATGAACTTCAATGATTTGGCAACAACCTGAGCTATGAAAGTGTCTTG 480  
QY 495 GCTCCCTGAAAGATATACAGTCCGACATTAATCTTCTACTATTTGGACAGAG 554  
Db 481 GCTCCCTGAAAGATATACAGTCCGACATTAATCTTCTACTATTTGGACAGAG 540  
QY 555 CCTGGAAGAAATTCATCATGTGAAAAACATCTTTAAGAAAGGCAATCTTTGGTGTTC 614  
Db 541 CCTGGAAGAAATTCATCATGTGAAAAACATCTTTAAGAAAGGCAATCTTTGGTGTTC 600  
QY 615 CTTTATCTGACCAAGTGAAGATTCAGATTTTGAACAAACAGTGTCCAAATTAATGT 674  
Db 601 CTTTATCTGACCAAGTGAAGATTCAGATTTTGAACAAACAGTGTCCAAATTAATGT 660  
QY 675 CAAAGATTAATGCAAGAAAAATTAACCATCTTCAATATATAGCTTTAACTTCCGTGT 734  
Db 661 CAAAGATTAATGCAAGAAAAATTAACCATCTTCAATATATAGCTTTAACTTCCGTGT 720  
QY 735 GAAACCTGATCCCTCCCATTTTAAACCTCTCCCTCCCAATGATGACCTATATGTGA 794  
Db 721 GAAACCTGATCCCTCCCATTTTAAACCTCTCTCTCCCAATGATGACCTATATGTGA 780  
QY 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAAAGTGAATCAATA 854  
Db 781 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAAAGTGAATCAATA 840  
QY 855 CAGCCAACTGAGACATATATGTTTTTCTACGTCGCAAGAGCTTAAATGTGAAATCCAGA 914  
Db 841 CAGCCAACTGAGACATATATGTTTTTCTACGTCGCAAGAGCTTAAATGTGAAATCCAGA 900  
QY 915 ATTGGAAGAAATGTGGAATATCATCTTGTTCATAGTTCCTCGGTCTTCTCTATAC 974  
Db 901 ATTGGAAGAAATGTGGAATATCATCTTGTTCATAGTTCCTCGGTCTTCTCTATAC 960  
QY 975 TTGGAACAGAGTCAGATAAGTCAAAACAATAATTATGCTATGAGATGACAAACT 1034  
Db 961 TTGGAACAGAGTCAGATAAGTCAAAACAATAATTATGCTATGAGATGACAAACT 1020  
QY 1035 CTGAGATATTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1094  
Db 1021 CTGAGATATTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1080  
QY 1095 AACCATGTTACTGATTTGTCACATCGTCGAGGTCGACATCATAGTACTCCGCTTTA 1154  
Db 1081 AACCATGTTACTGATTTGTCACATCGTCGAGGTCGACATCATAGTACTCCGCTTTA 1140  
QY 1155 CCTAAAAGGCTCAAGATTTATTTATTTCTCCATTCCTGATCTCGGCAAGATTTTAA 1214  
Db 1141 CCTAAAAGGCTCAAGATTTATTTATTTCTCCATTCCTGATCTCGGCAAGATTTTAA 1200  
QY 1215 AGAAATGTTTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1274  
Db 1201 AGAAATGTTTGGAGCCAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1260  
QY 1275 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1334  
Db 1261 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATAGAAAACCTGAAGAAAGCTC 1320  
QY 1335 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
Db 1321 TCAGTATGAGATTAATTTATTTTATTTTACCTTCACTGTGACCTTGAGAGA 1369



RESULT 7  
US-09-543-679A-2903  
; Sequence 2903, Application US/09543679A  
; Patent No. 7034007  
; GENERAL INFORMATION:  
; APPLICANT: NYCE, Jonathan W.  
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,  
; COMPOSITIONS, KIT & METHOD FOR TREATMENT  
; OF AIRWAY DISORDERS ASSOCIATED WITH  
; BRONCHOCONSTRICION, LONG INFLAMMATION,  
; NUMBER OF SEQUENCES: 3111  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; City: Cranbury  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-R  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: N/A  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/543,679A  
; FILING DATE: 13-Apr-2000  
; CLASSIFICATION: UNKNOWN  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 60/127,958  
; FILING DATE: 1998-08-03  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-0067191b  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 2903:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4039 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2903:  
US-09-543-679A-2903  
Query Match 86.6%; Score 1198; DB 5; Length 4039;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CGCGCTACGGAACCTCAGCAGCTGTGACAAATTGAGTGTCTGTGTAACCTCTG 194  
DB 121 CGCGCTACGGAACCTCAGCAGCTGTGACAAATTGAGTGTCTGTGTAACCTCTG 180  
QY 195 CACAGTAATGTGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATAGTA 254  
DB 181 CACAGTAATGTGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGATGCTATAGTA 240  
QY 255 TTTTATGATTTTGGGACAAACAAGTAAGAAATAGTCCGGAATCGTGGTCAAT 314  
DB 241 TTTTATGATTTTGGGACAAACAAGTAAGAAATAGTCCGGAATCGTGGTCAAT 300  
QY 315 AGAAGTACCCCTGATGAGAGATTGTCTGCAAGTGGGCTCCAGTGTGACCAATGA 374  
DB 301 AGAAGTACCCCTGATGAGAGATTGTCTGCAAGTGGGCTCCAGTGTGACCAATGA 360  
QY 375 GAGTGAGAGCCCTAGCATTTTGTGTAAGAAATGATCTACCCCGAAGATGATCTGTA 434  
DB 361 GAGTGAGAGCCCTAGCATTTTGTGTAAGAAATGATCTACCCCGAAGATGATCTGTA 420  
QY 435 GTCTGTGTGACTGAACCTTCATGATTTTGGCAACAACCTGAGTACATGAAGTGTCTTG 494

DB 421 GTCTGTGTGACTGAGCTTCATGATTTTGGCAACAACCTGAGTACATGAAGTGTCTTG 480  
QY 495 GCTCCCTGGAAGAAATCCAGTCCCGACATTAATCTCTCTACTATTTGGCAGAGAG 554  
DB 481 GCTCCCTGGAAGAAATCCAGTCCCGACATTAATCTCTCTACTATTTGGCAGAGAG 540  
QY 555 CCTGGAAGAAATTCATGATGTGAAACATCTTTAGAGAGGCCAATACTTGTGTTGC 614  
DB 541 CCTGGAAGAAATTCATGATGTGAAACATCTTTAGAGAGGCCAATACTTGTGTTGC 600  
QY 615 CTTTATCTGACCAAGATGAGATTTCCAGTTTGAACAACAGTGTCCAAATATAGT 674  
DB 601 CTTTATCTGACCAAGATGAGATTTCCAGTTTGAACAACAGTGTCCAAATATAGT 660  
QY 675 CAAGATATGACGAGAAATTTAAACATCTCTCAATATATGTGCTTTAATCCCTGT 734  
DB 661 CAAGATATGACGAGAAATTTAAACATCTCTCAATATATGTGCTTTAATCCCTGT 720  
QY 735 GAAACCTGATCTCTCAATATTTAAACCTCTCTCCACAAATGATGACCTATATGCA 794  
DB 721 GAAACCTGATCTCTCAATATTTAAACCTCTCTCCACAAATGATGACCTATATGCA 780  
QY 795 ATGGAGAAATCCAGAAATTTTATAGCAGATGCTATTTTATGAGATGAGATCAATA 854  
DB 781 ATGGAGAAATCCAGAAATTTTATAGCAGATGCTATTTTATGAGATGAGATCAATA 840  
QY 855 CAGCCAAATCAGACACATATGTTTCTTACAGTCCAAAGGCTAATATGTGAATCCAGA 914  
DB 841 CAGCCAAATCAGACACATATGTTTCTTACAGTCCAAAGGCTAATATGTGAATCCAGA 900  
QY 915 ATTGAGAGAAATGTGAGAAATCATCTTGTTCATGTCCTGCTGCTCTCTCTGATAC 974  
DB 901 ATTGAGAGAAATGTGAGAAATCATCTTGTTCATGTCCTGCTGCTCTCTCTGATAC 960  
QY 975 TTGGAACACAGTCAAGATTAAGTCAAAACAATTAAGTATGCTATGAGATGACAACT 1034  
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QY 1035 CTGAGATTAATGAGACCAAGAAATGAGTATAGTATGAGACCGCAATTCACACTCTAT 1094  
DB 1021 CTGAGATTAATGAGACCAAGAAATGAGTATAGTATGAGACCGCAATTCACACTCTAT 1080  
QY 1095 AACCATGTTATCTATTTGTTCCAGTCACTGTCGAGAGTGCAATCATATCTCTGCTTTA 1154  
DB 1081 AACCATGTTATCTATTTGTTCCAGTCACTGTCGAGAGTGCAATCATATCTCTGCTTTA 1140  
QY 1155 CTTAAAAAGGCTCAAGATTTATTTATTTCCCTCCCAATTCCTGATCCTGCAAGATTTTAA 1214  
DB 1141 CTTAAAAAGGCTCAAGATTTATTTATTTCCCTCCCAATTCCTGATCCTGCAAGATTTTAA 1200  
QY 1215 AGAATGTTTGGAGACCAAGATGATATCTGCACTGGAAGAGTACGACATCTATGA 1274  
DB 1201 AGAATGTTTGGAGACCAAGATGATATCTGCACTGGAAGAGTACGACATCTATGA 1260  
QY 1275 GAAGCAAAACCAAGAGAAACCGACCTGTGATGCTGATGAAAACCTGAAGAAAGCTC 1334  
DB 1261 GAAGCAAAACCAAGAGAAACCGACCTGTGATGCTGATGAAAACCTGAAGAAAGCTC 1320  
QY 1335 TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAAAGA 1383  
DB 1321 TCAGTATGAGATTAATTTTATTTTACCTTCACTGTGACCTTGAGAAAGA 1369  
RESULT 8  
US-09-193-707-5  
; Sequence 5, Application US/09193707  
; Patent No. 6524792  
; GENERAL INFORMATION:  
; APPLICANT: Renner, Wolfgang A.  
; APPLICANT: Orberger, Georg H.  
; APPLICANT: Koller, Daniel  
; APPLICANT: Bailey, James E.

```

; TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,
; TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES WITH
; FILE REFERENCE: 8358-0005-999
; CURRENT APPLICATION NUMBER: US/09/193,707
; CURRENT FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 11927
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-193-707-5

Query Match      86.6%; Score 1198; DB 3; Length 11927;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      135  CCGGCTTAAGGAACTCAGCCACCTGTGACAAATTGGAGTGTCTCTGTTGAAAACTCTG 134
DB      7763  CCGGCTTAAGGAACTCAGCCACCTGTGACAAATTGGAGTGTCTCTGTTGAAAACTCTG 7822
QY      195  CACAGTAATATGAGCATGTGATCCACCCGAGGAGCCAGCTCAAAATTGTATGTATAGTA 254
DB      7823  CACAGTAATATGAGCATGTGATCCACCCGAGGAGCCAGCTCAAAATTGTATGTATAGTA 7882
QY      255  TTTTACTATTTTGGGACAAACAAAGTAAGAAATAGCTCCGGAATCTGTCGTTCAAT 314
DB      7883  TTTTACTATTTTGGGACAAACAAAGTAAGAAATAGCTCCGGAATCTGTCGTTCAAT 7942
QY      315  AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTACACCAATGA 374
DB      7943  AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTACACCAATGA 8002
QY      375  GAGTGAGAGCCGATGATTTGGTTGAAAAATGATCTACCCCGAAGGATATCCTGA 434
DB      8003  GAGTGAGAGCCGATGATTTGGTTGAAAAATGATCTACCCCGAAGGATATCCTGA 8062
QY      435  GTCTGCTGTGACTGAATCTTCAATGATGTTGGCACAACCTGAGTACATGAAGTCTTGG 494
DB      8063  GTCTGCTGTGACTGAATCTTCAATGATGTTGGCACAACCTGAGTACATGAAGTCTTGG 8122
QY      495  GCTCCCTGGAAGAAATACCAAGTCCGACATACTATCTCTCTACTATTGGACAGAG 554
DB      8123  GCTCCCTGGAAGAAATACCAAGTCCGACATACTCTCTACTATTGGACAGAG 8182
QY      555  CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATPACTTTGGTTGTC 614
DB      8183  CCTGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATPACTTTGGTTGTC 8242
QY      615  CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGAGTGTCCAAATAATGT 674
DB      8243  CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGAGTGTCCAAATAATGT 8302
QY      675  CAAAGTAATGACGAAAAATTAACCATCTTCAATATATGTGCTTTAACTTCCGCTGT 734
DB      8303  CAAAGTAATGACGAAAAATTAACCATCTTCAATATATGTGCTTTAACTTCCGCTGT 8362
QY      735  GAAACCTGATCCCTCCCATATTAAAAACCTCTCTCCCAATAGATAGCACTATATGCA 794
DB      8363  GAAACCTGATCCCTCCCATATTAAAAACCTCTCTCCCAATAGATAGCACTATATGCA 8422
QY      795  ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTTTATAGAGTAGAAGTCAATAA 854
DB      8423  ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTTTTATAGAGTAGAAGTCAATAA 8482
QY      855  CAGCCAAACTGAGACACATATATGTTTCTACGTCGAAGAGCTPAATGTGAGAAATCAG 914
DB      8483  CAGCCAAACTGAGACACATATATGTTTCTACGTCGAAGAGCTPAATGTGAGAAATCAG 8542
QY      915  ATTGAGAGAAATGTGAGAAATCATCTGTTCAAGGTGCCGAGTCTTCTCTGATAC 974
DB      8543  ATTGAGAGAAATGTGAGAAATCATCTGTTCAAGGTGCCGAGTCTTCTCTGATAC 8602
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QY      975  TTTGAACACAGTCAGATAAGTCAAAACAAATAAGTTATGCTATAGAGATGACAAACT 1034
DB      8603  TTTGAACACAGTCAGATAAGTCAAAACAAATAAGTTATGCTATAGAGATGACAAACT 8662
QY      1035  CTGAGTAATTTGAGACCAAGAAATAGATATAGGTAAAGGCCCAATCTCACTCAAT 1094
DB      8663  CTGAGTAATTTGAGACCAAGAAATAGATATAGGTAAAGGCCCAATCTCACTCAAT 8722
QY      1095  AACCATGTACTCATGTTCCAGTCACTGTCGAGGTGCAATCATATGTAATCTCTGCTTAA 1154
DB      8723  AACCATGTACTCATGTTCCAGTCACTGTCGAGGTGCAATCATATGTAATCTCTGCTTAA 8782
QY      1155  CCTAAAAAGCTTCAGATTTATATATTCCTCCATTTCTGATCTCGGCAAGATTTTAA 1214
DB      8783  CCTAAAAAGCTTCAGATTTATATATTCCTCCATTTCTGATCTCGGCAAGATTTTAA 8842
QY      1215  AGAAATGTTTGAAGACCAAGAAATAGATATCTGCACTGGAAGAAATAGACATCTATGA 1274
DB      8843  AGAAATGTTTGAAGACCAAGAAATAGATATCTGCACTGGAAGAAATAGACATCTATGA 8902
QY      1275  GAAGCAAAACCAAGAGAAACCGACTCTGTAGTGTATAGAAACCTGAAGAAACCTTC 1334
DB      8903  GAAGCAAAACCAAGAGAAACCGACTCTGTAGTGTATAGAAACCTGAAGAAACCTTC 8962
QY      1335  TCAGTATGAGATTAATTTATTTTACCTTCACTGTAACCTTGAGAGA 1383
DB      8963  TCAGTATGAGATTAATTTATTTTACCTTCACTGTAACCTTGAGAGA 9011

RESULT 9
US-09-543-679A-2905
; Sequence 2905, Application US/09543679A
; Patent No. 7034007
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCONSTRICITION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/543,679A
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2905:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14978 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2905;  
US-09-543-679A-2905

Query Match 86.6%; Score 1198; DB 5; Length 14978;

Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 135 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTGAGTGTCTGTGTTGAAAACCTGTG 194
DB 1381 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTGAGTGTCTGTGTTGAAAACCTGTG 1440
QY 195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 254
DB 1441 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 1500
QY 255 TTTTAGCATTTTGGCCACAAACAAGATAAGAAAATAGCTCCGGAATCTCGTCTCAAT 314
DB 1501 TTTTAGCATTTTGGCCACAAACAAGATAAGAAAATAGCTCCGGAATCTCGTCTCAAT 1560
QY 315 AGAAGTACCCCTGATGAGAGATTTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAAATGA 374
DB 1561 AGAAGTACCCCTGATGAGAGATTTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAAATGA 1620
QY 375 GAGTGAGAGCCTTACATTTTGTGAAAAATGCACTCAACCCGAGAGGTGATCTGA 434
DB 1621 GAGTGAGAGCCTTACATTTTGTGAAAAATGCACTCAACCCGAGAGGTGATCTGA 1680
QY 435 GTCTGCTGTGACCTTCAATGATGTTGGCAACACCTGACCTACATGAAGTGTCTTG 494
DB 1681 GTCTGCTGTGACCTTCAATGATGTTGGCAACACCTGACCTACATGAAGTGTCTTG 1740
QY 495 GTCCTCCGGAAGAAATACAGTCCGACACTAATCTCTACTATTGGGACAGAG 554
DB 1741 GTCCTCCGGAAGAAATACAGTCCGACACTAATCTCTACTATTGGGACAGAG 1800
QY 555 CCTGGAATAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATCTTGGTGTTC 614
DB 1801 CCTGGAATAAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATCTTGGTGTTC 1860
QY 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAACAGTGTCCAAATATGT 674
DB 1861 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAACAGTGTCCAAATATGT 1920
QY 675 CAAGGATATGCAAGGAAAAATTTAAACAATCTTCAATATAGTGGCTTTAATCTCCGTGT 734
DB 1921 CAAGGATATGCAAGGAAAAATTTAAACAATCTTCAATATAGTGGCTTTAATCTCCGTGT 1980
QY 735 GAAACCTGATCTTCCATATTTAAAACTCTCTCCCTCCACATGATGACCTATATGTGA 794
DB 1981 GAAACCTGATCTTCCATATTTAAAACTCTCTCTCCCTCCACATGATGACCTATATGTGA 2040
QY 795 ATGGGAGAAATCCACAGAAATTTTATAGCAATGCGTAATTTTATGAGTGAAGTCAATAA 854
DB 2041 ATGGGAGAAATCCACAGAAATTTTATAGCAATGCGTAATTTTATGAGTGAAGTCAATAA 2100
QY 855 CAGGCAAACTGAGACATATATGTTTCTACGTCGCAAGAGCTTAAATGTAGATCCAGA 914
DB 2101 CAGGCAAACTGAGACATATATGTTTCTACGTCGCAAGAGCTTAAATGTAGATCCAGA 2160
QY 915 ATTTGAGAGAAATGTGAGAGATACATCTTGTTCATGGTCCCTGTGTTCCTCTGATAC 974
DB 2161 ATTTGAGAGAAATGTGAGAGATACATCTTGTTCATGGTCCCTGTGTTCCTCTGATAC 2220
QY 975 TTTTGAACACGTCAAGATTAAGAGTCAAAACAATATGTTATGCTATAGAGATGCAAACT 1034
DB 2221 TTTTGAACACGTCAAGATTAAGAGTCAAAACAATATGTTATGCTATAGAGATGCAAACT 2280
QY 1035 CTGAGATTAATTTGAGGCAAGAAATGAGTATAGGTAAAGGCAATCCACACTTACAT 1094
DB 2281 CTGAGATTAATTTGAGGCAAGAAATGAGTATAGGTAAAGGCAATCCACACTTACAT 2340
QY 1095 AACCATGTTACTCATTTGTTCAATGCTGCGAGGTGCAATCATAGTACTCTCTGCTTTA 1154
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DB 2341 AACCATGTTACTCATTTGTTCAATGCTGCGAGGTGCAATCATAGTACTCTCTGCTTTA 2400
QY 1155 CCTAAAAAGCTCAAGATTAATATTTCCCTCCCAATTCCTGATCTGTGCAAGATTTTAA 1214
DB 2401 CCTAAAAAGCTCAAGATTAATATTTCCCTCCCAATTCCTGATCTGTGCAAGATTTTAA 2460
QY 1215 AGAATGTTTGGAGACCGAATGATGATGATCTGCACTGGAAGAGTGCATCTATGA 1274
DB 2461 AGAATGTTTGGAGACCGAATGATGATGATCTGCACTGGAAGAGTGCATCTATGA 2520
QY 1275 GAAGCAAAACCAAGAGGAAAAACCGAATCTGATGCTGATAGAAAACTGGAAGAGCTTC 1334
DB 2521 GAAGCAAAACCAAGAGGAAAAACCGAATCTGATGCTGATAGAAAACTGGAAGAGCTTC 2580
QY 1335 TCACTGATGAGATTAATTTTATTTTACCTTACTCTGATGACCTTGAGAGA 1383
DB 2581 TCACTGATGAGATTAATTTTATTTTACCTTACTCTGATGACCTTGAGAGA 2629
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## RESULT 10

US-09-825-561A-81

; Sequence 81, Application US/09825561A

; Patent No. 6777539

; GENERAL INFORMATION:

; APPLICANT: Sprechter, Cindy A.

; APPLICANT: No. 677539ak, Julia E.

; APPLICANT: West, James W.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Holly, Richard D.

; APPLICANT: Nelson, Andrew J.

; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS

; FILE REFERENCE: 00-22

; CURRENT APPLICATION NUMBER: US/09/825,561A

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/194,731

; PRIOR FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/222,121

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 86

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 81

; LENGTH: 966

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(966)

US-09-825-561A-81

Query Match 65.1%; Score 901; DB 3; Length 966;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 135 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTGAGTGTCTGTGTTGAAAACCTGTG 194
DB 15 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTGAGTGTCTGTGTTGAAAACCTGTG 74
QY 195 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 254
DB 75 CACAGTAATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTA 134
QY 255 TTTTAGCATTTTGGGGAACAACAAGTAAAGAAATAGCTCCGGAATCTCGTGTCAAT 314
DB 135 TTTTAGCATTTTGGGGAACAACAAGTAAAGAAATAGCTCCGGAATCTCGTGTCAAT 194
QY 315 AGAAGTACCCCTGATGAGAGATTTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAAATGA 374
DB 195 AGAAGTACCCCTGATGAGAGATTTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAAATGA 254
QY 375 GAGTGAGAGCCTTACATTTTGTGAAAAATGCACTCAACCCGAGAGGTGATCTGA 434
DB 255 GAGTGAGAGCCTTACATTTTGTGAAAAATGCACTCAACCCGAGAGGTGATCTGA 314
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QY 435 GTCGTGCTGAGTGAATTCATGCAATTTGGCAAACTGAGCTAGATGAAGTCTTG 494
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|
|
QY 495 GCTCCCTGGAAGGAATACCACTGCTCCGACACTAATCTTACTCTTACTTATGGCAGAG 554
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Db 375 GCTCCCTGGAAGGAATACCACTGCTCCGACACTAATCTTACTCTTACTTATGGCAGAG 434
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QY 555 CCGGAAAAAATTCATCAATGTGAAAAATCTTAGAGAGGCAATPACTTGTGTTTC 614
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Db 435 CCGGAAAAAATTCATCAATGTGAAAAATCTTAGAGAGGCAATPACTTGTGTTTC 494
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|
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QY 615 CTTTGAATCGACCAAGAGTGAAGGATTCAGTTTGAACAACAGAGTCCAAAATAATGT 674
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|
Db 495 CTTTGAATCGACCAAGAGTGAAGGATTCAGTTTGAACAACAGAGTCCAAAATAATGT 554
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QY 675 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTTCCGTGT 734
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Db 555 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGCCTTTAACTTCCGTGT 614
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|
QY 735 GAAACCTGATCCCTCCACATATTAATAAAACCTCTCCTTCCACATGATGACCTATATGCA 794
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Db 615 GAAACCTGATCCCTCCACATATTAATAAAACCTCTCCTTCCACATGATGACCTATATGCA 674
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QY 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAAGTAGAATCAATA 854
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Db 735 CAGCCAAATCGACACATTAATGTTTCTTACGTCGAAGAGGCTTAATGTGAATCCAGA 794
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QY 975 TTGGAACACAGTCAGATTAAGATCAAAACAAATAAGTTATGCTATGAGATGACAAACT 1034
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|
Db 855 TTGGAACACAGTCAGATTAAGATCAAAACAAATAAGTTATGCTATGAGATGACAAACT 914
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QY 1035 CTGAGATTAATGAGCCAGAAATGAGTATAGTAAAGCGCAATTCCACA 1086
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Db 915 CTGAGATTAATGAGCCAGAAATGAGTATAGTAAAGCGCAATTCCACA 966
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RESULT 11
US-09-313-942-29
; Sequence 29, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2352)
US-09-313-942-29
Query Match 65.1%; Score 901; DB 3; Length 2355;
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 135 CGGCGCTTAGGAAACCTCAGCCACCTGTGCAATTTGAGTGTCTGTGAAAACTCTG 194
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Db 714 CGGCGCTTAGGAAACCTCAGCCACCTGTGCAATTTGAGTGTCTGTGAAAACTCTG 773
|
|
|
QY 195 CACAGTAATATGACATGGAATCCACCGAGGAGGCACTCAATTTAGTATATGTA 254
|
|
|
Db 774 CACAGTAATATGACATGGAATCCACCGAGGAGGCACTCAATTTAGTATATGTA 833
|
|
|
QY 255 TTTTATGCTATTTTGGGCAAAACAGATTAAGAAAAAGCTCCGGAAAACTGTGTTCAAT 314
|
|
|
Db 834 TTTTATGCTATTTTGGGCAAAACAGATTAAGAAAAAGCTCCGGAAAACTGTGTTCAAT 893
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|
|
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTATAGCAACAATGA 374
|
|
|
Db 894 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTATAGCAACAATGA 953
|
|
|
QY 375 GAGTGAAGGCTTAGCATTTTGGTTGAAAAATGCAATCTCACCCCGAAGGTGATCTGA 434
|
|
|
Db 954 GAGTGAAGGCTTAGCATTTTGGTTGAAAAATGCAATCTCACCCCGAAGGTGATCTGA 1013
|
|
|
QY 435 GTCGTGCTGAGTGAATTCATGCAATTTGGCAAACTGAGCTAGATGAAGTCTTG 494
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|
|
Db 1014 GTCGTGCTGAGTGAATTCATGCAATTTGGCAAACTGAGCTAGATGAAGTCTTG 1073
|
|
|
QY 495 GCTCCCTGGAAGGAATACCACTGCTCCGACACTAATCTTACTCTTACTTATGGCAGAG 554
|
|
|
Db 1074 GCTCCCTGGAAGGAATACCACTGCTCCGACACTAATCTTACTCTTACTTATGGCAGAG 1133
|
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QY 555 CCGGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATPACTTGTGTTTC 614
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Db 1134 CCGGAAAAAATTCATCAATGTGAAAAATCTTTAGAGAGGCAATPACTTGTGTTTC 1193
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QY 615 CTTTGAATCGACCAAGAGTGAAGGATTCAGTTTGAACAACAGAGTCCAAAATAATGT 674
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Db 1194 CTTTGAATCGACCAAGAGTGAAGGATTCAGTTTGAACAACAGAGTCCAAAATAATGT 1253
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QY 675 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATAGTGCCTTAACTTCCGTGT 734
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QY 735 GAAACCTGATCCCTCCACATATTAATAAAACCTCTTCCACATGATGACCTATATGCA 794
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Db 1314 GAAACCTGATCCCTCCACATATTAATAAAACCTCTTCCACATGATGACCTATATGCA 1373
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QY 795 ATGGAGAAATCCACAGAAATTTTATGCAAGTGCCTATTTTATGAAGTAGAATCAATA 854
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Db 1374 ATGGAGAAATCCACAGAAATTTTATGCAAGTGCCTATTTTATGAAGTAGAATCAATA 1433
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QY 855 CAGCCAAATCGACACATTAATGTTTCTACGTCGAAGAGGCTTAATGTGAATCCAGA 914
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Db 1434 CAGCCAAATCGACACATTAATGTTTCTACGTCGAAGAGGCTTAATGTGAATCCAGA 1493
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QY 915 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGATGCTGATGTTCTTCTGTATAC 974
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Db 1494 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGATGCTGATGTTCTTCTGTATAC 1553
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QY 1035 CTGAGATTAATGAGCCAGAAATGAGTATAGTAAAGCGCAATTCCACA 1086
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RESULT 12
US-10-282-162-29
; Sequence 29, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
FILE REFERENCE: REG 203-B-US
CURRENT FILING DATE: 2002-10-28
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: 09/787,835
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: PCT/US99/22045
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 29
LENGTH: 2355
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (2352)
US-10-282-162-29
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Query Match 65.1%; Score 901; DB 3; Length 2355;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 195 CACAGTAATATGACATGATGATCCACCGAGGAGCCAGCTCAATATTTGATGATGATGAT 254
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QY 255 TTTTACATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 314
DB 834 TTTTACATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 893
QY 315 AGAAGTACCCCTGAAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374
DB 894 AGAAGTACCCCTGAAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 953
QY 375 GAGTGAAGAACCTAGCATTTTGTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 434
DB 954 GAGTGAAGAACCTAGCATTTTGTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1013
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DB 1014 GTCTGCTGTACGTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1073
QY 495 GCTCCCTGAAAGAAATCCAGTCCCGACATTAATTAATTAATTAATTAATTAATTAATTAAT 554
DB 1074 GCTCCCTGAAAGAAATCCAGTCCCGACATTAATTAATTAATTAATTAATTAATTAATTAAT 1133
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DB 1134 CCTGGAAGAAATTCATCAATGTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1193
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DB 1194 CTTTGTATCTGACCAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1253
QY 675 CAAGATTAATGACGAAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 734
DB 1254 CAAGATTAATGACGAAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1313
QY 735 GAAACCTGATCTTCCACATATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 794
DB 1314 GAAACCTGATCTTCCACATATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1373
QY 795 ATGGAGAAATCCAGAAATTTTATAGCAATGCTTATTTATAGCAATGCTTATTTATAGCA 854
DB 1374 ATGGAGAAATCCAGAAATTTTATAGCAATGCTTATTTATAGCAATGCTTATTTATAGCA 1433
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DB 1494 ATTTGAGAAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 1553
QY 975 TTTGACACAGTCAGAAATTAAGTCAAAACAAATTAAGTATGATGAGATGACAACT 1034
DB 1554 TTTGACACAGTCAGAAATTAAGTCAAAACAAATTAAGTATGATGAGATGACAACT 1613
QY 1035 CTGAGTAATTTGAGCCCAAGAAATGAGTATGATGATGATGATGATGATGATGATGATG 1086
DB 1614 CTGAGTAATTTGAGCCCAAGAAATGAGTATGATGATGATGATGATGATGATGATGATG 1665
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RESULT 13

US-09-313-942-31

Sequence 31, Application US/09313942

Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

FILE REFERENCE: REG 203-A

CURRENT FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 2382

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1) ... (2379)

US-09-313-942-31

Query Match 65.1%; Score 901; DB 3; Length 2382;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 78 CGGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTGTTGAAAACCTCTG 137
QY 195 CACAGTAATATGACATGATGATCCACCGAGGAGCCAGCTCAATATTTGATGATGATGATG 254
DB 138 CACAGTAATATGACATGATGATCCACCGAGGAGCCAGCTCAATATTTGATGATGATGATG 197
QY 255 TTTTACATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 314
DB 198 TTTTACATTTTGGGCGACAAACAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 257
QY 315 AGAAGTACCCCTGAAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374
DB 258 AGAAGTACCCCTGAAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 317
QY 375 GAGTGAAGAACCTAGCATTTTGTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 434
DB 318 GAGTGAAGAACCTAGCATTTTGTGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 377
QY 435 GTCTGCTGTACGTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 494
DB 378 GTCTGCTGTACGTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 437
QY 495 GCTCCCTGAAAGAAATCCAGTCCCGACATTAATTAATTAATTAATTAATTAATTAATTAAT 554
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Db 438 GCTCCCTGGAAGGAATACCAATGCCGACACTAACTTACTCTCTACTATTGGACAGAAAG 497  
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Db 498 CCGGAAAAAATTCATCAATGTGTAATAACATCTTTAGAGAGGCCAACTACTTTGGTTTC 557  
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Qy 915 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTCTGTATAC 974  
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Qy 975 TTTGAAACACATGACATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 1034  
Db 918 TTTGAAACACATGACATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 977  
Qy 1035 CTGGAGTAATTTGGAGCCCAAGAAATGATAGTTAGTAAGAGCGCAATTCACA 1086  
Db 978 CTGGAGTAATTTGGAGCCCAAGAAATGATAGTTAGTAAGAGCGCAATTCACA 1029

RESULT 14  
US-10-282-162-31  
; Sequence 31, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; PRIOR FILING DATE: 1999-09-22  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 2382  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2379)  
US-10-282-162-31

Query Match 65.1%; Score 901; DB 3; Length 2382;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 951; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 135 CGCGCTACGAGAACTCAGCCACTGTGACAAATTTAGAGTGTCTGTGTAAGAACTCTG 194  
Db 78 CGCGCTACGAGAACTCAGCCACTGTGACAAATTTAGAGTGTCTGTGTAAGAACTCTG 137

Qy 195 CACAGTAATATGACATGGAATTCACCCGAGGAGCCAGCTCAATTTAGTCTATGTA 254  
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Qy 735 GAAACCTGATCTCCATATTTAAACCTCTCTTCCCAATGATGACCTATATGTGA 794  
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Db 858 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTCTGTATAC 917  
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Db 918 TTTGAAACACATGACATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 977  
Qy 1035 CTGGAGTAATTTGGAGCCCAAGAAATGATAGTTAGTAAGAGCGCAATTCACA 1086  
Db 978 CTGGAGTAATTTGGAGCCCAAGAAATGATAGTTAGTAAGAGCGCAATTCACA 1029

RESULT 15  
US-09-949-016-2679  
; Sequence 2679, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/231,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2679  
LENGTH: 701  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-2679

Query Match 46.5%; Score 643; DB 3; Length 701;  
Best Local Similarity 99.9%; Pred. No. 4,5e-312;  
Matches 693; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 37781012

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Published Applications NA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|------------------------|-------------------|
| 1          | 1198  | 86.6        | 4009   | 15 US-11-185-230-3     | Sequence 3, Appl1 |
| 2          | 1198  | 86.6        | 4009   | 16 US-11-182-384A-3    | Sequence 3, Appl1 |
| 3          | 1198  | 86.6        | 4009   | 16 US-11-183-599A-3    | Sequence 3, Appl1 |
| 4          | 1198  | 86.6        | 4038   | 8 US-10-671-697-8      | Sequence 8, Appl1 |
| 5          | 1198  | 86.6        | 4039   | 3 US-09-962-832-160    | Sequence 16, Appl |
| 6          | 1198  | 86.6        | 4039   | 3 US-09-880-107-3856   | Sequence 386, Ap  |
| 7          | 1198  | 86.6        | 4039   | 7 US-10-172-118-633    | Sequence 63, App  |
| 8          | 1198  | 86.6        | 4039   | 8 US-10-342-887-633    | Sequence 63, App  |
| 9          | 1198  | 86.6        | 4039   | 10 US-10-843-641A-6046 | Sequence 6046, Ap |
| 10         | 1198  | 86.6        | 4468   | 3 US-09-971-392-58     | Sequence 58, Appl |
| 11         | 1189  | 86.0        | 3880   | 3 US-09-822-846-109    | Sequence 109, App |
| 12         | 1179  | 85.2        | 1383   | 6 US-10-036-568-3      | Sequence 3, Appl1 |
| 13         | 1138  | 82.3        | 3906   | 12 US-10-745-586-32    | Sequence 32, Appl |
| 14         | 1105  | 79.9        | 1284   | 10 US-10-850-270-3     | Sequence 3, Appl1 |
| 15         | 1096  | 79.2        | 1572   | 9 US-10-278-698-6      | Sequence 6, Appl1 |
| 16         | 1096  | 79.2        | 1572   | 9 US-10-278-698-520    | Sequence 520, App |
| 17         | 901   | 65.1        | 966    | 3 US-09-825-561A-81    | Sequence 81, Appl |

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| 18 | 901 | 65.1 | 966  | 9 US-10-872-087-81  | Sequence 81, Appl |
| 19 | 901 | 65.1 | 2343 | 3 US-09-935-868-33  | Sequence 33, Appl |
| 20 | 901 | 65.1 | 2343 | 6 US-10-287-035-33  | Sequence 33, Appl |
| 21 | 901 | 65.1 | 2355 | 3 US-09-313-942-29  | Sequence 29, Appl |
| 22 | 901 | 65.1 | 2355 | 3 US-09-935-868-29  | Sequence 29, Appl |
| 23 | 901 | 65.1 | 2355 | 6 US-10-287-035-29  | Sequence 29, Appl |
| 24 | 901 | 65.1 | 2355 | 7 US-10-282-162-29  | Sequence 29, Appl |
| 25 | 901 | 65.1 | 2355 | 13 US-11-134-114-29 | Sequence 29, Appl |
| 26 | 901 | 65.1 | 2382 | 3 US-09-313-942-31  | Sequence 31, Appl |
| 27 | 901 | 65.1 | 2382 | 3 US-09-935-868-31  | Sequence 31, Appl |
| 28 | 901 | 65.1 | 2382 | 6 US-10-287-035-31  | Sequence 31, Appl |
| 29 | 901 | 65.1 | 2382 | 7 US-10-282-162-31  | Sequence 31, Appl |
| 30 | 901 | 65.1 | 2382 | 13 US-11-134-114-31 | Sequence 31, Appl |
| 31 | 900 | 65.1 | 1995 | 10 US-10-850-270-39 | Sequence 39, Appl |
| 32 | 899 | 65.0 | 2331 | 3 US-09-935-868-35  | Sequence 35, Appl |
| 33 | 899 | 65.0 | 2331 | 6 US-10-287-035-39  | Sequence 39, Appl |
| 34 | 850 | 61.5 | 2343 | 3 US-09-935-868-37  | Sequence 37, Appl |
| 35 | 850 | 61.5 | 2343 | 6 US-10-287-035-37  | Sequence 37, Appl |
| 36 | 850 | 61.5 | 2349 | 3 US-09-935-868-51  | Sequence 51, Appl |
| 37 | 850 | 61.5 | 2349 | 6 US-10-287-035-51  | Sequence 51, Appl |
| 38 | 850 | 61.5 | 2349 | 6 US-10-287-035-57  | Sequence 57, Appl |
| 39 | 848 | 61.3 | 2331 | 3 US-09-935-868-39  | Sequence 39, Appl |
| 40 | 848 | 61.3 | 2331 | 6 US-10-287-035-35  | Sequence 35, Appl |
| 41 | 848 | 61.3 | 2337 | 3 US-09-935-868-49  | Sequence 49, Appl |
| 42 | 848 | 61.3 | 2337 | 6 US-10-287-035-49  | Sequence 49, Appl |
| 43 | 848 | 61.3 | 2337 | 6 US-10-287-035-55  | Sequence 55, Appl |
| 44 | 840 | 60.7 | 2343 | 3 US-09-935-868-41  | Sequence 41, Appl |
| 45 | 840 | 60.7 | 2343 | 6 US-10-287-035-41  | Sequence 41, Appl |

ALIGNMENTS

RESULT 1  
US-11-185-230-3  
; Sequence 3, Application US/11185230  
; Publication No. US2005028216A1  
; GENERAL INFORMATION:  
; APPLICANT: Caput, Daniel  
; APPLICANT: Ferrara, Pascual  
; APPLICANT: Laurent, Patrick  
; APPLICANT: Vila, Natalio  
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity  
; FILE REFERENCE: IVD924 US CMT 1  
; CURRENT APPLICATION NUMBER: US/11/185,230  
; CURRENT FILING DATE: 2005-07-18  
; PRIOR APPLICATION NUMBER: PCT/FR96/01756  
; PRIOR FILING DATE: 1996-11-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 4009  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-11-185-230-3

Query Match 86.6%; Score 1198; DB 15; Length 4009;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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| QY | 135 | CGGCGCTACGGAACCTGACGACCTGACAAATTTGAGTCTCTGTGAAAACCTCTG   | 194 |
| DB | 111 | CGGCGCTACGGAACCTGACGACCTGACAAATTTGAGTCTCTGTGAAAACCTCTG   | 170 |
| QY | 195 | CACAGTAATATGACATGATCCACCCGAGGAGCCAGCTCAATTTGATGATGATGATA | 254 |
| DB | 171 | CACAGTAATATGACATGATCCACCCGAGGAGCCAGCTCAATTTGATGATGATGATA | 230 |
| QY | 255 | TTTATGATATTTTGGGACAAACAAAGTAAAGAAATGCTCCGAAATCTGCTTCAAT  | 314 |
| DB | 231 | TTTATGATATTTTGGGACAAACAAAGTAAAGAAATGCTCCGAAATCTGCTTCAAT  | 290 |



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QY 915 ATTTGAGAGAAATGTGAGATACATCTGTTTCATAGTCCCTGAGTCTTCTCTGATAC 974  
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Db 891 ATTTGAGAGAAATGTGAGATACATCTGTTTCATAGTCCCTGAGTCTTCTCTGATAC 950  
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Db 951 TTTGAAACACAGTCAGATTAAGAGTCAAAACAAATAGTTATGCTATGAGTAGCAAACT 1010  
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Db 1071 AACCATGTTACTGATGTTCCAGTCATGTCGAGGAGTCAATCATATGATCTCCCTCTTA 1130  
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Db 1131 CCTAAAGAGCTCAAGATTATTTATTTCCCTCCATTCCTGATCTGAGCAAGATTTTAA 1190  
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QY 1215 AGAATGTTTGGAGACCAAGATGATGATCTGTCACCTGAGAAAGTAGACATCTATGA 1274  
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Db 1191 AGAATGTTTGGAGACCAAGATGATGATCTGTCACCTGAGAAAGTAGACATCTATGA 1250  
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QY 1275 GAGGCAAAACCAAGAGGAAACCGACCTGTGATGTCGATAGAAACCTGAAAGAAAGCTC 1334  
| | | | |  
Db 1251 GAGGCAAAACCAAGAGGAAACCGACCTGTGATGTCGATAGAAACCTGAAAGAAAGCTC 1310  
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QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
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Db 1311 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1359  
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RESULT 3  
US-11-183-599A-3  
; Sequence 3, Application US/11183599A  
; Publication No. US20060035856A1  
; GENERAL INFORMATION:  
; APPLICANT: Caput, Daniel  
; APPLICANT: Ferrara, Pascual  
; APPLICANT: Laurent, Patrick  
; APPLICANT: Vila, Natalio  
; TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity  
; FILE REFERENCE: IVD924 US Div 1  
; CURRENT APPLICATION NUMBER: US/11/183,599A  
; PRIOR APPLICATION NUMBER: 09/077,817  
; PRIOR FILING DATE: 1998-09-14  
; PRIOR APPLICATION NUMBER: PCT/FR96/01756  
; PRIOR FILING DATE: 1996-11-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3  
; LENGTH: 4009  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-183-599A-3

Query Match 86.6%; Score 1198; DB 16; Length 4009;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CCGGCTTACGGAACCTGAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 194  
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Db 111 CCGGCTTACGGAACCTGAGCCACTGTGACAAATTTGAGTGTCTCTGTTGAAAACCTCTG 170  
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QY 195 CACAGTATATNGACATGGAATCCACCGAGGAGCCAGCTCAATTTAGTCTATGGTA 254  
| | | | |  
Db 171 CACAGTATATNGACATGGAATCCACCGAGGAGCCAGCTCAATTTAGTCTATGGTA 230  
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QY 255 TTTTATGTCATTTTGGGACAAACAAATTAAGAAAATAGTCTCCGAAACTGCTGTCAT 314  
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Db 231 TTTTATGTCATTTTGGGACAAACAAATTAAGAAAATAGTCTCCGAAACTGCTGTCAT 290  
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QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGGTGACCAATGA 374  
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Db 291 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGGTGACCAATGA 350  
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QY 375 GAGTGAAGCTTACATTTTGGTGAATAATGATCTCACCCCGAGAGGTATCCGA 434  
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QY 435 GTCTGCTGTCAGTGAATCTTCAATGCAATTTGGCAACACCTGAGCTACATGAAGTCTTG 494  
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QY 495 GCTCCCTGGAAGGATTCAGTCCGACACTAATATCTCTACTATTTGGCACAGAG 554  
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Db 471 GCTCCCTGGAAGGATTCAGTCCGACACTAATATCTCTACTATTTGGCACAGAG 530  
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Db 531 CTTGGAATAATTCATGATGTAACATCTTTAGGAAGGCCAATATCTTTGGTGTTC 590  
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QY 615 CTTTATCTGACCAAGATGAAGATTCAGTTTGAACAACACAGTGTCCAAATATAGT 674  
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Db 591 CTTTATCTGACCAAGATGAAGATTCAGTTTGAACAACACAGTGTCCAAATATAGT 650  
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QY 675 CAAGATATGCAAGAAAATTAACATCTTCAATATATGTCCTTTAACTTCCGTGT 734  
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Db 651 CAAGATATGCAAGAAAATTAACATCTTCAATATATGTCCTTTAACTTCCGTGT 710  
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QY 735 GAAACCTGATCTCCACATTTTAAACCTCTCTTCCACAAATGATGACCTATATGGA 794  
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Db 711 GAAACCTGATCTCCACATTTTAAACCTCTCTTCCACAAATGATGACCTATATGGA 770  
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QY 795 ATGGAGAAATCCACAGATTTTATTTAGACAGTCCCTATTTTATGAGTAGAGTCAATTA 854  
| | | | |  
Db 771 ATGGAGAAATCCACAGATTTTATTTAGACAGTCCCTATTTTATGAGTAGAGTCAATTA 830  
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QY 855 CAGCCAAATCTGAGACACATATGTTTCTACAGTCCAAAGAGCTTAAATGTGAATCCAGA 914  
| | | | |  
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Db 891 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATAGTCCCTGAGTCTTCTCTGATAC 950  
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QY 975 TTTGAAACACAGTCAGATTAAGAGTCAAAACAAATAGTTATGCTATGAGTAGCAAACT 1034  
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Db 951 TTTGAAACACAGTCAGATTAAGAGTCAAAACAAATAGTTATGCTATGAGTAGCAAACT 1010  
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QY 1035 CTGAGATTAATTGAGACCAAGAAATGAGTATGTAAGAGGCAATTCCACACTCTA 1094  
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Db 1011 CTGAGATTAATTGAGACCAAGAAATGAGTATGTAAGAGGCAATTCCACACTCTA 1070  
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QY 1095 AACCATGTTACTGATGTTCCAGTCATGTCGAGGAGTCAATCATATGATCTCCCTCTTA 1154  
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Db 1071 AACCATGTTACTGATGTTCCAGTCATGTCGAGGAGTCAATCATATGATCTCCCTCTTA 1130  
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QY 1155 CCTAAAGAGCTCAAGATTATTTATTTCCCTCCATTCCTGATCTGAGCAAGATTTTAA 1214  
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Db 1191 AGAATGTTTGGAGACCAAGATGATGATCTGTCACCTGAGAAAGTAGACATCTATGA 1250  
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; Sequence 160, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 160
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-160
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Query Match      86.6%; Score 1198; DB 3; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      135  CGGCGCTACGAACTCAGCCACCTGTGACAAATTGAGTGTCTGTGTAACCACTCTG 194
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DB      121  CGGCGCTACGAACTCAGCCACCTGTGACAAATTGAGTGTCTGTGTAACCACTCTG 180
QY      195  CACAGTAATATGACATGTAATCCACCCGAGGAGCCAGCTCAATTGTATGTAATGTA 254
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DB      181  CACAGTAATATGACATGTAATCCACCCGAGGAGCCAGCTCAATTGTATGTAATGTA 240
QY      255  TTTTACTGATTTTGGGACAAACAAGTAAATAATAGCTCCGAAACCTGTGTTCAAT 314
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DB      241  TTTTACTGATTTTGGGACAAACAAGTAAATAATAGCTCCGAAACCTGTGTTCAAT 300
QY      315  AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGA 374
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DB      301  AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGGTCCGAGTGTGACCAATGA 360
QY      375  GAGTGAAGAGCTTATGATTTGGTTGTAATAATGATCTCAACCCCGAAGGTATCTTGA 434
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DB      361  GAGTGAAGAGCTTATGATTTGGTTGTAATAATGATCTCAACCCCGAAGGTATCTTGA 420
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DB      421  GTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY      495  GCTCCCTGGAAGAAATACCAAGTCCGACACTAATCTTCTACTATTTGGACAGAGAG 554
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DB      481  GCTCCCTGGAAGAAATACCAAGTCCGACACTAATCTTCTACTATTTGGACAGAGAG 540
QY      555  CCTGGAATAAATTCATCAATGTGAAATCATCTTTAGAGAGGCGCAATACCTTGGTTC 614
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DB      601  CTTTGTATGACCAAGTGAAGATTCAGTTTGAACAACAAGTGTCCAATTAATGTGT 660
QY      675  CAAGATTAATGACGAAATAATTAACCATCTTCAATATATGATGATGATGATGATGAT 724
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DB      661  CAAGATTAATGACGAAATAATTAACCATCTTCAATATATGATGATGATGATGATGAT 720
QY      735  GAAACCTGATCTTCCATATTAATAAATCTTCTTCCATATATGATGATGATGATGAT 794
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DB      721  GAAACCTGATCTTCCATATTAATAAATCTTCTTCCATATATGATGATGATGATGAT 780
QY      795  ATGGAGATATCCACAGATTTTATATGAGATGATGATGATGATGATGATGATGATGAT 854
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DB      841  CAGCCAAATCTGAGACATATATGTTTTCTAAGTCCAAAGAGCTTAATGTGAATCCAGA 900
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DB      901  ATTTGAGAAATGTGAGAAATACATCTTTTCAATGATGATGATGATGATGATGATGAT 960
QY      975  TTTGAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTATGATGATGATGATGAT 1034
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DB      961  TTTGAACACAGTCAGAAATAGAGTCAAAACAAATTAAGTATGATGATGATGATGAT 1020
QY      1035  CTGAGATTAATGAGCCAAAGAAATGAGTATAGTATAGAGCCGAATTCACACTCTAT 1094
      |||
DB      1021  CTGAGATTAATGAGCCAAAGAAATGAGTATAGTATAGAGCCGAATTCACACTCTAT 1080
QY      1095  AACCATGTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1154
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DB      1081  AACCATGTACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY      1155  CTTAAAAAGCTCAGATTAATTAATTCCTCCCAATTCCTGATCCTGCAAGATTTTAA 1214
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DB      1141  CTTAAAAAGCTCAGATTAATTAATTCCTCCCAATTCCTGATCCTGCAAGATTTTAA 1200
QY      1215  AGAATGTTTGGAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1274
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DB      1201  AGAATGTTTGGAGACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY      1275  GAAGCAAAACCAAGAGAAACCGACTCTGTATGATGATGATGATGATGATGATGATGAT 1334
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DB      1261  GAAGCAAAACCAAGAGAAACCGACTCTGTATGATGATGATGATGATGATGATGATGAT 1320
QY      1335  TCAGTATGAGATTAATTAATTTTACCTTCACTGATGATGATGATGATGATGATGAT 1383
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DB      1321  TCAGTATGAGATTAATTAATTTTACCTTCACTGATGATGATGATGATGATGATGAT 1369
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## RESULT 6

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US-09-880-107-3856
; Sequence 3856, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3856
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y10659
US-09-880-107-3856
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Query Match      86.6%; Score 1198; DB 3; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      135  CGGCGCTACGAACTCAGCCACCTGTGACAAATTGAGTGTCTGTGTAACCACTCTG 194
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DB      121  CGGCGCTACGAACTCAGCCACCTGTGACAAATTGAGTGTCTGTGTAACCACTCTG 180
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QY 255 TTTTATCATTTTGGGACAAACAAGTAAAGTAATAGCTCCGGAAATCGTGTTCAT 314  
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QY 375 GAGTGAAGAGCTTACATTTTGGTGAAGAAATGATCTCACCCCGAAGGTATCTTGA 434  
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QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACCAACAGTGTCCAAATATGCT 674  
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DB 661 CAAGATAATGCAAGAAAAATTAACCATCTTCAATATAGTGTCTTAACTTCCGCTGT 720  
QY 735 GAAACCTGATCTCCACATATTAATAAACTCTCTCTCCACAAATGATGACTATATGTGA 794  
DB 721 GAAACCTGATCTCCACATATTAATAAACTCTCTCTCCACAAATGATGACTATATGTGA 780  
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QY 855 CAGCCAACTGAGACACATATGTTTCTAGCTCCAGAGAGCTAAATGTAGAGATCCAGA 914  
DB 841 CAGCCAACTGAGACACATATGTTTCTAGCTCCAGAGAGCTAAATGTAGAGATCCAGA 900  
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DB 901 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGCTCCCTGGTGTCTTCCGTATAC 960  
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DB 1081 AACCATGTTACTCATTTGTCAGTCAATGTCGACAGGTGCAATCATATGATCTCTGCTTTA 1140  
QY 1155 CTTAAAGAAAGGCTCAAGATTATATATTCCTCCATTCCTGATCTGTGGCAAGATTTTAA 1214  
DB 1141 CTTAAAGAAAGGCTCAAGATTATATATTCCTCCATTCCTGATCTGTGGCAAGATTTTAA 1200  
QY 1215 AGAAATGTTTGAAGACAGAAATGATGATCTGCACTGGAAGAAAGTACGATCTATGA 1274  
DB 1201 AGAAATGTTTGAAGACAGAAATGATGATCTGCACTGGAAGAAAGTACGATCTATGA 1260  
QY 1275 GAAGCAAAACCAAGAGGAAACGACCTCTGTATGCTGATGAAAACTTGAAGAAAGCTTC 1334

DB 1261 GAAGCAAAACCAAGAGGAAACCGACTGTGTAGTGTGATGAAAACTTGAAGAAAGCTTC 1320  
QY 1335 TCAGTATGAGAGTAATTTATTTTAACTTCACTGTGACCTTGAGAGAG 1383  
DB 1321 TCAGTATGAGAGTAATTTATTTTAACTTCACTGTGACCTTGAGAGAG 1369  
RESULT 7  
US-10-172-118-633  
; Sequence 633, Application US/10172118  
; Publication No. US20030224374A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Chris  
; APPLICANT: Van 't Veer, Laura  
; APPLICANT: Van de Vijver, Marc  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-175-999  
; CURRENT APPLICATION NUMBER: US/10/172, 118  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/380, 770  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 633  
; LENGTH: 4039  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: NM\_001560  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-633  
Query Match 86.6%; Score 1198; DB 7; Length 4039;  
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Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 135 CGGCTTAAGGAACTCAGCCACCTGTGCAAAATTTGAGTGTCTCTTGAAGAACTCTG 194  
DB 121 CGGCTTAAGGAACTCAGCCACCTGTGCAAAATTTGAGTGTCTCTTGAAGAACTCTG 180  
QY 195 CACAGTAATATGAGACATGAGATCCACCGAGGAGCAGCTCAATTTAGTATGTA 254  
DB 181 CACAGTAATATGAGACATGAGATCCACCGAGGAGCAGCTCAATTTAGTATGTA 240  
QY 255 TTTTATCATTTTGGGACAAACAAGTAAAGTAATAGCTCCGGAAATCGTGTTCAT 314  
DB 241 TTTTATCATTTTGGGACAAACAAGTAAAGTAATAGCTCCGGAAATCGTGTTCAT 300  
QY 315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA 374  
DB 301 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCAGTGTAGCAACAATGA 360  
QY 375 GAGTGAAGAGCTTACATTTTGGTGAAGAAATGATCTCACCCCGAAGGTATCTTGA 434  
DB 361 GAGTGAAGAGCTTACATTTTGGTGAAGAAATGATCTCACCCCGAAGGTATCTTGA 420  
QY 435 GTCTGCTGAGCTGAACTTCAATGCAATTTGGGCACAACCTGAGCTACATGAAGTCTTG 494  
DB 421 GTCTGCTGAGCTGAGCTTCAATGCAATTTGGGCACAACCTGAGCTACATGAAGTCTTG 480  
QY 495 GCTCCCTGGAAGGAAATACAGTCCGCACTAACTACTCTCTACTATTGGACAGAG 554  
DB 481 GCTCCCTGGAAGGAAATACAGTCCGCACTAACTACTCTCTACTATTGGACAGAG 540  
QY 555 CTTGGAATAATTCATCATATGTGAAAAATCTTTAGAGAGGCCAATATCTTGGTGTTC 614  
DB 541 CTTGGAATAATTCATCATATGTGAAAAATCTTTAGAGAGGCCAATATCTTGGTGTTC 600  
QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACCAACAGTGTCCAAATATGCT 674



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Db 601 CTTTATCTGACCAAGTGAAGATTCAGTTTTCAGCAACACAGTGTCCAAATATATGCT 660
Qy 675 CAGGATATGACGAGGAAAAATTAACCATCCCTCAATATAGGCTTTAACTCCCGCT 734
Db 661 CAGGATATGACGAGGAAAAATTAACCATCCCTCAATATAGGCTTTAACTCCCGCT 720
Qy 735 GAAACCTGATCCTCCACATATTTAAACCTCTCCTTCCACATGATGACCTTATGTCGA 794
Db 721 GAAACCTGATCCTCCACATATTTAAACCTCTCCTTCCACATGATGACCTTATGTCGA 780
Qy 795 ATGGAGATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGTGAAGTCAATAA 854
Db 781 ATGGAGATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGTGAAGTCAATAA 840
Qy 855 CAGCCAACTGAGACACATATGTTTCTTACCTCCAAAGGCTAATATGAGAAATCCAGA 914
Db 841 CAGCCAACTGAGACACATATGTTTCTTACCTCCAAAGGCTAATATGAGAAATCCAGA 900
Qy 915 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGGTCCCTGCTTCTTCTGATAC 974
Db 901 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGGTCCCTGCTTCTTCTGATAC 960
Qy 975 TTTGAAACAGTCAAGATTAAGATCAAAACAAATAGTATGCTATGAGATGACAAACT 1034
Db 961 TTTGAAACAGTCAAGATTAAGATCAAAACAAATAGTATGCTATGAGATGACAAACT 1020
Qy 1035 CTGAGATATTTGAGCCCAAGAAATGATAGTATGAGTGAAGGCAATTTCCACTTACAT 1094
Db 1021 CTGAGATATTTGAGCCCAAGAAATGATAGTATGAGTGAAGGCAATTTCCACTTACAT 1080
Qy 1095 AACCATGTTACTATTTCTCAGTATGCTGCTGAGTGCATCATAGTATCTGCTTAA 1154
Db 1081 AACCATGTTACTATTTCTCAGTATGCTGCTGAGTGCATCATAGTATCTGCTTAA 1140
Qy 1155 CCTAAAAAGGCTCAAGATTTATATATCCCTCAATTCCTGATCCTGCAAGATTTTAA 1214
Db 1141 CCTAAAAAGGCTCAAGATTTATATATCCCTCAATTCCTGATCCTGCAAGATTTTAA 1200
Qy 1215 AGAATGTTTGAAGACCAAGATGATGATCTGCTGCACTGGAAGATTCGACATTTAGA 1274
Db 1201 AGAATGTTTGAAGACCAAGATGATGATCTGCTGCACTGGAAGATTCGACATTTAGA 1260
Qy 1275 GAAGCAAAACCAAGGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGAGAAAGCCTC 1334
Db 1261 GAAGCAAAACCAAGGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGAGAAAGCCTC 1320
Qy 1335 TCACTGATGAGATATTTATTTTACCTTCACTGCTGACCTTGAGAGAA 1383
Db 1321 TCACTGATGAGATATTTATTTTACCTTCACTGCTGACCTTGAGAGAA 1369

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## RESULT 8

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US-10-342-887-633
; Sequence 633, Application US/10342887
; Publication No. US20040058340n1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 50/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14

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; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 633
; LENGTH: 4039
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-633

Query Match      86.6%; Score 1198; DB 8; Length 4039;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 135 CGCCCTCAGGAAATCGACCACTGTCACAAATTTGAGTGTCTGTGTAAGAACTCTG 194
Db 121 CGCCCTCAGGAAATCGACCACTGTCACAAATTTGAGTGTCTGTGTAAGAACTCTG 180
Qy 195 CACAGTATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGTATGTGTA 254
Db 181 CACAGTATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTTGTATGTGTA 240
Qy 255 TTTTAGTATTTTGGCCGACAAACAAAGATTAAGAAATAGCTCCGAACTCGTCTTCAAT 314
Db 241 TTTTAGTATTTTGGCCGACAAACAAAGATTAAGAAATAGCTCCGAACTCGTCTTCAAT 300
Qy 315 AGAAGTACCCCTGATGAGAGATTTTCTGCAAGTGGGTCCCGATGAGACCAATGA 374
Db 301 AGAAGTACCCCTGATGAGAGATTTTCTGCAAGTGGGTCCCGATGAGACCAATGA 360
Qy 375 GAGTGAAGGCTAGCATTTTGTGTAAGAAATGATCTACCCCGAGAGGATCTCTGA 434
Db 361 GAGTGAAGGCTAGCATTTTGTGTAAGAAATGATCTACCCCGAGAGGATCTCTGA 420
Qy 435 GTCTGCTGTAAGTCAATCTTCAATGCTTGGCAACACTGAGCTACATGAAGTGTCTTG 494
Db 421 GTCTGCTGTAAGTCAATCTTCAATGCTTGGCAACACTGAGCTACATGAAGTGTCTTG 480
Qy 495 GCTCCCTGGAAGAAATCCAGTCCCGACACTAATCTCTCTAATTTGGCAGAGAG 554
Db 481 GCTCCCTGGAAGAAATCCAGTCCCGACACTAATCTCTCTAATTTGGCAGAGAG 540
Qy 555 CCTGAAAAAATTCATCAATGTAAGAAACATCTTTAGAGAGGCCAATCTTTGGTGTTC 614
Db 541 CCTGAAAAAATTCATCAATGTAAGAAACATCTTTAGAGAGGCCAATCTTTGGTGTTC 600
Qy 615 CTTTATCTGACCAAGTGAAGATTCAGTTTGAACAAACAGTGTCCAAATATAGGT 674
Db 601 CTTTATCTGACCAAGTGAAGATTCAGTTTGAACAAACAGTGTCCAAATATAGGT 660
Qy 675 CAAGATATATGACAGAAAAATTAACCATCTTCAATATATAGTCTTAACTCCCGGT 734
Db 661 CAAGATATATGACAGAAAAATTAACCATCTTCAATATATAGTCTTAACTCCCGGT 720
Qy 735 GAAACCTGATCCTCCACATATTTAAACCTCTCCTTCCACATGATGACCTATATGTCGA 794
Db 721 GAAACCTGATCCTCCACATATTTAAACCTCTCCTTCCACATGATGACCTATATGTCGA 780
Qy 795 ATGGAGATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGTGAAGTCAATAA 854
Db 781 ATGGAGATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGTGAAGTCAATAA 840
Qy 855 CAGCCAACTGAGACACATATGTTTCTTACCTCCAAAGGCTAATATGAGAAATCCAGA 914
Db 841 CAGCCAACTGAGACACATATGTTTCTTACCTCCAAAGGCTAATATGAGAAATCCAGA 900
Qy 915 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGGTCCCTGCTTCTTCTGATAC 974
Db 901 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGGTCCCTGCTTCTTCTGATAC 960
Qy 975 TTTGAAACAGTCAAGATTAAGATCAAAACAAATAGTATGCTATGAGATGACAAACT 1034
Db 961 TTTGAAACAGTCAAGATTAAGATCAAAACAAATAGTATGCTATGAGATGACAAACT 1020

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QY 1035 CTGAGTAATTTGAGCCAGAAATGAGTATAGGTAGAGAGCCAAATTCACACTCTACAT 1094  
DB 1021 CTGAGTAATTTGAGCCAGAAATGAGTATAGGTAGAGAGCCAAATTCACACTCTACAT 1080  
QY 1095 AACCATGTTACTGATTTGTCAGATCGTCGAGAGGCAATCATAGTACTCTGCTTTA 1154  
DB 1081 AACCATGTTACTGATTTGTCAGATCGTCGAGAGGCAATCATAGTACTCTGCTTTA 1140  
QY 1155 CCTAAAAGGCTCAAGATTATTTATTTCTCTCCAAATTCCTGATCCTGGCAAGATTTTAA 1214  
DB 1141 CCTAAAAGGCTCAAGATTATTTATTTCTCTCCAAATTCCTGATCCTGGCAAGATTTTAA 1200  
QY 1215 AGAAATGTTTGAGACCAAGATGATGATCTCTGCACTGGAAGAATGACATCTATGA 1274  
DB 1201 AGAAATGTTTGAGACCAAGATGATGATCTCTGCACTGGAAGAATGACATCTATGA 1260  
QY 1275 GAAGCAAAACCAAGAGAGAAACCGACTCTGATGCTGATGAGAAAACCTGAAGAAGCTC 1334  
DB 1261 GAAGCAAAACCAAGAGAGAAACCGACTCTGATGCTGATGAGAAAACCTGAAGAAGCTC 1320  
QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
DB 1321 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1369

## RESULT 9

US-10-843-641A-6046  
; Sequence 6046, Application US/10843641A  
; Publication No. US2005006454A1  
; GENERAL INFORMATION:  
; APPLICANT: Avalon Pharmaceuticals, Inc.  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using  
; FILE REFERENCE: 689290-189  
; CURRENT APPLICATION NUMBER: US/10/843,641A  
; PRIOR FILING DATE: 2004-05-12  
; PRIOR APPLICATION NUMBER: US/09/873,367  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US/09/954,531  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/09/954,456  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,436  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/962,832  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/09/964,824  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/09/967,768  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: US/09/968,007  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,347  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/09/969,708  
; PRIOR FILING DATE: 2001-10-03  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 8447  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6046  
; LENGTH: 4039  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-843-641A-6046

Query Match 86.6%; Score 1198; DB 10; Length 4039;  
Best Local Similarity 99.9%; Pired. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTTACGAGAACTCAGCCACTGTGACAAATTTGAGTCTCTGTTGAAAACCTCTG 194  
DB 121 CGGCGCTTACGAGAACTCAGCCACTGTGACAAATTTGAGTCTCTGTTGAAAACCTCTG 180

QY 195 CACAGTAATTTGAGCACTGGATTCACCCGAGGAGCCAGCTCAAAATTTGATGTATGGTA 254  
DB 181 CACAGTAATTTGAGCACTGGATTCACCCGAGGAGCCAGCTCAAAATTTGATGTATGGTA 240  
QY 255 TTTTATGATTTTGGGACCAACAAATAGATAGAGTCCGGAAATCGTCTCAAT 314  
DB 241 TTTTATGATTTTGGGACCAACAAATAGATAGAGTCCGGAAATCGTCTCAAT 300  
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 374  
DB 301 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAATGA 360  
QY 375 GAGTGAAGAGCTTACGATTTTGGTTGAAAATGCAATCTCACCCCGAAGGATCTCTGA 434  
DB 361 GAGTGAAGAGCTTACGATTTTGGTTGAAAATGCAATCTCACCCCGAAGGATCTCTGA 420  
QY 435 GTCTGCTGATGACTGAATCAATGATTTTGGGCAACCTGAGCTACATGAAGTCTTGG 494  
DB 421 GTCTGCTGATGACTGAATCAATGATTTTGGGCAACCTGAGCTACATGAAGTCTTGG 480  
QY 495 GCTCCCTGGAAGGAATACGATCCGACACTAACTACTCTCTACTATTGGCACAAG 554  
DB 481 GCTCCCTGGAAGGAATACGATCCGACACTAACTACTCTCTACTATTGGCACAAG 540  
QY 555 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATCTTGGTTGTC 614  
DB 541 CTTGAAAAAATTCATCAATGTGAAAACATCTTTAGAGAAGGCCAATCTTGGTTGTC 600  
QY 615 CTTTATGATGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGAT 674  
DB 601 CTTTATGATGACCAAGTGAAGATTCAGTTTGAACAACAGTGTCCAAATTAATGAT 660  
QY 675 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATAGTCCCTTAACTTCCGATG 734  
DB 661 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATAGTCCCTTAACTTCCGATG 720  
QY 735 GAAACCTGATCCTCCCATATTTAAAACTCTCTCTCCCAATGATGACCTATATGTGA 794  
DB 721 GAAACCTGATCCTCCCATATTTAAAACTCTCTCTCCCAATGATGACCTATATGTGA 780  
QY 795 ATGGAGAAATCCACAAATTTTATTTAGAGATGCTATTTTGAAGTGAAGTCAATA 854  
DB 781 ATGGAGAAATCCACAAATTTTATTTAGAGATGCTATTTTGAAGTGAAGTCAATA 840  
QY 855 CAGCCAACTGAGACACATATGTTTCTACGTCGAAGAGGCTTAATGTGAGATCCAGA 914  
DB 841 CAGCCAACTGAGACACATATGTTTCTACGTCGAAGAGGCTTAATGTGAGATCCAGA 900  
QY 915 ATTTGAGAAATGTGAGAAATCATCTTGTTCATGTCCTGCTGTTCTTCTGATAC 974  
DB 901 ATTTGAGAAATGTGAGAAATCATCTTGTTCATGTCCTGCTGTTCTTCTGATAC 960  
QY 975 TTTTGAACAGTCAAGATTAAGATCAAAACAATAAGTTATGCTATGAGAGTGAACAAT 1034  
DB 961 TTTTGAACAGTCAAGATTAAGATCAAAACAATAAGTTATGCTATGAGAGTGAACAAT 1020  
QY 1035 CTGAGTAATTTGAGCCAGAAATGAGTATAGGTAGAGAGCCAAATTCACACTCTACAT 1094  
DB 1021 CTGAGTAATTTGAGCCAGAAATGAGTATAGGTAGAGAGCCAAATTCACACTCTACAT 1080  
QY 1095 AACCATGTTACTGATTTGTCAGATCGTCGAGAGGCAATCATAGTACTCTGCTTTA 1154  
DB 1081 AACCATGTTACTGATTTGTCAGATCGTCGAGAGGCAATCATAGTACTCTGCTTTA 1140  
QY 1155 CCTAAAAGGCTCAAGATTATTTATTTCTCTCCAAATTCCTGATCCTGGCAAGATTTTAA 1214  
DB 1141 CCTAAAAGGCTCAAGATTATTTATTTCTCTCCAAATTCCTGATCCTGGCAAGATTTTAA 1200  
QY 1215 AGAAATGTTTGAGACCAAGATGATGATCTCTGCACTGGAAGAATGACATCTATGA 1274  
DB 1201 AGAAATGTTTGAGACCAAGATGATGATCTCTGCACTGGAAGAATGACATCTATGA 1260  
QY 1275 GAAGCAAAACCAAGAGAGAAACCGACTCTGATGCTGATGAGAAAACCTGAAGAAGCTC 1334

Db 1261 GAAGCAACCAAGAGGAAACCGACTGTAGTCTGATAGAAAACCTGAAGAACCTC 1320  
Qy 1335 TCAGTGTGAGATATTTATTTTACCTCAGCTGTACCTGTGAGAA 1383  
Db 1321 TCAGTGTGAGATATTTATTTTACCTCAGCTGTACCTGTGAGAA 1369

RESULT 10  
US-09-971-392-58  
; Sequence 58, Application US/09971392  
; Publication No. US20030134283A1  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, David P.  
; APPLICANT: Pearson, Cecilia I.  
; APPLICANT: Cocks, Benjamin G.  
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0029 US  
; CURRENT APPLICATION NUMBER: US/09/971,392  
; PRIOR FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: 60/237,652  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ. ID NOS: 260  
; SOFTWARE: PERL Program  
; SEQ ID NO 58  
; LENGTH: 4466  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Template ID: 331428.2  
; LOCATION: 1874-2179, 4212, 4229, 4239, 4254, 4309, 4328, 4335, 4338  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-971-392-58

Query Match 86.6%; Score 1198; DB 3; Length 4466;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 135 CGGCGCTACGGAACCTGAGCCAGCTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 194  
Db 158 CGGCGCTACGGAACCTGAGCCAGCTGTGACAAATTTGAGTGTCTGTGTAACCTCTG 217  
Qy 195 CACAGTAATATGACATGATGATCCACCCGAGGAGCCAGCTCAATTTGATGATGATGTA 254  
Db 218 CACAGTAATATGACATGATGATCCACCCGAGGAGCCAGCTCAATTTGATGATGATGTA 277  
Qy 255 TTTTATGATTTTGGGACAAACAGATAGAAAATAGCTCCGGAACCTGCTGTCAT 314  
Db 278 TTTTATGATTTTGGGACAAACAGATAGAAAATAGCTCCGGAACCTGCTGTCAT 337  
Qy 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAAATGA 374  
Db 338 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCAACAAATGA 397  
Qy 375 GAGTGAAGACCTTACGATTTTGTGTAATAATGATCTACCCCGAAGAGTATCTCTGA 434  
Db 398 GAGTGAAGACCTTACGATTTTGTGTAATAATGATCTACCCCGAAGAGTATCTCTGA 457  
Qy 435 GTCTGCTGTGACGAACTTCAATGATGATTTGGGACAACTGAGCTACATGAAAGTCTTG 494  
Db 458 GTCTGCTGTGACGAGCTTCAATGATGATTTGGGACAACTGAGCTACATGAAAGTCTTG 517  
Qy 495 GCTTCCTGGAAGATTCAGTCTCCGACCTAACTATATCTCTACTATTTGGGACAGAG 554  
Db 518 GCTTCCTGGAAGATTCAGTCTCCGACCTAACTATATCTCTACTATTTGGGACAGAG 577  
Qy 555 CCTGGAAGAAATTCATATATGTAAGAAACATCTTTAGGAGAGGCCAATCTTTGGTCTC 614  
Db 578 CCTGGAAGAAATTCATATATGTAAGAAACATCTTTAGGAGAGGCCAATCTTTGGTCTC 637  
Qy 615 CTTTGAATCTGACCAAGATGAGATTCAGTTTGAACCAACAGATGTCCAAATATATGT 674

Db 638 CTTTGAATCTGACCAAGATGAGATTCAGTTTGAACCAACAGATGTCCAAATATATGT 697  
Qy 675 CAAGATATATGCGAGAAAATTTAAACCATCTTCAATATATGCTTTAACTTCCGCTGT 734  
Db 698 CAAGATATATGCGAGAAAATTTAAACCATCTTCAATATATGCTTTAACTTCCGCTGT 757  
Qy 735 GAAACCTGATCTTCCATATTTAAACCTCTCTCTTCCAAATATGATGACCTATATGTGA 794  
Db 758 GAAACCTGATCTTCCATATTTAAACCTCTCTCTTCCAAATATGATGACCTATATGTGA 817  
Qy 795 ATGGAGAAATCCACAGATTTTATTTAGCAGATGCTATTTTATGAACTAGATCAATAA 854  
Db 818 ATGGAGAAATCCACAGATTTTATTTAGCAGATGCTATTTTATGAACTAGATCAATAA 877  
Qy 855 CAGCCAAATCAGACATATATGTTTCTACAGTCCAGAGAGCTTAAATGTAGATCCAGA 914  
Db 878 CAGCCAAATCAGACATATATGTTTCTACAGTCCAGAGAGCTTAAATGTAGATCCAGA 937  
Qy 915 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGCTCCGCTGCTCTGATAC 974  
Db 938 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGCTCCGCTGCTCTGATAC 997  
Qy 975 TTTGACACAGTACAGATTAAGATCAAAACAAATTAATTTATGCTATGAGATGACAAACT 1034  
Db 998 TTTGACACAGTACAGATTAAGATCAAAACAAATTAATTTATGCTATGAGATGACAAACT 1057  
Qy 1035 CTGAGATATTTGAGACCCAAAGAAATGATATAGTATAGAGAGCCATTCACACTCTACAT 1094  
Db 1058 CTGAGATATTTGAGACCCAAAGAAATGATATAGTATAGTATAGAGAGCCATTCACACTCTACAT 1117  
Qy 1095 AACCATGTAATGATGCTTCCAGTACATGCTGAGAGGACATCATATGCTCCGCTTAA 1154  
Db 1118 AACCATGTAATGATGCTTCCAGTACATGCTGAGAGGACATCATATGCTCCGCTTAA 1177  
Qy 1155 CCTTAAAGAGCTCAGATTTATTTATTTCCCTCCAAATCTGATCTGCAAGATTTTAA 1214  
Db 1178 CCTTAAAGAGCTCAGATTTATTTATTTCCCTCCAAATCTGATCTGCAAGATTTTAA 1237  
Qy 1215 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGAGAGAGTATGACATCTATGA 1274  
Db 1238 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGAGAGAGTATGACATCTATGA 1297  
Qy 1275 GAGCAACCAAGAGGAAACGACCTGTAGAGCTGATGAGAAACCTGAAGAAAGCTC 1334  
Db 1298 GAGCAACCAAGAGGAAACGACCTGTAGAGCTGATGAGAAACCTGAAGAAAGCTC 1357  
Qy 1335 TCAGTGTGAGATATTTATTTTACCTTCACTGTGACCTGAGAGA 1383  
Db 1358 TCAGTGTGAGATATTTATTTTACCTTCACTGTGACCTGAGAGA 1406

RESULT 11  
US-09-822-846-109  
; Sequence 109, Application US/09822846  
; Publication No. US20030027139A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: LaVallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steinger II, Robert J.  
; APPLICANT: Bowman, Michael R.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Howes, Steven H.  
; APPLICANT: Resnick, Richard J.

```
APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 109
LENGTH: 3880
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-846-109
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Query Match 86.0%; Score 1189; DB 3; Length 3880;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1239; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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144 GGAATCTGACCCAGTGTGACAAATTTGAGTGTCTGTGAAAACCTCTGCACAGTAAT 203
2 GGAATCTGACCCAGTGTGACAAATTTGAGTGTCTGTGAAAACCTCTGCACAGTAAT 61
204 ATGACATGGAATCCACCCGAGGAGGAGCCAGCTCAATTTGATCTATGTTTATGTC 263
62 ATGACATGGAATCCACCCGAGGAGGAGCCAGCTCAATTTGATCTATGTTTATGTC 121
264 TTTGGCCGACAAACAGATTAAGAAATAGCTCCGAAAACCTGCTTCAATAGAGTACC 323
122 TTTGGCCGACAAACAGATTAAGAAATAGCTCCGAAAACCTGCTTCAATAGAGTACC 181
324 CCTGATAGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATAGAGTGAAG 383
182 CCTGATAGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATAGAGTGAAG 241
384 GCTTACATTTTGTGAAAATAGCTTCAACCCCGAAGGTGATCTGAGTCTGCTGT 443
242 GCTTACATTTTGTGAAAATAGCTTCAACCCCGAAGGTGATCTGAGTCTGCTGT 301
444 GACTGAACTTCAATGATTTGGGCAACCTGAGCTACATGAAATGTTCTGCTGCTG 503
302 GACTGAACTTCAATGATTTGGGCAACCTGAGCTACATGAAATGTTCTGCTGCTG 361
504 AAGGATATCCAGTCCCGACACTACTACTCTCTACTATTTGGACAGAGCTGGAAA 563
362 AAGGATATCCAGTCCCGACACTACTACTCTCTACTATTTGGACAGAGCTGGAAA 421
564 AATTCAATCAATGTAAGAAACATCTTTAGAGAGGCCAATCTTTGTTGTTCTTGA 623
422 AATTCAATCAATGTAAGAAACATCTTTAGAGAGGCCAATCTTTGTTGTTCTTGA 481
624 GACCAAGTGAAGAGATTTCCAGTTTGAACAACAAGTGTCAAAATATGTTCAAGATA 683
482 GACCAAGTGAAGAGATTTCCAGTTTGAACAACAAGTGTCAAAATATGTTCAAGATA 541
684 TGCAGAAAAAATTAACCAATCTTCAATATAGTGCCTTTAATCTCCGTTGAAACCTGA 743
542 TGCAGAAAAAATTAACCAATCTTCAATATAGTGCCTTTAATCTCCGTTGAAACCTGA 601
744 TCTTCACATATTTAAACCTCTCTTCCAAATGATGACCTATATGTCGCAATGGAGAA 803
602 TCTTCACATATTTAAACCTCTCTTCCCAATGATGACCTATATGTCGCAATGGAGAA 661
804 TCCAGAGATTTTATAGAGAGATGCTATTTTATGAGATGAAAGTCAATTAACGCCAAC 863
662 TCCAGAGATTTTATAGAGAGATGCTATTTTATGAGATGAAAGTCAATTAACGCCAAC 721
864 TGAGACATATATGTTTCTAGCTCCAGAGGCTTAATATGAGAAATCCAGAAATTTGAG 923
722 TGAGACATATATGTTTCTAGCTCCAGAGGCTTAATATGAGAAATCCAGAAATTTGAG 781
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924 AATGTGAGAAATATATCTTTGTTTCATGTCCTCTGTTGTTCTTCTGATATCTTTGAAC 983
782 AATGTGAGAAATATATCTTTGTTTCATGTCCTCTGTTGTTCTTCTGATATCTTTGAAC 841
984 AGTCAGAAATTAAGGTGAAAACCAATTAAGTCTTGAAGATGAAACCTCGAGATTA 1043
842 AGTCAGAAATTAAGGTGAAAACCAATTAAGTCTTGAAGATGAAACCTCGAGATTA 901
1044 TTGAGACCAAGAAATAGTATAGTAAAGAGCCCAATTCACACTACATTAACATGTT 1103
902 TTGAGACCAAGAAATAGTATAGTAAAGAGCCCAATTCACACTACATTAACATGTT 961
1104 ACTCATTTGTCAGTATGTCGAGAGTGCATATGATGATCTCTGCTTAACTTAAAG 1163
962 ACTCATTTGTCAGTATGTCGAGAGTGCATATGATGATCTCTGCTTAACTTAAAG 1021
1164 GCTCAAGATTAATATTTCCCTCCATTCCTGATCTCTGCAAGATTTTAAAGAAATGTT 1223
1022 GCTCAAGATTAATATTTCCCTCCATTCCTGATCTCTGCAAGATTTTAAAGAAATGTT 1081
1224 TGAGACCAAGAAATAGTATATCTGCACTGGAAGAGTACGACATCTATGAGAGCAAC 1283
1082 TGAGACCAAGAAATAGTATATCTGCACTGGAAGAGTACGACATCTATGAGAGCAAC 1141
1284 CAAGAGAAACCGACTCTGTAGTGTGATGAAACCTGAAGAAAGCTTCAATGATG 1343
1142 CAAGAGAAACCGACTCTGTAGTGTGATGAAACCTGAAGAAAGCTTCAATGATG 1201
1344 GAGATATATTTATTTTACCTTCACTGTGACCTTGAGAAAG 1383
1202 GAGATATATTTATTTTACCTTCACTGTGACCTTGAGAAAG 1241
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## RESULT 12

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US-10-036-568-3
Sequence 3, Application US/10036568
Publication No. US20020090682A1
GENERAL INFORMATION:
APPLICANT: Willson, Tracy
APPLICANT: Nicols, A.
APPLICANT: Hilton, Douglas J.
APPLICANT: Metcalf, Donald
TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
FILE REFERENCE: ENCODING SAME
CURRENT APPLICATION NUMBER: US/10/036,568
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US/09/051,843
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 3
LENGTH: 1383
TYPE: DNA
ORGANISM: Human IL-13 receptor alpha-chain
FEATURE:
NAME/KEY: CDS
LOCATION: (61)..(1338)
US-10-036-568-3
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Query Match 85.2%; Score 1179; DB 6; Length 1383;

Best Local Similarity 99.7%; Pred. No. 0; Matches 1379; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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1 GAGCTTAACACGAGCAAGAGTTTAAACAGTGCAGGCGGCTTCCAGGCGAGAGCTGC 60
1 GAGCTTAACACGAGCAAGAGTTTAAACAGTGCAGGCGGCTTCCAGGCGAGAGCTGC 60
61 ATGGAATGCGCGGCGGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
61 ATGGAATGCGCGGCGGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
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[illegible]

| Db  | 1201 | GGCAAGATTTTAAAGAAATTTTGGAGACCGAGATGATGATCTTGCACTGGAAGAG     | 1260 |                        |      |
|---|------|---|------|------------------------|------|
| QY  | 1261 | TACGACATCTATGAGAAGCAAAACCAAGAGAAA                           | CGA  | CTCTAGTGTCTGATGA       | 1320 |
| Db  | 1261 | TACGACATCTATGAGAAGCAAAACCAAGAGAAA                           | CCG  | ACTCTGATAGTCTGATGA     | 1320 |
| QY  | 1321 | CTGAAGAAAGCCTCTCAAGTATGAGATATTTT                            | TTT  | TACCTTCACTGTGACCTTGAGA | 1380 |
| Db  | 1321 | CTGAAGAAAGCCTCTCAAGTATGAGATATTTT                            | TTT  | TACCTTCACTGTGACCTTGAGA | 1380 |
| QY  | 1381 | AGA 1383  |      |                        |      |
| Db  | 1381 | AGA 1383  |      |                        |      |
| RESULT 13   |      |   |      |                        |      |
| US-10-745-586-32  |      |   |      |                        |      |
| ; Sequence 32, Application US/10745586                                    |      |   |      |                        |      |
| ; Publication No. US2006006327A1  |      |   |      |                        |      |
| ; GENERAL INFORMATION:  |      |   |      |                        |      |
| ; APPLICANT: Jacobs, Kenneth  |      |   |      |                        |      |
| ; APPLICANT: McCoy, John M.   |      |   |      |                        |      |
| ; APPLICANT: Lavallee, Edward R.  |      |   |      |                        |      |
| ; APPLICANT: Collins-Racie, Lisa A.                                       |      |   |      |                        |      |
| ; APPLICANT: Evans, Cheryl  |      |   |      |                        |      |
| ; APPLICANT: Merberg, David   |      |   |      |                        |      |
| ; APPLICANT: Treacy, Maurice  |      |   |      |                        |      |
| ; APPLICANT: Bowman, Michael R.   |      |   |      |                        |      |
| ; APPLICANT: Spaulding, Vikki   |      |   |      |                        |      |
| ; APPLICANT: Agostino, Michael J.   |      |   |      |                        |      |
| ; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM |      |   |      |                        |      |
| ; FILE REFERENCE: GI 6011-18X   |      |   |      |                        |      |
| ; CURRENT APPLICATION NUMBER: US/10/745, 586                              |      |   |      |                        |      |
| ; PRIOR FILING DATE: 2003-12-29   |      |   |      |                        |      |
| ; PRIOR APPLICATION NUMBER: US/09/398, 829                                |      |   |      |                        |      |
| ; PRIOR FILING DATE: 1999-09-17   |      |   |      |                        |      |
| ; NUMBER OF SEQ ID NOS: 283   |      |   |      |                        |      |
| ; SOFTWARE: PatentIn Ver. 2.0   |      |   |      |                        |      |
| ; SEQ ID NO 32  |      |   |      |                        |      |
| ; LENGTH: 3906  |      |   |      |                        |      |
| ; TYPE: DNA   |      |   |      |                        |      |
| ; ORGANISM: Homo sapiens  |      |   |      |                        |      |
| US-10-745-586-32  |      |   |      |                        |      |
| Query Match 82.3%; Score 1138; DB 12; Length 3906;                        |      |   |      |                        |      |
| Best Local Similarity 99.8%; Pred. No. 0;                                 |      |   |      |                        |      |
| Matches 1238; Conservative 0; Mismatches 2; Indels 0; Gaps 0;             |      |   |      |                        |      |
| QY  | 144  | GGAACCTCAGCCACTGTGACCAATTTGAGTGTCTGTTGAAAACCTCGACAGTAAT     | 203  |                        |      |
| Db  | 1    | GGAACCTCAGCCACTGTGACCAATTTGAGTGTCTGTTGAAAACCTCGACAGTAAT     | 60   |                        |      |
| QY  | 204  | ATGACATGGAATCCACCAGGAGGCCAGCTCAATTTGATCTATGATATTTTACTCA     | 263  |                        |      |
| Db  | 61   | ATGACATGGAATCCACCAGGAGGCCAGCTCAATTTGATCTATGATATTTTACTCA     | 120  |                        |      |
| QY  | 264  | TTTTGGGACCAACAGATTAAGAAATAGTCTCCGAAAACCTGCTGTTCAATAGAGTACC  | 323  |                        |      |
| Db  | 121  | TTTTGGGACCAACAGATTAAGAAATAGTCTCCGAAAACCTGCTGTTCAATAGAGTACC  | 180  |                        |      |
| QY  | 324  | CCCTAATGAGAGGATTTGTCTGCAAGTGGGGGTCCCACTGATAGACCAATAGAGTGAAG | 383  |                        |      |
| Db  | 181  | CCCTAATGAGAGGATTTGTCTGCAAGTGGGGGTCCCACTGATAGACCAATAGAGTGAAG | 240  |                        |      |
| QY  | 384  | GCCTAGCATTTTGGTTGAAAATGCAATCTCACCCCGAAGAGGTGATCTGAGTCTGCTGT | 443  |                        |      |
| Db  | 241  | GCCTAGCATTTTGGTTGAAAATGCAATCTCACCCCGAAGAGGTGATCTGAGTCTGCTGT | 300  |                        |      |
| QY  | 444  | GACTGAATCTTCAATGCAATTTGGGCAAACTGAGCTATATGAATGTCTTGGCTCCCTGG | 503  |                        |      |
| Db  | 301  | GACTGAATCTTCAATGCAATTTGGGCAAACTGAGCTATATGAATGTCTTGGCTCCCTGG | 360  |                        |      |

QY 504 AAGGAATACAGTCCGACACTAATACTCTCTAATTGGACAGAAAGCTGGAAA 563  
DB 361 AAGGAATACAGTCCGACACTAATACTCTCTAATTGGACAGAAAGCTGGAAA 420  
QY 564 AATTCATCATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTGTCTTGTATCT 623  
DB 421 AATTCATCATGTGAAAACATCTTTAGAGAGGCCAATCTTTGGTGTCTTGTATCT 480  
QY 624 GACCAAGTGAAGAGATTCAGTTTGAACAACAGTGTCCAATATATGTCAAGATTA 683  
DB 481 GACCAAGTGAAGAGATTCAGTTTGAACAACAGTGTCCAATATATGTCAAGATTA 540  
QY 684 TGCAGAAAAATTAACCATCTTCAATATATGTCTTAACTCCGCTGAAACCTGA 743  
DB 541 TGCAGAAAAATTAACCATCTTCAATATATGTCTTAACTCCGCTGAAACCTGA 600  
QY 744 TCCTCCACATATTAATAAAGCTCTCCCTCCACATATATGTCTTAACTCCGCTGAA 803  
DB 601 TCCTCCACATATTAATAAAGCTCTCCCTCCACATATATGTCTTAACTCCGCTGAA 660  
QY 804 TCCACAGAAATTTATTAGCAGATGCTTATTTATGAAGTAGAAGTCAATAACGCCAAC 863  
DB 661 TCCACAGAAATTTATTAGCAGATGCTTATTTATGAAGTAGAAGTCAATAACGCCAAC 720  
QY 864 TGAACACATATATGTTTCTACGTCAGAGGCTMAATGTAGAGATCCAGAAATTTGAG 923  
DB 721 TGAACACATATATGTTTCTACGTCAGAGGCTMAATGTAGAGATCCAGAAATTTGAG 780  
QY 924 AATATGAGAGATATCATCTTTGTTTCATGATGCTCCGCTGTTCTTCTGATATCTTGAAC 983  
DB 781 AATATGAGAGATATCATCTTTGTTTCATGATGCTCCGCTGTTCTTCTGATATCTTGAAC 840  
QY 984 AGTCAGAAATTAAGTCAAAAACAATATATGATGATAGAGATGACAACTCTGAGATTA 1043  
DB 841 AGTCAGAAATTAAGTCAAAAACAATATATGATGATAGAGATGACAACTCTGAGATTA 900  
QY 1044 TTGGAGCCAGAAATGATATAGTAAAGAGCGCAATTCACACTTACATAACCATGTT 1103  
DB 901 TTGGAGCCAGAAATGATATAGTAAAGAGCGCAATTCACACTTACATAACCATGTT 960  
QY 1104 ACTCATTTGTTCCGATCATGTCGCGAGTGCAATCATATGATCTCTGTTTACCTAAAG 1163  
DB 961 ACTCATTTGTTCCGATCATGTCGCGAGTGCAATCATATGATCTCTGTTTACCTAAAG 1020  
QY 1164 GCTCAAGATTTATATATTCCTCCCAATTCCTGATTCCTGCGAAGATTTTAAAGAAATGTT 1223  
DB 1021 GCTCAAGATTTATATATTCCTCCCAATTCCTGATTCCTGCGAAGATTTTAAAGAAATGTT 1080  
QY 1224 TGGAGACCAAGATGATATCTTGCACTGGAAGAAATGACATCTATGAGAGCAAC 1283  
DB 1081 TGGAGACCAAGATGATATCTTGCACTGGAAGAAATGACATCTATGAGAGCAAC 1140  
QY 1284 CAAGAGGAAACCGACTCTGTATGCTGATAGAAAACCTGAAGAAAGCTCTCATGATG 1343  
DB 1141 CAAGAGGAAACCGACTCTGTATGCTGATAGAAAACCTGAAGAAAGCTCTCATGATG 1200  
QY 1344 GAGATATATTTATTTTACCTTCACTGAGCTTGAAGAGA 1383  
DB 1201 GAGATATATTTATTTTACCTTCACTGAGCTTGAAGAGA 1240

RESULT 14  
US-10-850-270-3  
; Sequence 3, Application US/10850270  
; Publication No. US20050058645A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd (For all States except the US)  
; APPLICANT: Dunlop, Felicity (US only)  
; APPLICANT: Baca, Manuel (US only)  
; APPLICANT: Nash, Andrew (US only)  
; APPLICANT: Fabri, Louis (US only)  
; TITLE OF INVENTION: Novel peptides

FILE REFERENCE: 12175890/EU  
; CURRENT APPLICATION NUMBER: US/10/850,270  
; CURRENT FILING DATE: 2004-05-20  
; PRIOR APPLICATION NUMBER: AU PS1301  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: AU 2003900437  
; PRIOR FILING DATE: 2003-02-03  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1284  
; TYPE: DNA  
; ORGANISM: human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1284)  
; OTHER INFORMATION:  
US-10-850-270-3

Query Match 79.9%; Score 1105; DB 10; Length 1284;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1205; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 135 CGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 194  
DB 78 CGCGCTACGGAACCTCAGCCACCTGTGACAAATTTGAGTGTCTGTTGAAAACCTCTG 137  
QY 195 CACAGTAATATGACATGGAATCCACCGAGGGAGCCAGTCAATTTGATGTATAGTTA 254  
DB 138 CACAGTAATATGACATGGAATCCACCGAGGGAGCCAGTCAATTTGATGTATAGTTA 197  
QY 255 TTTTATGATATTTTGGGACAAACAAGATTAAGAAATAGCTCCGGAATCTGTGTCAT 314  
DB 198 TTTTATGATATTTTGGGACAAACAAGATTAAGAAATAGCTCCGGAATCTGTGTCAT 257  
QY 315 AGAAGTACCCCTGATATGAGAGATTTGTCTGCAAGTGGGTCCCATGTATGACCAATGA 374  
DB 258 AGAAGTACCCCTGATATGAGAGATTTGTCTGCAAGTGGGTCCCATGTATGACCAATGA 317  
QY 375 GAGTGAAGAGCCAGCATTTTGGTGAATAATGATCTCACCCCGAAGGATGATCTGA 434  
DB 318 GAGTGAAGAGCCAGCATTTTGGTGAATAATGATCTCACCCCGAAGGATGATCTGA 377  
QY 435 GTCTGCTGATGACATTTCAATGATTTGGACAACTGAGCTACATGATGATGTTCTTG 494  
DB 378 GTCTGCTGATGATGACATTTCAATGATTTGGACAACTGAGCTACATGATGATGTTCTTG 437  
QY 495 GCTTCCCTGGAAGAAATCCAGTCCGACACTAATCTTACTTCTTACTATTTGGCAGAA 554  
DB 438 GCTTCCCTGGAAGAAATCCAGTCCGACACTAATCTTACTTCTTACTATTTGGCAGAA 497  
QY 555 CCGTGAATAAATCATCAATGTGAATAACATCTTTAGAGAGCCAACTCTTGGTGTTC 614  
DB 498 CCGTGAATAAATCATCAATGTGAATAACATCTTTAGAGAGCCAACTCTTGGTGTTC 557  
QY 615 CTTTGATCTGACCAAGATGAGGATTCAGTTTGAACAACAAGTGTCCAATAATATGTT 674  
DB 558 CTTTGATCTGACCAAGATGAGGATTCAGTTTGAACAACAAGTGTCCAATAATATGTT 617  
QY 675 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATATGAGTCTTTAACTTCCGTGT 734  
DB 618 CAAGATTAATGCAAGAAAAATTAACCATCTTCAATATATGAGTCTTTAACTTCCGTGT 677  
QY 735 GAAACCTGATCCGCAATATTAATAAAGCTCTCCCAATGATGACCTATATATGGA 794  
DB 678 GAAACCTGATCCGCAATATTAATAAAGCTCTCCCAATGATGACCTATATATGGA 737  
QY 795 ATGGAGAAATCCACAGAAATTTATGAGATGCTTATTTATGAAGTGAAGTCAATA 854  
DB 738 ATGGAGAAATCCACAGAAATTTATGAGATGCTTATTTATGAAGTGAAGTCAATA 797  
QY 855 CAGCCAACTGAGACATATATGTTTCTACGTCAGAGGCTTAATGTGAAGATCCAGA 914



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Db 798 CAGCCAACTGAGACACATAATGTTTCTACGTCACAAAGGCTAAATGTGAAATCCAGA 857
Qy 915 ATTTGAGAGAAATGAGAAATACATCTTGTTCATGTCCTGGTGTCTTCTCTGATAC 974
Db 858 ATTTGAGAGAAATGAGAAATACATCTTGTTCATGTCCTGGTGTCTTCTCTGATAC 917
Qy 975 TTTGAAACGACGTCAAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 1034
Db 918 TTTGAAACGACGTCAAGATTAAGAGTCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 977
Qy 1035 CTGAGATTAATGAGGCCAAGAAATGAGTATAGTAAAGGCAATTCACATCTATCAT 1094
Db 978 CTGAGATTAATGAGGCCAAGAAATGAGTATAGTAAAGGCAATTCACATCTATCAT 1037
Qy 1095 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGTCAATCATAGTACTCTGCTTAA 1154
Db 1038 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGTCAATCATAGTACTCTGCTTAA 1097
Qy 1155 CCTTAAAAAGGCTCAAGATTTATTTATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTAA 1214
Db 1098 CCTTAAAAAGGCTCAAGATTTATTTATTTCCCTCCCAATTCCTGATCCTGGCAAGATTTTAA 1157
Qy 1215 AGAATGTTTGGAGACCAAGATTAAGTATGATCTGCACTGGAAGAAATGCAATCTATGA 1274
Db 1158 AGAATGTTTGGAGACCAAGATTAAGTATGATCTGCACTGGAAGAAATGCAATCTATGA 1217
Qy 1275 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGGAAGAAAGCTC 1334
Db 1218 GAAGCAAAACCAAGAGAGAAACCGACTCTGTAGTGTGATAGAAAACCTGGAAGAAAGCTC 1277
Qy 1335 TCAGTGA 1341
Db 1278 TCAGTGA 1284

RESULT 15
US-10-278-698-6
; Sequence 6, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmueller, Bruno
; APPLICANT: Hauptl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1572
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-6

Query Match 79.2%; Score 1096; DB 9; Length 1572;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 342 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGACCAATGA 401
Qy 375 GAGTGAAGGCTTGACATTTTGTGAAAAATGATCTCACCCAGAGGATCCGGA 434
Db 402 GAGTGAAGGCTTGACATTTTGTGAAAAATGATCTCACCCAGAGGATCCGGA 461
Qy 435 GTCTGCTGTGACTGAATCTTCATGATCTTTGGCACAACCTGAGCTACATGAAGTGTCTTG 494
Db 462 GTCTGCTGTGATTTAGGCTTCAATGATCTTTGGCACAACCTGAGCTACATGAAGTGTCTTG 521
Qy 495 GCTCCCTGGAAGGAATTAACAGTCCCGACACTAATCTCTCTCTATATTTGGCACAAG 554
Db 522 GCTCCCTGGAAGGAATTAACAGTCCCGACACTAATCTCTCTCTATATTTGGCACAAG 581
Qy 555 CCTGGAATAAATTCATCAATGTTGAAAACATCTTTAGAGAGCCAAATCTTTGGTGTTC 614
Db 582 CCTGGAATAAATTCATCAATGTTGAAAACATCTTTAGAGAGCCAAATCTTTGGTGTTC 641
Qy 615 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTCCAAATPAATGAT 674
Db 642 CTTTGATCTGACCAAGTGAAGATTCAGTTTGAACAACAAGTCCAAATPAATGAT 701
Qy 675 CAAGATTAATGAGAAAAATTTAAACCATCTTCAATTAATAGTGCCTTTAATCTCCGAT 734
Db 702 CAAGATTAATGAGAAAAATTTAAACCATCTTCAATTAATAGTGCCTTTAATCTCCGAT 761
Qy 735 GAAACCTGATCCCTCCACATTAATAAACCTCTCTTCCACATATGATGACCTTAATGCA 794
Db 762 GAAACCTGATCCCTCCACATTAATAAACCTCTCTTCCACATATGATGACCTTAATGCA 821
Qy 795 ATGGAGAAATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGAGCAATPA 854
Db 822 ATGGAGAAATCCACAGAAATTTTATAGAGATGCTTATTTATAGAGAGCAATPA 881
Qy 855 CAGCCAAACTGAGACATTAATGTTTCTAGCTCAAGAGGCTAAATGTGAAATCCAGA 914
Db 882 CAGCCAAACTGAGACATTAATGTTTCTAGCTCAAGAGGCTAAATGTGAAATCCAGA 941
Qy 915 ATTTGAGAGAAATGTGAGAAATACATCTTTGTCATGTCCTGCTGTCTTCTGATAC 974
Db 942 ATTTGAGAGAAATGTGAGAAATACATCTTTGTCATGTCCTGCTGTCTTCTGATAC 1001
Qy 975 TTTGAAACAGCTCAGAAATTAAGAGTCAAAACAAATTAATTAATGATAGATGCAACT 1034
Db 1002 TTTGAAACAGCTCAGAAATTAAGAGTCAAAACAAATTAATTAATGATAGATGCAACT 1061
Qy 1035 CTGAGATTAATGAGCCCAAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1094
Db 1062 CTGAGATTAATGAGCCCAAGAAATGAGTATAGTAAAGACGCAATTCACACTCTACAT 1121
Qy 1095 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGTGCATCATATGATCTCTGCTTAA 1154
Db 1122 AACCATGTTACTCATTTGTTCCAGTCATGTCGACAGTGCATCATATGATCTCTGCTTAA 1181
Qy 1155 CCTTAAAAAGGCTCAAGATTTATTTATTTCCCTCCCAATTCCTGAGCTCCGCAAGATTTTAA 1214
Db 1182 CCTTAAAAAGGCTCAAGATTTATTTATTTCCCTCCCAATTCCTGAGCTCCGCAAGATTTTAA 1241
Qy 1215 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAAATGATCTATGA 1274
Db 1242 AGAATGTTTGGAGACCAAGATGATGATCTCTGCACTGGAAGAAATGATCTATGA 1301
Qy 1275 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATGAGAAACCTGGAAGAAAGCTC 1334
Db 1302 GAAGCAAAACCAAGAGAGAAACGACTCTGTAGTGTGATGAGAAACCTGGAAGAAAGCTC 1361
Qy 1335 TCAGTGAATGAGATTAATTTATTTTTCCTTCACTGAGCACTTGAAGA 1383
Db 1362 TCAGTGAATGAGATTAATTTATTTTACCTTCACTGAGCACTTGAAGA 1410

Search completed: July 7, 2006, 23:48:48
Job time : 1929 secs
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GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: July 7, 2006, 23:16:46 ; Search time 204 Seconds  
(without alignments)  
8814.136 Million cell updates/sec

Title: US-09-051-843D-3

Perfect score: 1383  
Sequence: 1 gagctctacacgcagcaagg.....tcactgtcacttgagaaga 1383

Scoring table: OLIGO\_NTIC

Gapop 60.0, Gapext 60.0

Searched: 844069 seqs, 650066433 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1687978

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

1: Published Applications NA New:  
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3: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US06\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                      | Description        |
|------------|-------|-------------|--------|-------------------------|--------------------|
| 1          | 1198  | 86.6        | 2139   | 8 US-11-266-748A-25722  | Sequence 25722, A  |
| 2          | 1198  | 86.6        | 4006   | 8 US-11-266-748A-56241  | Sequence 56241, A  |
| 3          | 958   | 69.3        | 2741   | 8 US-11-266-748A-185183 | Sequence 185183, A |
| 4          | 923   | 66.7        | 975    | 8 US-11-266-748A-192679 | Sequence 192679, A |
| 5          | 923   | 66.7        | 975    | 8 US-11-266-748A-226550 | Sequence 226550, A |
| 6          | 846   | 61.2        | 1016   | 8 US-11-266-748A-54658  | Sequence 54658, A  |
| 7          | 811   | 58.6        | 1294   | 8 US-11-266-748A-73628  | Sequence 73628, A  |
| 8          | 811   | 58.6        | 1294   | 8 US-11-266-748A-107924 | Sequence 107924, A |
| 9          | 811   | 58.6        | 1294   | 8 US-11-266-748A-126439 | Sequence 126439, A |
| 10         | 587   | 42.4        | 902    | 8 US-11-266-748A-54614  | Sequence 54614, A  |
| 11         | 278   | 20.1        | 1297   | 8 US-11-266-748A-73627  | Sequence 73627, A  |
| 12         | 278   | 20.1        | 1297   | 8 US-11-266-748A-107923 | Sequence 107923, A |
| 13         | 278   | 20.1        | 1297   | 8 US-11-266-748A-126438 | Sequence 126438, A |
| 14         | 63    | 4.6         | 583    | 8 US-11-266-748A-51095  | Sequence 51095, A  |
| 15         | 26    | 1.9         | 1264   | 7 US-11-218-305-11789   | Sequence 11789, A  |
| 16         | 26    | 1.9         | 2037   | 6 US-10-449-902-12101   | Sequence 12101, A  |
| 17         | 26    | 1.9         | 2961   | 6 US-10-511-455-53      | Sequence 53, A     |
| 18         | 26    | 1.9         | 3428   | 6 US-10-511-455-51      | Sequence 51, A     |
| 19         | 26    | 1.9         | 6975   | 7 US-11-218-305-11790   | Sequence 11790, A  |
| 20         | 26    | 1.9         | 755217 | 8 US-11-266-748A-29045  | Sequence 29045, A  |
| 21         | 25    | 1.8         | 719    | 6 US-10-953-349-51494   | Sequence 51494, A  |
| 22         | 25    | 1.8         | 1107   | 6 US-10-449-902-28133   | Sequence 28133, A  |
| 23         | 25    | 1.8         | 1137   | 6 US-10-449-902-10726   | Sequence 10726, A  |
| 24         | 25    | 1.8         | 1152   | 6 US-10-449-902-14304   | Sequence 14304, A  |

|    |    |     |      |                         |                    |
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| 25 | 25 | 1.8 | 2513 | 6 US-10-449-902-24182   | Sequence 24182, A  |
| 26 | 25 | 1.8 | 2818 | 6 US-10-449-902-14434   | Sequence 14434, A  |
| 27 | 25 | 1.8 | 3572 | 6 US-10-449-902-24102   | Sequence 24102, A  |
| 28 | 23 | 1.7 | 1140 | 7 US-11-218-305-3444    | Sequence 3444, A   |
| 29 | 23 | 1.7 | 1791 | 7 US-11-218-305-15541   | Sequence 15541, A  |
| 30 | 23 | 1.7 | 1809 | 6 US-10-449-902-22993   | Sequence 22993, A  |
| 31 | 23 | 1.7 | 1816 | 6 US-10-449-902-7949    | Sequence 7949, A   |
| 32 | 23 | 1.7 | 1905 | 7 US-11-218-305-18984   | Sequence 18984, A  |
| 33 | 23 | 1.7 | 4536 | 7 US-11-218-305-33747   | Sequence 33747, A  |
| 34 | 22 | 1.6 | 1000 | 8 US-11-266-748A-206504 | Sequence 206504, A |
| 35 | 22 | 1.6 | 1000 | 8 US-11-266-748A-222027 | Sequence 222027, A |
| 36 | 22 | 1.6 | 1000 | 8 US-11-266-748A-287725 | Sequence 287725, A |
| 37 | 22 | 1.6 | 1000 | 8 US-11-266-748A-339154 | Sequence 339154, A |
| 38 | 22 | 1.6 | 1000 | 8 US-11-266-748A-390454 | Sequence 390454, A |
| 39 | 22 | 1.6 | 1000 | 8 US-11-266-748A-481172 | Sequence 481172, A |
| 40 | 22 | 1.6 | 1080 | 7 US-11-174-307B-4763   | Sequence 4763, A   |
| 41 | 22 | 1.6 | 1134 | 7 US-11-218-305-10524   | Sequence 10524, A  |
| 42 | 22 | 1.6 | 1149 | 6 US-10-953-349-40071   | Sequence 40071, A  |
| 43 | 22 | 1.6 | 1324 | 6 US-10-953-349-33381   | Sequence 33381, A  |
| 44 | 22 | 1.6 | 1457 | 7 US-11-174-307B-1093   | Sequence 1093, A   |
| 45 | 22 | 1.6 | 2091 | 7 US-11-218-305-16780   | Sequence 16780, A  |

## ALIGNMENTS

RESULT 1  
US-11-266-748A-25722  
Sequence 25722, Application US/11266748A  
Publication No. US20060134663A1  
GENERAL INFORMATION:  
APPLICANT: Hartkin, Paul  
APPLICANT: Johnston, Patrick  
APPLICANT: Mulligan, Karl  
TITLE OF INVENTION: Transcriptome Microarray Technology and  
FILE REFERENCE: 55815-0102 (319189)  
CURRENT APPLICATION NUMBER: US/11/266, 748A  
PRIOR FILING DATE: 2005-11-03  
PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105507.0  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105484.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662, 276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700, 293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 483996  
SOFTWARE: Patent version 3.3  
SEQ ID NO 25722  
LENGTH: 2139  
TYPE: DNA  
ORGANISM: Homo Sapiens  
US-11-266-748A-25722  
Query Match 86.6%; Score 1198; DB 8; Length 2139;  
Best local similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 135 CGGCCCTACGGAACCTGACCTGTCGCTCTGTTGAAACCTCTG 194  
DB 108 CGGCCCTACGGAACCTGACCTGTCGCTCTGTTGAAACCTCTG 167  
OY 195 CACAGTATATGACATGGAATCCACCCGAGGAGCCAGCTCAATTGTAGTCTATGTTA 254

Db 168 CACAGTAATATGAGCATGGAATCCACCGAGGAGCCAGCTCAAAATTGATGCTATGGA 227  
QY 255 TTTTACTGATTTTGGGACAAACAGATAGAAAAATAGTCCGGAAAATCTGCTGTCAT 314  
Db 228 TTTTACTGATTTTGGGACAAACAGATAGAAAAATAGTCCGGAAAATCTGCTGTCAT 287  
QY 315 AGAAGTAACCTGTAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTGACCAATGA 374  
Db 288 AGAAGTAACCTGTAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTGACCAATGA 347  
QY 375 GAGTGAAGCCATGAGATTTTGGTGAATAATGATCTCAACCCCGAAGGATGATCCTGA 434  
Db 348 GAGTGAAGCCATGAGATTTTGGTGAATAATGATCTCAACCCCGAAGGATGATCCTGA 407  
QY 435 GTCTGCTGTGACTGAATTCATATGATATTTGGCAACAACCTGAGTACATGAAGTTCCTG 494  
Db 408 GTCTGCTGTGACTGAAGTTCATATGATATTTGGCAACAACCTGAGTACATGAAGTTCCTG 467  
QY 495 GCTCCCTGGAAGATATCCAGTCCCGACACTAACTATATCTCTACTATTTGGACAGAG 554  
Db 468 GCTCCCTGGAAGATATCCAGTCCCGACACTAACTATATCTCTACTATTTGGACAGAG 527  
QY 555 CCGGAAAAAATTCATCAATGTAATAAATCATCTTTAGAGAGGCCAATCTTGGTGTTC 614  
Db 528 CCGGAAAAAATTCATCAATGTAATAAATCATCTTTAGAGAGGCCAATCTTGGTGTTC 587  
QY 615 CTTTGATCTGACCAAGTGAAGATTCAGTCTTTGAACAACAAGTGTCCAAATATGT 674  
Db 588 CTTTGATCTGACCAAGTGAAGATTCAGTCTTTGAACAACAAGTGTCCAAATATGT 647  
QY 675 CAAAGTAATGCAAGAAAAATTAAACCATCTTCAATATATGTGCTTTAACTTCCGTGT 734  
Db 648 CAAAGTAATGCAAGAAAAATTAAACCATCTTCAATATATGTGCTTTAACTTCCGTGT 707  
QY 735 GAAACCTGATCCCTCAATTTAAAAAATCTCTCTTCCAAATGATGAGCTATATGGA 794  
Db 708 GAAACCTGATCCCTCAATTTAAAAAATCTCTCTTCCAAATGATGAGCTATATGGA 767  
QY 795 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAGTAGAAGTCAATTA 854  
Db 768 ATGGAGAAATCCACAGAAATTTTATAGCAGATGCTATTTTATGAGTAGAAGTCAATTA 827  
QY 855 CAGCCAAATCTGAGACATATGTTTTTATGCTCAAGAGGCTTAATGTGAGAAATCCAGA 914  
Db 828 CAGCCAAATCTGAGACATATGTTTTTATGCTCAAGAGGCTTAATGTGAGAAATCCAGA 887  
QY 915 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGAGTCCCTGAGTCTTCTCTGATAC 974  
Db 888 ATTTGAGAAATGTGAGAAATACATCTTGTTCATGAGTCCCTGAGTCTTCTCTGATAC 947  
QY 975 TTTGAACACAGTCAGATAGATCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 1034  
Db 948 TTTGAACACAGTCAGATAGATCAAAACAAATTAAGTTATGCTATGAGATGACAAACT 1007  
QY 1035 CTGAGATATTTGAGCCCAAGAAATGAGTATAGTAAAGCCGAATTCACACTCTACAT 1094  
Db 1008 CTGAGATATTTGAGCCCAAGAAATGAGTATAGTAAAGCCGAATTCACACTCTACAT 1067  
QY 1095 AACCAAGTATCTGATGTTCCAGTCCGTCGAGAGGCAATCATAGTATCTCTCGCTTAA 1154  
Db 1068 AACCAAGTATCTGATGTTCCAGTCCGTCGAGAGGCAATCATAGTATCTCTCGCTTAA 1127  
QY 1155 CCTAAAGAGCTCAAGTTATTTATATTCCTCCCAATTCCTGATCTGGCAAGATTTTAA 1214  
Db 1128 CCTAAAGAGCTCAAGTTATTTATATTCCTCCCAATTCCTGATCTGGCAAGATTTTAA 1187  
QY 1215 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGGAGAAAGTACGACATCTATGA 1274  
Db 1188 AGAATGTTTGGAGACCAAGATGATGATCTGCACTGGAGAAAGTACGACATCTATGA 1247  
QY 1275 GAAAGCAACCAAGAGAAACCGACCTGTGATGCTGATGAGAAACCTGAGAAAGCTC 1334  
Db 1248 GAAAGCAACCAAGAGAAACCGACCTGTGATGCTGATGAGAAACCTGAGAAAGCTC 1307

QY 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1383  
Db 1308 TCAGTATGAGATTAATTTATTTTACCTTCACTGTGACCTTGAGAGA 1356

RESULT 2  
US-11-266-748A-56241  
; Sequence 56241, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcription Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; CURRENT FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 56241  
; LENGTH: 4006  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-56241

Query Match 86.6%; Score 1198; DB 8; Length 4006;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CCGGCTACGGAACCTCAGCCACCTGTGACCAATTTGAGTGTCTGTTGAAAACTCTG 194  
Db 121 CCGGCTACGGAACCTCAGCCACCTGTGACCAATTTGAGTGTCTGTTGAAAACTCTG 180  
QY 195 CACAGTAATATGAGATGGAATCCACCGAGGAGCCAGTCAATTTGATGCTATGGA 254  
Db 181 CACAGTAATATGAGATGGAATCCACCGAGGAGCCAGTCAATTTGATGCTATGGA 240  
QY 255 TTTTACTGATTTTGGGACAAACAGATAGAAAAATAGTCCGGAAAATCTGCTGTCAT 314  
Db 241 TTTTACTGATTTTGGGACAAACAGATAGAAAAATAGTCCGGAAAATCTGCTGTCAT 300  
QY 315 AGAAGTAACCTGTAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTGACCAATGA 374  
Db 301 AGAAGTAACCTGTAATGAGAGATTTGTCTGCAAGTGGGCTCCAGTGTGACCAATGA 360  
QY 375 GAGTGAAGCCATGAGATTTTGGTGAATAATGATCTCAACCCCGAAGGATGATCCTGA 434  
Db 361 GAGTGAAGCCATGAGATTTTGGTGAATAATGATCTCAACCCCGAAGGATGATCCTGA 420  
QY 435 GTCTGCTGTGACTGAATTCATATGATATTTGGCAACAACCTGAGTACATGAAGTTCCTG 494  
Db 421 GTCTGCTGTGACTGAAGTTCATATGATATTTGGCAACAACCTGAGTACATGAAGTTCCTG 480  
QY 495 GCTCCCTGGAAGATATCCAGTCCCGACACTAACTATATCTCTACTATTTGGACAGAG 554

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Db 481 GCTCCCTGGAAGAAATACCACTCCCGACACTAATCTCTTACTTATTTGGCAGAG 540
QY 555 CTTGGAAGAAATTCATCATGTGTGAAAACATCTTTAGAGAGCCAAATCTTTGGTGTTC 614
Db 541 CTTGGAAGAAATTCATCATGTGTGAAAACATCTTTAGAGAGCCAAATCTTTGGTGTTC 600
QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACACACAGTGTCCAAATATGTGT 674
Db 601 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACACACAGTGTCCAAATATGTGT 660
QY 675 CAAGGATTAATGCGAGGAAATTAACATCCTTCAATATGTGTCTTAATCTCCGCTGT 734
Db 661 CAAGGATTAATGCGAGGAAATTAACATCCTTCAATATGTGTCTTAATCTCCGCTGT 720
QY 735 GAAACCTGATCTCTCACAATATTAATAACCTCTCTTCCACAATATGATGATGATGCA 794
Db 721 GAAACCTGATCTCTCACAATATTAATAACCTCTCTTCCACAATATGATGATGATGCA 780
QY 795 ATGGAGAAATCCACAGAAATTTTATTTAGCAGATGCTTATTTATGAGATGAGATCAAT 854
Db 781 ATGGAGAAATCCACAGAAATTTTATTTAGCAGATGCTTATTTATGAGATGAGATCAAT 840
QY 855 CAGCCAAATCTGACACATATATGTTTCTAGCTCCAGAGGCTTAATGTGAGATCCAGA 914
Db 841 CAGCCAAATCTGACACATATATGTTTCTAGCTCCAGAGGCTTAATGTGAGATCCAGA 900
QY 915 ATTTGAGAGAAATGTGAGAAATACATCTGTGTTTCTAGTGTCTCTGTTCTCTGATAC 974
Db 901 ATTTGAGAGAAATGTGAGAAATACATCTGTGTTTCTAGTGTCTCTGTTCTCTGATAC 960
QY 975 TTTGAAACAGTCAAGATTAAGAGTCAAAACAAATTAATGTTATGCTATGAGATGCAAACT 1034
Db 961 TTTGAAACAGTCAAGATTAAGAGTCAAAACAAATTAATGTTATGCTATGAGATGCAAACT 1020
QY 1035 CTGAGATTAATTTGAGAGCCAAAGATGATTAATGTTAAGAGGCAATTCACACTCTAT 1094
Db 1021 CTGAGATTAATTTGAGAGCCAAAGATGATTAATGTTAAGAGGCAATTCACACTCTAT 1080
QY 1095 AACCATGTTTCTCATGTTCTCAGTCACTGTGCGAGGCAATCAATATCTCCGCTTAA 1154
Db 1081 AACCATGTTTCTCATGTTCTCAGTCACTGTGCGAGGCAATCAATATCTCCGCTTAA 1140
QY 1155 CCTTAAAGAGGCTCAAGATTAATTAATCTCCCAATCTCTGATCTCTGCAAGATTTTAA 1214
Db 1141 CCTTAAAGAGGCTCAAGATTAATTAATCTCCCAATCTCTGATCTCTGCAAGATTTTAA 1200
QY 1215 AGAAATGTTTGAAGACCAAGATGATGATCTCTGCACTGGAAGAGTACGATCTATGA 1274
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QY 1275 GAAGCAAAACCAAGAGGAAACCGACTGTGTAAGTCTGATAGAAAACCTGAAAGAGCTC 1334
Db 1261 GAAGCAAAACCAAGAGGAAACCGACTGTGTAAGTCTGATAGAAAACCTGAAAGAGCTC 1320
QY 1335 TCAGTGAATGAGATTAATTTTATTTTACCTTCACTGTGACCTGTGAGAGA 1383
Db 1321 TCAGTGAATGAGATTAATTTTATTTTACCTTCACTGTGACCTGTGAGAGA 1369
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## RESULT 3

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US-11-266-748A-185183
; Sequence 185183, Application US/11266748A
; Publication NO. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; PRIOR APPLICATION NUMBER: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
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;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105482.6
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105483.4
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105507.0
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105485.9
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: EP 04105484.2
;; PRIOR FILING DATE: 2004-11-03
;; PRIOR APPLICATION NUMBER: US 60/662, 276
;; PRIOR FILING DATE: 2005-03-14
;; PRIOR APPLICATION NUMBER: US 60/700, 293
;; PRIOR FILING DATE: 2005-07-18
;; NUMBER OF SEQ ID NOS: 483996
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 185183
;; LENGTH: 2741
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1520)..(1834)
;; OTHER INFORMATION: n is a, c, g, or t
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (2177)..(2186)
;; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-185183
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Query Match 69.3%; Score 958; DB 8; Length 2741;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1008; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 375 GAGTGAGAACCTAGCATTTTGTGTAATAATGATCTCAACCCAGAGGTGATCTCGA 434
Db 44 GAGTGAGAACCTAGCATTTTGTGTAATAATGATCTCAACCCAGAGGTGATCTCGA 103
QY 435 GTCTGCTGTGATCGAATTTCAATGATGATTTGGCACAACCTGAGTCAATGAAATGTTCTTG 494
Db 104 GTCTGCTGTGATCGAATTTCAATGATGATTTGGCACAACCTGAGTCAATGAAATGTTCTTG 163
QY 495 GCTCCCTGGAAGAAATCCAGTCCCGACCTAATCTCTAATGTTGGCAGAGAAG 554
Db 164 GCTCCCTGGAAGAAATCCAGTCCCGACCTAATCTCTAATGTTGGCAGAGAAG 223
QY 555 CTTGGAAGAAATTCATCATGTGTGAAAACATCTTTAGAGAGCCAAATCTTTGGTGTTC 614
Db 224 CTTGGAAGAAATTCATCATGTGTGAAAACATCTTTAGAGAGCCAAATCTTTGGTGTTC 283
QY 615 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACACACAGTGTCCAAATATGTGT 674
Db 284 CTTTGAATCTGACCAAGTGAAGATTCAGTTTGAACACACAGTGTCCAAATATGTGT 343
QY 675 CAAGGATTAATGCGAGGAAATTAACATCCTTCAATATGTGTCTTAATCTCCGCTGT 734
Db 344 CAAGGATTAATGCGAGGAAATTAACATCCTTCAATATGTGTCTTAATCTCCGCTGT 403
QY 735 GAAACCTGATCTCTCACAATATTAATAACCTCTCTTCCACAATATGATGATGATGCA 794
Db 404 GAAACCTGATCTCTCACAATATTAATAACCTCTCTTCCACAATATGATGATGATGCA 463
QY 795 ATGGAGAAATCCACAGAAATTTTATTTAGCAGATGCTTATTTATGAGATGAGATCAAT 854
Db 464 ATGGAGAAATCCACAGAAATTTTATTTAGCAGATGCTTATTTATGAGATGAGATCAAT 523
QY 855 CAGCCAAATCTGACACATATATGTTTCTAGCTCCAGAGGCTTAATGTGAGATCCAGA 914
Db 524 CAGCCAAATCTGACACATATATGTTTCTAGCTCCAGAGGCTTAATGTGAGATCCAGA 583
QY 915 ATTTGAGAGAAATGTGAGAAATACATCTGTGTTTCTAGTGTCTCTGTTCTCTGATAC 974
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Db 584 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTTCTTCTGTATAC 643  
Qy 975 TTGGAACACAGTCAGATAAAGTCAAAACAAATAAGTTATGCTATGAGATGACAAACT 1034  
Db 644 TTTGAACACAGTCAGATAAAGTCAAAACAAATAAGTTATGCTATGAGATGACAAACT 703  
Qy 1035 CTGAGTAATTTGAGCCAGAAATGAGTATAGTTAAGAAAGCAATTCCACTCTACAT 1094  
Db 704 CTGAGTAATTTGAGCCAGAAATGAGTATAGTTAAGAAAGCAATTCCACTCTACAT 763  
Qy 1095 AACCATGTTACTCATTTGTCCTGACATCGTCGAGGAGCAATCATAGTACTCCGGCTTA 1154  
Db 764 AACCATGTTACTCATTTGTCCTGACATCGTCGAGGAGCAATCATAGTACTCCGGCTTA 823  
Qy 1155 CCTAAAAGGCTCAAGATTATTAATTCCTCCCAATTCCTGATCTGGCAAGATTTTAA 1214  
Db 824 CCTAAAAGGCTCAAGATTATTAATTCCTCCCAATTCCTGATCTGGCAAGATTTTAA 883  
Qy 1215 AGAAATGTTTGAGACCAAGATGATGATCTCTGCACTGGAAAGATGACATCTATGA 1274  
Db 884 AGAAATGTTTGAGACCAAGATGATGATCTCTGCACTGGAAAGATGACATCTATGA 943  
Qy 1275 GAAGCAACCAAGAGAGAAACGACCTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1334  
Db 944 GAAGCAACCAAGAGAGAAACGACCTCTGATGCTGATAGAAAACCTGAAGAAAGCTC 1003  
Qy 1335 TCAGTATGAGATTAATTTATTTTACCTTCACTGACCTTGAGAGA 1383  
Db 1004 TCAGTATGAGATTAATTTATTTTACCTTCACTGACCTTGAGAGA 1052

RESULT 4  
US-11-266-748A-192679  
; Sequence 192679, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnston, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcriptome Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266,748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662,276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700,293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 483996  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 192679  
; LENGTH: 975  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-11-266-748A-192679

Query Match 66.7%; Score 923; DB 8; Length 975;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 135 CGGCCTACGGAATCTACGCCACCTGTGACAAATTTGAGTGTCTGTGTAAGAACTCTG 194

Db 2 CGGCCTACGGAATCTACGCCACCTGTGACAAATTTGAGTGTCTGTGTAAGAACTCTG 61  
Qy 195 CACAGTAATATGACATGGAATCCACCCGAGGAGGACCAATTAATGATCTATGTA 254  
Db 62 CACAGTAATATGACATGGAATCCACCCGAGGAGGACCAATTAATGATCTATGTA 121  
Qy 255 TTTTACTCATTTTGGCGCAAAACAGATTAAGAAATAGTCCGGAAATCTGCTTCAT 314  
Db 122 TTTTACTCATTTTGGCGCAAAACAGATTAAGAAATAGTCCGGAAATCTGCTTCAT 181  
Qy 315 AGAAGTACCCCTGAATGAGAGATTGTCTGCAAGTGGGGTCCAGTATGACCAATGA 374  
Db 182 AGAAGTACCCCTGAATGAGAGATTGTCTGCAAGTGGGGTCCAGTATGACCAATGA 241  
Qy 375 GAGTGAAGAGCCTAGCATTTTGGTTGAAAAATGATCTGACCCCGAAGAGTATCTGA 434  
Db 242 GAGTGAAGAGCCTAGCATTTTGGTTGAAAAATGATCTGACCCCGAAGAGTATCTGA 301  
Qy 435 GTCTGCTGATCTGAATCTTCAATGCACTTTGGCAAACTGAGTACATGAAGTCTTG 494  
Db 302 GTCTGCTGATCTGAATCTTCAATGCACTTTGGCAAACTGAGTACATGAAGTCTTG 361  
Qy 495 GCTCCCTGGAAGGAATACCAAGTCCGACACTAATCTACTACTATTTGGCAGAG 554  
Db 362 GCTCCCTGGAAGGAATACCAAGTCCGACACTAATCTACTACTATTTGGCAGAG 421  
Qy 555 CCTGAAAAAATTCATCAATGTAAGAAACATCTTTAGAGAGGCAATACCTTGGTTC 614  
Db 422 CCTGAAAAAATTCATCAATGTAAGAAACATCTTTAGAGAGGCAATACCTTGGTTC 481  
Qy 615 CTTTGTCTGACCAAGTGAAGATTCCAGTTTGAACACACAGTGTCCAAATAATG 674  
Db 482 CTTTGTCTGACCAAGTGAAGATTCCAGTTTGAACACACAGTGTCCAAATAATG 541  
Qy 675 CAAGATAATGACGAAAAATTAACCATCTTCAATATAGTCCCTTAATCCGCTG 734  
Db 542 CAAGATAATGACGAAAAATTAACCATCTTCAATATAGTCCCTTAATCCGCTG 601  
Qy 735 GAAACCTGATCTCCCATATTAATAAACCCTCTCCCAATGATGACCTATATGTA 794  
Db 602 GAAACCTGATCTCCCATATTAATAAACCCTCTCCCAATGATGACCTATATGTA 661  
Qy 795 ATGGAGAAATCCACAGATTTTATTAAGCATGCTATTTTATGAAGTGAAGTCAATA 854  
Db 662 ATGGAGAAATCCACAGATTTTATTAAGCATGCTATTTTATGAAGTGAAGTCAATA 721  
Qy 855 CAGCCAACTGAGACATTAATGTTTCTACGTCGAAGGCTAAATGAGAAATCCAGA 914  
Db 722 CAGCCAACTGAGACATTAATGTTTCTACGTCGAAGGCTAAATGAGAAATCCAGA 781  
Qy 915 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGCTGTTCTCTGATAC 974  
Db 782 ATTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGCTGTTCTCTGATAC 841  
Qy 975 TTGGAACACAGTCAGATAAAGTCAAAACAAATAAGTTATGCTATGAGATGACAACT 1034  
Db 842 TTTGAACACAGTCAGATAAAGTCAAAACAAATAAGTTATGCTATGAGATGACAACT 901  
Qy 1035 CTGAGTAATTTGAGCCAGAAATGAGTATAGTTAAGAAAGCAATTCCACTCTACAT 1094  
Db 902 CTGAGTAATTTGAGCCAGAAATGAGTATAGTTAAGAAAGCAATTCCACTCTACAT 961  
Qy 1095 AACCATGTTACTCA 1108  
Db 962 AACCATGTTACTCA 975

RESULT 5  
US-11-266-748A-226550  
; Sequence 226550, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:

```
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
PRIOR FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 236550
LENGTH: 975
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-226550
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Query Match 66.7%; Score 923; DB 8; Length 975;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 973; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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135 CGCGCCGACGAACTGAGCAGCCTGAGCAAAATTTGAGTCTCTGTGAAACCTCTG 194
2 CGGCCCTACGGAACCTGAGCAGCCTGAGCAAAATTTGAGTCTCTGTGAAACCTCTG 61
195 CACAGTAATATGACATGAAATCCAGCCGAGGAGCCAGCTCAATATGATGATGTA 254
62 CACAGTAATATGACATGAAATCCAGCCGAGGAGCCAGCTCAATATGATGATGTA 121
255 TTTTATGATTTTGGCGCAACAAGATAGAAAATAGCTCCGAACTGCTGAT 314
122 TTTTATGATTTTGGCGCAACAAGATAGAAAATAGCTCCGAACTGCTGAT 181
315 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCTCCAGTGTACCAATGA 374
182 AGAAGTACCCCTGATGAGAGATTTGTCTGCAAGTGGGTCCTCCAGTGTACCAATGA 241
375 GAGTGAAGCCTTGAATTTTGTGAAAATGATCTCAACCCAGAGGTGATCTCTGA 434
242 GAGTGAAGCCTTGAATTTTGTGAAAATGATCTCAACCCAGAGGTGATCTCTGA 301
435 GTCTGCTGATCTGATCAATGATTTTGGCAACAGCTGATCAATGATGATGTTCTTG 494
302 GTCTGCTGATCTGATCAATGATTTTGGCAACAGCTGATCAATGATGATGTTCTTG 361
495 GCTCCCTGGAAGAAATCCAGTCCGACATCAATCTACTCTACTATTGGGACAGAG 554
362 GCTCCCTGGAAGAAATCCAGTCCGACATCAATCTACTCTACTATTGGGACAGAG 421
555 CTTGGAATAATTCATGATGTAATCATTTTGAAGAGCCCAATCTTTGTTGTTTC 614
422 CTTGGAATAATTCATGATGTAATCATTTTGAAGAGCCCAATCTTTGTTGTTTC 481
615 CTTTATGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGGTGCAAAATAGT 674
482 CTTTATGATCTGACCAAGTGAAGATTCAGTTTGAACAACAGGTGCAAAATAGT 541
675 CAAAGATATGACAGAAATAATTAACCATCTTCAATATAGTGCTTTAACTTCCGTGT 734
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542 CAAGATATATCAGGAAAAATTAACATCTTCAATATAGTGCTTTAACTTCCGTGT 601
735 GAAACCTGATCTCCATATATTAACCTCTCTCTCCATATGATGATGATGATGCA 794
602 GAAACCTGATCTCCATATATTAACCTCTCTCTCCATATGATGATGATGATGCA 661
795 ATGGAGAAATCCAGAAATTTTATAGAGATGCTATTTATAGAGAGAGAGCAATTA 854
662 ATGGAGAAATCCAGAAATTTTATAGAGATGCTATTTATAGAGAGAGAGCAATTA 721
855 CAGCCAACTGAGACATATATGTTTCTACGTCAGAGGCTAATATGAGATCCAGA 914
722 CAGCCAACTGAGACATATATGTTTCTACGTCAGAGGCTAATATGAGATCCAGA 781
915 ATTTGAGAGAAATGAGAAATATCATCTTTTATGATGCTCCCTGCTTCTCTGATAC 974
782 ATTTGAGAGAAATGAGAAATATCATCTTTTATGATGCTCCCTGCTTCTCTGATAC 841
975 TTTGACACAGTCAAGATTAAGAGTCAAAACAAATAGTTATGATGAGATGACAACT 1034
842 TTTGACACAGTCAAGATTAAGAGTCAAAACAAATAGTTATGATGAGATGACAACT 901
1035 CTGAGTAATTTGAGCCAGAAATGATATAGTAAAGGCAATTCACACTCTACAT 1094
902 CTGAGTAATTTGAGCCAGAAATGATATAGTAAAGGCAATTCACACTCTACAT 961
1095 AACCATGTTACTCA 1108
962 AACCATGTTACTCA 975
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RESULT 6

US-11-266-748A-54658

Sequence 54658, Application US/11266748A

Publication No. US2006013463A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcription Microarray Technology and

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

PRIOR FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE: PatentIn version 3.3

SEQ ID NO 54658

LENGTH: 1016

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (60)..(60)

OTHER INFORMATION: n is a, c, g, or t

US-11-266-748A-54658

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Query Match      61.2%; Score 846; DB 8; Length 1016;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 886; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 135 CGGCGCTACGGAACCTCAGCACCTGTGACAAATTTGAGTGTCTGTGTGAAAAACCTCTG 194
DB 79 CGGCGCTACGGAACCTCAGCACCTGTGACAAATTTGAGTGTCTGTGTGAAAAACCTCTG 138
QY 195 CACAGTAATATGACATGGAATCCACCAGGAGGAGCCAGTCAATTTGATGTATGTA 254
DB 139 CACAGTAATATGACATGGAATCCACCAGGAGGAGCCAGTCAATTTGATGTATGTA 198
QY 255 TTTTACTGATTTTGGGACAAACAAGTAAGAAATAGCTCCGGAACCTGTGTTAAT 314
DB 199 TTTTACTGATTTTGGGACAAACAAGTAAGAAATAGCTCCGGAACCTGTGTTAAT 258
QY 315 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCCAAATGA 374
DB 259 AGAAGTACCCCTGAATGAGAGATTTGTCTGCAAGTGGGGTCCAGTGTAGCCAAATGA 318
QY 375 GAGTGAAGACCTAGCATTTTGTGTAATAATGATCTCAACCCAGAGGTGATCTCTGA 434
DB 319 GAGTGAAGACCTAGCATTTTGTGTAATAATGATCTCAACCCAGAGGTGATCTCTGA 378
QY 435 GTCTGCTGTGACTGGAATCTTAATGATCTTGGGACACCTGATCACTGAAGTGTCTTG 494
DB 379 GTCTGCTGTGACTGGAATCTTAATGATCTTGGGACACCTGATCACTGAAGTGTCTTG 438
QY 495 GCTCCCTGGAAGGAATCCAGTCCCGACACTAATCTACTCTCTACTATTGGGACAGAG 554
DB 439 GCTCCCTGGAAGGAATCCAGTCCCGACACTAATCTACTCTCTACTATTGGGACAGAG 498
QY 555 CCTGGAATAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATATCTTGGTGTTC 614
DB 499 CCTGGAATAATTCATCAATGTGAAAAATCTTTAGAGAGGCCAATATCTTGGTGTTC 558
QY 615 CTTTGAATCTGACCAAAAGTGAAGATTCAGTTTGAACAACAAGTCCAAATATGAT 674
DB 559 CTTTGAATCTGACCAAAAGTGAAGATTCAGTTTGAACAACAAGTCCAAATATGAT 618
QY 675 CAAGATTAATGCGAGAAAAATTTAAACCATCTCAATATAGTGCCTTAATCTCCGCTG 734
DB 619 CAAGATTAATGCGAGAAAAATTTAAACCATCTCAATATAGTGCCTTAATCTCCGCTG 678
QY 735 GAAACCTGATCTCTCAATATTAATAAATCTCTCTTCCACATGATGATGATATGTCGA 794
DB 679 GAAACCTGATCTCTCAATATTAATAAATCTCTCTTCCACATGATGATGATATGTCGA 738
QY 795 ATGGGGAATCCACAGATTTTATAGCAGATGCTATTTTATGAGAGTGAAGTCAATTA 854
DB 739 ATGGGGAATCCACAGATTTTATAGCAGATGCTATTTTATGAGAGTGAAGTCAATTA 798
QY 855 CAGCCAAACTGAGACACATTAATGTTTCTAGGTCGAAGAGGCTAAATAGTGAATCCAGA 914
DB 799 CAGCCAAACTGAGACACATTAATGTTTCTAGGTCGAAGAGGCTAAATAGTGAATCCAGA 858
QY 915 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTCTTCTCTGATAC 974
DB 859 ATTTGAGAGAAATGTGAGAAATACATCTTGTTCATGTCCTGTGTCTTCTCTGATAC 918
QY 975 TTTGAAACACAGTCAAGATTAAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAA 1031
DB 919 TTTGAAACACAGTCAAGATTAAGAGTCAAAACAAATTAAGTATGCTATGAGATGACAA 975
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## RESULT 7

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US-11-266-748A-73628/c
; Sequence 73628; Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
```

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; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73628
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)-(30)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-73628

Query Match      58.6%; Score 811; DB 8; Length 1294;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 ATGTGAAAATCTTTAGAGAGGCCAATATCTTGTGTGTCTTGTGATCGCAAGT 632
DB 1099 ATGTGAAAATCTTTAGAGAGGCCAATATCTTGTGTGTCTTGTGATCGCAAGT 1040
QY 633 GAAGATTCAGTTTGAACACACAGTGTCCAAATATAGTGAAGATTAATGACAGAA 692
DB 1039 GAAGATTCAGTTTGAACACACAGTGTCCAAATATAGTGAAGATTAATGACAGAA 690
QY 693 AATTAACCATCTTCAATATAGTGCCTTAACTTCCGCTGGAACCTGATCTCCACA 752
DB 979 AATTAACCATCTTCAATATAGTGCCTTAACTTCCGCTGGAACCTGATCTCCACA 720
QY 753 TATTAATAAATCTCTCTCCACATGATGACCTATATGTGCAATGGAGAAATCCAGAA 812
DB 919 TATTAATAAATCTCTCTCCACATGATGACCTATATGTGCAATGGAGAAATCCAGAA 860
QY 813 TTTTATAGCAGATGCTATTTTATGAGAGTGAAGTCAATTAACGCAATCGACACACA 872
DB 799 TTTTATAGCAGATGCTATTTTATGAGAGTGAAGTCAATTAACGCAATCGACACACA 800
QY 873 TAAATGTTTCTAGCTCAAGAGGCTAAATGTGGAATCCAGATTTGAGAGAAATGTGA 932
DB 799 TAAATGTTTCTAGCTCAAGAGGCTAAATGTGGAATCCAGATTTGAGAGAAATGTGA 740
QY 933 GAATACATCTTGTTCATGATGCTCCGTGTGTCTTCTGATATCTTTGAACACAGTCAAGT 992
DB 739 GAATACATCTTGTTCATGATGCTCCGTGTGTCTTCTGATATCTTTGAACACAGTCAAGT 680
QY 993 AAGAGTCAAAACAAATTAAGTATGCTATGAGAGTGAACAACTTGGAGTAATGGAGCCA 1052
DB 679 AAGAGTCAAAACAAATTAAGTATGCTATGAGAGTGAACAACTTGGAGTAATGGAGCCA 620
QY 1053 AGAATGAGATATGATGAAGAGGCAATTCACACACTCTACATTAACCATGTTACTGTT 1112
DB 619 AGAATGAGATATGATGAAGAGGCAATTCACACACTCTACATTAACCATGTTACTGTT 560
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QY 1113 TCAGTCATGTCGACGAGTGCAATCATAGTATCTCTGCTTACCTTAAAGGCTCAAGAT 1172  
DB 559 TCCAGTCATGTCGACGAGTGCAATCATAGTATCTCTGCTTACCTTAAAGGCTCAAGAT 500  
QY 1173 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 1232  
DB 499 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 440  
QY 1233 GAATGATGATATCTGTCGACGAGAGTACGACATCATATGAGAGCAACCAAGAGAGA 1292  
DB 439 GAATGATGATATCTGTCGACGAGAGTACGACATCATATGAGAGCAACCAAGAGAGA 380  
QY 1293 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTGATGATGAGATTAAT 1352  
DB 379 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTGATGATGAGATTAAT 320  
QY 1353 TATTTTACCTTCACTGTGACCTTGAGAGA 1383  
DB 319 TATTTTACCTTCACTGTGACCTTGAGAGA 289

## RESULT 8

US-11-266-748A-107924/C  
; Sequence 107924, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnson, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcription Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266, 748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105484.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US 60/662, 276  
; PRIOR FILING DATE: 2005-03-14  
; PRIOR APPLICATION NUMBER: US 60/700, 293  
; PRIOR FILING DATE: 2005-07-18  
; NUMBER OF SEQ ID NOS: 48396  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 107924  
; LENGTH: 1294  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (30)..(30)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-107924

Query Match 58.6%; Score 811; DB 8; Length 1294;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 ATGTGAAAACATCTTTAGAGAGGCCAATACTTGTGTTCTTTGATCTGACCAAGT 632  
DB 1099 ATGTGAAAACATCTTTAGAGAGGCCAATACTTGTGTTCTTTGATCTGACCAAGT 1040  
QY 633 GAAGGATTCAGTTTGAACAACAACAGTGTCCCAATATAGTCAAGATATGACAGAAA 692  
DB 1039 GAAGGATTCAGTTTGAACAACAACAGTGTCCCAATATAGTCAAGATATGACAGAAA 980

QY 693 AATTAACCATCTTCAATATAGTCCCTTACTTCCGCTGAGAACTGATCTCCACA 752  
DB 979 AATTAACCATCTTCAATATAGTCCCTTACTTCCGCTGAGAACTGATCTCCACA 920  
QY 753 TATTAAAAACCTCTCTTCCCAATATGATGACCTATATGTGCAATGGAGAAATCCACAGA 812  
DB 919 TATTAAAAACCTCTCTTCCCAATATGATGACCTATATGTGCAATGGAGAAATCCACAGA 860  
QY 813 TTTTATAGAGATGCTTATTTTATGAAATGAGTCAATTAACGCCCAATGAGACACA 872  
DB 859 TTTTATAGAGATGCTTATTTTATGAAATGAGTCAATTAACGCCCAATGAGACACA 800  
QY 873 TATGTTTTCTACGTCACAGAGGCTAATATGAGATCCAGAAATTTGAGAAATGTGGA 932  
DB 799 TATGTTTTCTACGTCACAGAGGCTAATATGAGATCCAGAAATTTGAGAAATGTGGA 740  
QY 933 GAATACATCTTGTTCATGCTCCCTGCTGATCTCTGATATCTTTGAAACACAGTCAGAT 992  
DB 739 GAATACATCTTGTTCATGCTCCCTGCTGATCTCTGATATCTTTGAAACACAGTCAGAT 680  
QY 993 AAGAGTCAAAACCAATATAGTATCTATGAGATGACAAACTCTGAGTAATTTGAGACCA 1052  
DB 679 AAGAGTCAAAACCAATATAGTATGCTATGAGATGACAAACTCTGAGTAATTTGAGACCA 620  
QY 1053 AGAAATGATATGATGATAGAGAGGCAATTCACACTACATTAACATGTTACTCATTTGT 1112  
DB 619 AGAAATGATATGATGATAGAGAGGCAATTCACACTACATTAACATGTTACTCATTTGT 560  
QY 1113 TCAGTCATGTCGACGAGTGCAATCATAGTATCTCTGCTTACCTTAAAGGCTCAAGAT 1172  
DB 559 TCCAGTCATGTCGACGAGTGCAATCATAGTATCTCTGCTTACCTTAAAGGCTCAAGAT 500  
QY 1173 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 1232  
DB 499 TATTATATTCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGGAGACA 440  
QY 1233 GAATGATGATATCTGTCGACGAGAGTACGACATCATATGAGAGCAACCAAGAGAGA 1292  
DB 439 GAATGATGATATCTGTCGACGAGAGTACGACATCATATGAGAGCAACCAAGAGAGA 380  
QY 1293 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTGATGATGAGATTAAT 1352  
DB 379 AACCGACTCTGTAGTGTCTGATAGAAAACCTGAGAAAAGCCTCTGATGATGAGATTAAT 320  
QY 1353 TATTTTACCTTCACTGTGACCTTGAGAGA 1383  
DB 319 TATTTTACCTTCACTGTGACCTTGAGAGA 289

## RESULT 9

US-11-266-748A-126439  
; Sequence 126439, Application US/11266748A  
; Publication No. US20060134663A1  
; GENERAL INFORMATION:  
; APPLICANT: Harkin, Paul  
; APPLICANT: Johnson, Patrick  
; APPLICANT: Mulligan, Karl  
; TITLE OF INVENTION: Transcription Microarray Technology and  
; FILE REFERENCE: 55815-0102 (319189)  
; CURRENT APPLICATION NUMBER: US/11/266, 748A  
; PRIOR FILING DATE: 2005-11-03  
; PRIOR APPLICATION NUMBER: EP 04105479.2  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105482.6  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105483.4  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105507.0  
; PRIOR FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: EP 04105485.9  
; PRIOR FILING DATE: 2004-11-03

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; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126439
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1265)..(1265)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-126439

Query Match      58.6%; Score 811; DB 8; Length 1294;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 811; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 573 ATGTGAAACATCTTTTGAAGAAGCCCAATCTTGGTTGCTTCTTGATCTGACCAAGT 632
   |||||||
DB 196 ATGTGAAACATCTTTTGAAGAAGCCCAATCTTGGTTGCTTCTTGATCTGACCAAGT 255

QY 633 GAAGAGTCCAGTTTGAACAACACAGTGCCTTAACTTCCCGTGTGAACCTGATCCTCCACA 692
   |||||||
DB 256 GAAGAGTCCAGTTTGAACAACACAGTGCCTTAACTTCCCGTGTGAACCTGATCCTCCACA 315

QY 693 AATTTAAACATCTCTTCAATATAGTCCCTTAACTTCCCGTGTGAACCTGATCCTCCACA 752
   |||||||
DB 316 AATTTAAACATCTCTTCAATATAGTCCCTTAACTTCCCGTGTGAACCTGATCCTCCACA 375

QY 753 TATTTAAAACTCTCTCTTCCCAATGATGACTATATGTGCATGGAGAAATCCACGAA 812
   |||||||
DB 376 TATTTAAAACTCTCTCTTCCCAATGATGACTATATGTGCATGGAGAAATCCACGAA 435

QY 813 TTTTATTAAGAGATGCTATTTTATGAAGTGAAGTCAATTAACGCCAACTGAGACACA 872
   |||||||
DB 436 TTTTATTAAGAGATGCTATTTTATGAAGTGAAGTCAATTAACGCCAACTGAGACACA 495

QY 873 TAAATGTTTCTACGTCGAAGAGCTAATATGAGAAATCCAGAAATTTGAGAAATGTGA 932
   |||||||
DB 496 TAAATGTTTCTACGTCGAAGAGCTAATATGAGAAATCCAGAAATTTGAGAAATGTGA 555

QY 933 GAATACATCTTGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 992
   |||||||
DB 556 GAATACATCTTGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 615

QY 993 AAGAGTCAAAACAAATTAAGTATGCTATGAGAGTGAAGAACTCTGGAGTATTTGAGACCA 1052
   |||||||
DB 616 AAGAGTCAAAACAAATTAAGTATGCTATGAGAGTGAAGAACTCTGGAGTATTTGAGACCA 675

QY 1053 AGAAATAGATATAGGTAGAAGCGCAATTCACACTCTACATAACCAATGTTACTCATTTG 1112
   |||||||
DB 676 AGAAATAGATATAGGTAGAAGCGCAATTCACACTCTACATAACCAATGTTACTCATTTG 735

QY 1113 TCCAGTATCGTGCAGGTGCAATCATATGATCTCTGCTTTTAACTTAAAGAAAGCTCAAGAT 1172
   |||||||
DB 736 TCCAGTATCGTGCAGGTGCAATCATATGATCTCTGCTTTTAACTTAAAGAAAGCTCAAGAT 795

QY 1173 TATTAATTTCCCTCCCAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGAAGCCA 1232
   |||||||
DB 796 TATTAATTTCCCTCCCAATTCCTGATCTCTGCAAGATTTTAAAGAAATGTTTGAAGCCA 855

QY 1233 GAATGATGATATCTGTGACTGGAAGAGTACGATCTATGAGAGCAACCAAGAGAGA 1292
   |||||||
DB 856 GAATGATGATATCTGTGACTGGAAGAGTACGATCTATGAGAGCAACCAAGAGAGA 915

QY 1293 AACCGACTCTGTAGTGTGTATGAGAAAACCTGAAGAAAACCTCTGAGTATGAGATATTT 1352
   |||||||
DB 916 AACCGACTCTGTAGTGTGTATGAGAAAACCTGAAGAAAACCTCTGAGTATGAGATATTT 975
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QY 1353 TATTTTACCTTCACTGTGACCTTGAGAGA 1383
   |||||||
DB 976 TATTTTACCTTCACTGTGACCTTGAGAGA 1006

RESULT 10
US-11-266-748A-54614
; Sequence 54614, Application US/1126748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54614
; LENGTH: 902
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (872)..(872)
; OTHER INFORMATION: n is a, c, g, or t
; NAME/KEY: misc feature
; LOCATION: (902)..(902)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-54614

Query Match      42.4%; Score 587; DB 8; Length 902;
Best Local Similarity 100.0%; Pred. No. 3,6e-308;
Matches 587; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 GGGAGAAATCCACAGAAATTTTATGAGAGTGCCTATTTTATGAAGTGAAGTCAATPACA 856
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DB 27 GGGAGAAATCCACAGAAATTTTATGAGAGTGCCTATTTTATGAAGTGAAGTCAATPACA 86

QY 857 GCCAAACTGAGACACATATGTTTCTACGTCGAAGAGCTTAATGTGAGAAATCCAGAAAT 916
   |||||||
DB 87 GCCAAACTGAGACACATATGTTTCTACGTCGAAGAGCTTAATGTGAGAAATCCAGAAAT 146

QY 917 TTGAGAGAAATGTGAGAAATACATCTGTTTCAATGCTCCCTGAGTCTTCTGATPACT 976
   |||||||
DB 147 TTGAGAGAAATGTGAGAAATACATCTGTTTCAATGCTCCCTGAGTCTTCTGATPACT 206

QY 977 TGAACACAGTCAGATTAAGAGTCAAAAACAATTAAGTATGCTATGAGATGAGACAACTCT 1036
   |||||||
DB 207 TGAACACAGTCAGATTAAGAGTCAAAAACAATTAAGTATGCTATGAGATGAGACAACTCT 266

QY 1037 GGAGTAATTTGAGACCAAGAAATGAGTATAGGTAGAAGCGCAATTCACACTTACATAA 1096
   |||||||
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Db 267 GGAGTAATTGGAGCCCAAGAAATGATATAGTAAAGAGCGCAATTCCACTCTACATVA 326
Qy 1097 CCATGTACTTACTTGTTCAGTCAATCGTCGAGGTCAGTATAGTACTCTGCTTACC 1156
Db 327 CCATGTACTTACTTGTTCAGTCAATCGTCGAGGTCAGTATAGTACTCTGCTTACC 386
Qy 1157 TAAAAAGGCTCAAGATTATATATTCCTCCCAATTCTGATCTGGCAAGATTTTAAAG 1216
Db 387 TAAAAAGGCTCAAGATTATATATTCCTCCCAATTCTGATCTGGCAAGATTTTAAAG 446
Qy 1217 AAATGTTGGAGACAGATATATATCTGCACTGGAGAAATAGACATCTATAGAGA 1276
Db 447 AAATGTTGGAGACAGATATATATCTGCACTGGAGAAATAGACATCTATAGAGA 506
Qy 1277 AGCAACCAAGAGAGAAACCGACTCTGATGCTGATGAGAAACCTGAGAAAGCTCTC 1336
Db 507 AGCAACCAAGAGAGAAACCGACTCTGATGCTGATGAGAAACCTGAGAAAGCTCTC 566
Qy 1337 AGTATGAGATATATATTTTACCTTCACTGATGACCTTGAGAGA 1383
Db 567 AGTATGAGATATATATTTTACCTTCACTGATGACCTTGAGAGA 613
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RESULT 11
US-11-266-748A-73627
; Sequence 73627, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73627
; LENGTH: 1297
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60)..(60)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (81)..(168)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (170)..(171)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (174)..(174)
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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (180)..(180)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (184)..(184)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1011)..(1121)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1125)..(1125)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1133)..(1133)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1142)..(1187)
; OTHER INFORMATION: n is a, c, g, or t
; US-11-266-748A-73627
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Query Match 20.1%; Score 278; DB 8; Length 1297;

Best Local Similarity 99.7%; Pred. No. 2.6e-140;

Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1055 AAATGATATAGGTAAAGAGCGCAATTCACACTCTACATATACCATGTTACTATGTTTC 1114
Db 217 AAATGATATAGGTAAAGAGCGCAATTCACACTCTACATATACCATGTTACTATGTTTC 276
Qy 1115 CAGTCATGTCGAGAGGTGCAATATAGTACTCTGCTTTACTTAAAGAGCTCAAGATTA 1174
Db 277 CAGTCATGTCGAGAGGTGCAATATAGTACTCTGCTTTACTTAAAGAGCTCAAGATTA 336
Qy 1175 TTATATTCCTCCCAATTCCTCGATCCGCGAAGATTTTAAAGAAATGTTGGAGACGAGA 1234
Db 337 TTATATTCCTCCCAATTCCTCGATCCGCGAAGATTTTAAAGAAATGTTGGAGACGAGA 396
Qy 1235 ATGATGATACTCTGCACTGAGAGAGATGACATCTATGAGAGCAAAACCAAGAGGAAA 1294
Db 397 ATGATGATACTCTGCACTGAGAGAGATGACATCTATGAGAGCAAAACCAAGAGGAAA 456
Qy 1295 CCGACTCTGTAGTGTGATGAGAAACCTGAGAAAGCCTCTCAGTGTAGATTAATTTTA 1354
Db 457 CCGACTCTGTAGTGTGATGAGAAACCTGAGAAAGCCTCTCAGTGTAGATTAATTTTA 516
Qy 1355 TTTTACCTTCACTGATGACCTTGAGAGA 1383
Db 517 TTTTACCTTCACTGATGACCTTGAGAGA 545
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RESULT 12
US-11-266-748A-107923
; Sequence 107923, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
```

PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105483.4  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105507.0  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105484.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662,276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 483996  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 107923  
LENGTH: 1297  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (60)..(60)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (81)..(168)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (170)..(171)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (174)..(174)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (180)..(180)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (184)..(184)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1011)..(1121)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1125)..(1125)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1133)..(1133)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1138)..(1140)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1142)..(1187)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-266-748A-107923

Query Match 20.1%; Score 278; DB 8; Length 1297;  
Best Local Similarity 99.7%; Pred. No. 2,6e-140;  
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1055 AATGAGTATAGGTAAAGCGCAATTCCACTTACATTAACCATGTTACTGATTGTC 1114

|||||  
Db 217 AATGAGTATAGGTAAAGCGCAATTCCACTTACATTAACCATGTTACTGATTGTC 276  
1115 CAGTCATCGTCGAGGTGCATCATAGTACTCTGCTTACCTAAAGGCTCAAGATTA 1174  
QY 277 CAGTCATCGTCGAGGTGCATCATAGTACTCTGCTTACCTAAAGGCTCAAGATTA 336  
1175 TTATATCCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGAAGACCA 1234  
Db 337 TTATATCCCTCCCAATTCCTGATCCTGGCAAGATTTTAAAGAAATGTTTGAAGACCA 396  
QY 1235 ATGATGATCTGTGCACTGGAAGAGTACGATCTATAGAGCAACCAAGAGGAAA 1294  
Db 397 ATGATGATCTGTGCACTGGAAGAGTACGATCTATAGAGCAACCAAGAGGAAA 456  
QY 1295 CCGACTCTGTAGTGCATGAGAAAACCTGAAGAAAGCCTCAGTATGAGATTAATTTA 1354  
Db 457 CCGACTCTGTAGTGCATGAGAAAACCTGAAGAAAGCCTCAGTATGAGATTAATTTA 516  
QY 1355 TTTTACCTTCACTGTGACCTTGAGAGA 1383  
Db 517 TTTTACCTTCACTGTGACCTTGAGAGA 545

RESULT 13  
US-11-266-748A-126438/c  
Sequence 126438, Application US/11266748A  
Publication No. US20060134663A1  
GENERAL INFORMATION:  
APPLICANT: Harkin, Paul  
APPLICANT: Johnston, Patrick  
TITLE OF INVENTION: Transcriptome Microarray Technology and  
FILE REFERENCE: 55815-0102 (319189)  
CURRENT APPLICATION NUMBER: US/11/266,748A  
PRIOR FILING DATE: 2005-11-03  
PRIOR APPLICATION NUMBER: EP 04105479.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105482.6  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105483.4  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105485.9  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: EP 04105484.2  
PRIOR FILING DATE: 2004-11-03  
PRIOR APPLICATION NUMBER: US 60/662,276  
PRIOR FILING DATE: 2005-03-14  
PRIOR APPLICATION NUMBER: US 60/700,293  
PRIOR FILING DATE: 2005-07-18  
NUMBER OF SEQ ID NOS: 483996  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 126438  
LENGTH: 1297  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (111)..(156)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
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FEATURE:  
NAME/KEY: misc\_feature  
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OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature

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OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (177)..(287)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (1114)..(1114)
OTHER INFORMATION: n is a, c, g, or t
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OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (1130)..(1217)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1238)..(1238)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-126438
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Query Match 20.1%; Score 278; DB 8; Length 1297;

Best Local Similarity 99.7%; Pred. No. 2.6e-140; Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1055 AATGAGTATAGTAAAGACGCAATTCACACTCTACATACCATCTTCTCTGTC 1114
DB 1081 AATGAGTATAGTAAAGACGCAATTCACACTCTACATACCATCTTCTCTGTC 1022
QY 1115 CAGTCATCTGCGAGGTGCAATCTCTCTCTTCTCTTAAAGAGCTCAAGT 1174
DB 1021 CAGTCATCTGCGAGGTGCAATCTCTCTCTTCTCTTAAAGAGCTCAAGT 962
QY 1175 TTATATTCCTCCAAATTCCTGATCTGCGAAGATTTTAAAGAAATTTGGAGCCGA 1234
DB 961 TTATATTCCTCCAAATTCCTGATCTGCGAAGATTTTAAAGAAATTTGGAGCCGA 902
QY 1235 ATGATGATCTCTGCACTGAGAGAGTACGACATCTTATGAGAGCAACCAAGAGGAA 1294
DB 901 ATGATGATCTCTGCACTGAGAGAGTACGACATCTTATGAGAGCAACCAAGAGGAA 842
QY 1295 CCGACTCTGTAGTGTGATGAGAAACCTGAGAAAGCTTCTAGTGTGAGATTAATTTA 1354
DB 841 CCGACTCTGTAGTGTGATGAGAAACCTGAGAAAGCTTCTAGTGTGAGATTAATTTA 782
QY 1355 TTTTACCTTCACTGAGACCTTGAGAGA 1383
DB 781 TTTTACCTTCACTGAGACCTTGAGAGA 753
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## RESULT 14

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US-11-266-748A-51095
Sequence 51095, Application US/11266748A
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
```

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CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 51095
LENGTH: 583
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (572)..(572)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-51095
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Query Match 4.6%; Score 63; DB 8; Length 583;

Best Local Similarity 100.0%; Pred. No. 1.5e-23; Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 CTGAGAAACCTCTCAGTATGAGATTAATTTTACCTTCACTGAGCTTGAGA 60
QY 1381 AGA 1383
DB 61 AGA 63
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## RESULT 15

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US-11-218-305-11789
Sequence 11789, Application US/11218305
Publication No. US2006014195A1
GENERAL INFORMATION:
APPLICANT: MONSANTO TECHNOLOGY, LLC
APPLICANT: McIsaid, Paul L.
APPLICANT: Tao, Nengsheng
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53660)B
CURRENT APPLICATION NUMBER: US/11/218,305
CURRENT FILING DATE: 2005-09-01
PRIOR APPLICATION NUMBER: US 60/606,880
PRIOR FILING DATE: 2004-09-01
NUMBER OF SEQ ID NOS: 25043
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11789
LENGTH: 1264
TYPE: DNA
ORGANISM: Zea mays
US-11-218-305-11789
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Query Match 1.9%; Score 26; DB 7; Length 1264;

Best Local Similarity 100.0%; Pred. No. 0.002; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 111 CGGCGGCGGGGCGGGGCGGGGCGG 136
DB 315 CGGCGGCGGGGCGGGGCGGGGCGG 340
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Search completed: July 7, 2006, 23:52:18  
Job time : 205 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2006, 01:35:08 ; Search time 195 Seconds  
(without alignments)  
998.842 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 2320

Sequence: 1 MEWPRLCGHMLLFCAGGS.....OTKETDVLVLEIKKASQ 426

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID       | Description        |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1          | 2320   | 100.0       | 426    | 2  | AAW09822 | AAW09822 Human int |
| 2          | 2309.5 | 99.5        | 427    | 2  | AAW24973 | AAW24973 Human int |
| 3          | 2309.5 | 99.5        | 427    | 4  | AAB19807 | AAB19807 Human int |
| 4          | 2309.5 | 99.5        | 427    | 8  | ADL17812 | ADL17812 Human int |
| 5          | 2309.5 | 99.5        | 427    | 8  | ADL82843 | ADL82843 Human PRO |
| 6          | 2309.5 | 99.5        | 427    | 8  | ADN04504 | ADN04504 Antipori  |
| 7          | 2309.5 | 99.5        | 427    | 8  | ADN62575 | ADN62575 Human int |
| 8          | 2309.5 | 99.5        | 427    | 8  | ABM82441 | ABM82441 Tumour-as |
| 9          | 2309.5 | 99.5        | 427    | 9  | AEC31473 | AEC31473 Human IL- |
| 10         | 2309.5 | 99.5        | 427    | 10 | AEE93788 | AEE93788 Human int |
| 11         | 2309.5 | 99.5        | 427    | 10 | AEE57817 | AEE57817 Acti-IL-1 |
| 12         | 2303.5 | 99.3        | 427    | 8  | ADL17813 | ADL17813 Human int |
| 13         | 2302.5 | 99.2        | 427    | 8  | ADP17835 | ADP17835 Human IL- |
| 14         | 2302.5 | 99.2        | 427    | 8  | ADL17814 | ADL17814 Human int |
| 15         | 2296.5 | 99.0        | 427    | 4  | AAB19808 | AAB19808 Human int |
| 16         | 2230.5 | 96.1        | 414    | 8  | ADX97531 | ADX97531 Pancreat  |
| 17         | 1878   | 80.9        | 403    | 4  | AAU69132 | AAU69132 Canine in |
| 18         | 1875.5 | 80.8        | 793    | 3  | AAU92208 | AAU92208 IL-13/IL- |
| 19         | 1875.5 | 80.8        | 793    | 7  | ABM02181 | ABM02181 Human IL- |
| 20         | 1784.5 | 76.9        | 664    | 3  | ADP17841 | ADP17841 Chimeric  |
| 21         | 1779.5 | 76.7        | 784    | 3  | AAU92207 | AAU92207 IL-13/IL- |
| 22         | 1779.5 | 76.7        | 784    | 7  | ABW02180 | ABW02180 Human IL- |
| 23         | 1769   | 76.2        | 322    | 5  | AAE13745 | AAE13745 Human sol |

|    |       |      |     |   |          |                    |
|----|-------|------|-----|---|----------|--------------------|
| 24 | 1741  | 75.0 | 776 | 9 | AEC31482 | AEC31482 Human IL- |
| 25 | 1741  | 75.0 | 776 | 9 | AEC31484 | AEC31484 Human IL- |
| 26 | 1741  | 75.0 | 776 | 9 | AEC31478 | AEC31478 Human IL- |
| 27 | 1741  | 75.0 | 776 | 9 | AEC31486 | AEC31486 Human IL- |
| 28 | 1741  | 75.0 | 776 | 9 | AEC31480 | AEC31480 Human IL- |
| 29 | 1714  | 73.9 | 426 | 2 | AAW09821 | AAW09821 Mouse int |
| 30 | 1696  | 73.1 | 424 | 9 | ADX97888 | ADX97888 Murine IL |
| 31 | 1536  | 66.2 | 286 | 4 | AAU90678 | AAU90678 Human DAL |
| 32 | 942   | 40.6 | 177 | 2 | AAU58987 | AAU58987 Homo sapi |
| 33 | 465   | 20.0 | 134 | 8 | ADP84617 | ADP84617 Human bre |
| 34 | 463   | 20.0 | 172 | 8 | ADP84616 | ADP84616 Human bre |
| 35 | 463   | 20.0 | 226 | 8 | ADQ65618 | ADQ65618 Novel hum |
| 36 | 414.5 | 17.9 | 82  | 8 | ADQ26844 | ADQ26844 Human rec |
| 37 | 329   | 14.2 | 386 | 8 | AAU69135 | AAU69135 Canine in |
| 38 | 318   | 13.7 | 398 | 2 | AAU22212 | AAU22212 Sequence  |
| 39 | 318   | 13.7 | 415 | 2 | AAU22211 | AAU22211 Sequence  |
| 40 | 318   | 13.7 | 415 | 2 | AAU22217 | AAU22217 Sequence  |
| 41 | 318   | 13.7 | 415 | 5 | ADZ58697 | ADZ58697 Mouse IL- |
| 42 | 310   | 13.4 | 365 | 4 | AAU69136 | AAU69136 Canine in |
| 43 | 304.5 | 13.1 | 561 | 4 | AAU69138 | AAU69138 Canine IL |
| 44 | 303.5 | 13.1 | 561 | 4 | AAU69141 | AAU69141 Canine IL |
| 45 | 302   | 13.0 | 372 | 2 | AAW36616 | AAW36616 Celebus m |

## ALIGNMENTS

|          |   |                                      |
|----------|---|--------------------------------------|
| RESULT 1 | AAW09822  | standard; protein; 426 AA.           |
| ID       | AAW09822;   |                                      |
| XX       | AAW09822;   |                                      |
| AC       | AAW09822;   |                                      |
| XX       | AAW09822;   |                                      |
| DT       | 15-JUL-1997   | (first entry)                        |
| XX       |   |                                      |
| DE       | Human interleukin-12 receptor alpha chain NR4.                        |                                      |
| XX       |   |                                      |
| KW       | NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine; |                                      |
| KW       | allergy; asthma; therapy.   |                                      |
| XX       |   |                                      |
| OS       | Homo sapiens.   |                                      |
| XX       |   |                                      |
| FT       | Key   | Location/Qualifiers                  |
| FT       | Peptide   | 1..27                                |
| FT       | Protein   | /label= Sig_peptide                  |
| FT       | Domain  | 28..426                              |
| FT       | Domain  | /label= Mat_protein                  |
| FT       | Domain  | 28..118                              |
| FT       | Domain  | /label= Extracellular domain         |
| FT       | Domain  | /note= "Ig-like domain"              |
| FT       | Modified-site   | 36                                   |
| FT       | Modified-site   | /label= N-glycosylation site         |
| FT       | Modified-site   | 104                                  |
| FT       | Domain  | /label= N-glycosylation site         |
| FT       | Domain  | 119..342                             |
| FT       | Modified-site   | /label= Hemoreceptor_receptor-domain |
| FT       | Region  | 137                                  |
| FT       | Region  | /label= N-glycosylation site         |
| FT       | Domain  | 326..330                             |
| FT       | Domain  | /label= WSDMS_motif                  |
| FT       | Domain  | 343..366                             |
| FT       | Domain  | /label= Transmembrane_domain         |
| FT       | Domain  | 367..426                             |
| FT       | Domain  | /label= Cytoplasmic_tail             |
| XX       | WC9715663-A1.   |                                      |
| XX       | 01-MAY-1997.  |                                      |
| PD       |   |                                      |
| XX       | 23-OCT-1996;  | 96MO-AUD000668.                      |
| XX       | 23-OCT-1995;  | 95AU-00006135.                       |
| PR       | 22-DEC-1995;  | 95AU-00007276.                       |



```
PR 09-SEP-1996; 96AU-00002208.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;
XX WPI; 1997-259018/23.
XX N-PSDB; AAT6165.
XX
XX DNA encoding animal haemopoietin receptor which interacts with
XX interleukin-13 - useful to treat asthma, allergy or condition exacerbated
XX by IgE production.
XX
XX Claim 5; Page 52-54; 93pp; English.
XX
XX Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822),
XX designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain.
XX The human NR4 amino acid sequence was deduced from a composite DNA
XX sequence (AAT6165) derived from bone marrow cDNA clones. Recombinant
XX NR4, or fusion proteins including NR4, can be produced in transformed
XX host cells. The receptor molecules and their components are useful in the
XX development of a range of agonists, antagonists, therapeutics and
XX diagnostic reagents based on ligand interaction with its receptor. esp.
XX for the development of cpds. capable of modulating the activity of IL-13
XX and related cytokines such as interleukin-4 for the treatment of allergy,
XX asthma and other conditions relating to IgE
XX
XX SQ Sequence 426 AA;
XX
XX Query Match 100.0%; Score 2320; DB 2; Length 426;
XX Best Local Similarity 100.0%; Pred. No. 4, 6e-212;
XX Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNLVSVENLCTVIMTNPPGASN 60
XX Db 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNLVSVENLCTVIMTNPPGASN 60
XX
XX QY 61 CSLMYFSHFQDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 120
XX Db 61 CSLMYFSHFQDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 120
XX
XX QY 121 EGGPESAVTELOCIWHNLSTYKCSWLPGRNTSPDTNNTLYYHRSLEKIHQENIFREGQ 180
XX Db 121 EGGPESAVTELOCIWHNLSTYKCSWLPGRNTSPDTNNTLYYHRSLEKIHQENIFREGQ 180
XX
XX QY 181 YFGCSFDLTQVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 240
XX Db 181 YFGCSFDLTQVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 240
XX
XX QY 241 DLYVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYVQAKCENPEFERNVENTSCFMVPG 300
XX Db 241 DLYVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYVQAKCENPEFERNVENTSCFMVPG 300
XX
XX QY 301 VLPDTLNTVIRIKRKNKLCYEDDKLMSNSQEMSIGKRRNSTLYITMLLIVPIVAGAI 360
XX Db 301 VLPDTLNTVIRIKRKNKLCYEDDKLMSNSQEMSIGKRRNSTLYITMLLIVPIVAGAI 360
XX
XX QY 361 VLLLYLKRLLKIIIFPPIPDGKIFKEMFGQNDTLLHMKYDIYEKQTEETS VVLIEN 420
XX Db 361 VLLLYLKRLLKIIIFPPIPDGKIFKEMFGQNDTLLHMKYDIYEKQTEETS VVLIEN 420
XX
XX QY 421 LKKAQSQ 426
XX Db 421 LKKAQSQ 426
XX
XX RESULT 2
XX AAW24973
XX ID AAW24973 standard; protein; 427 AA.
XX AC AAW24973;
XX XX
XX DT 22-JUN-1998 (first entry)
```

```
XX
XX DE Human interleukin-13 alpha receptor.
XX
XX KM Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
XX
XX OS Homo sapiens.
XX
XX PN WO9720926-A1.
XX
XX PD 12-JUN-1997.
XX
XX PF 07-NOV-1996; 96WO-FR001756.
XX
XX PR 06-DEC-1995; 95FR-00014424.
XX
XX XX (SNFI ) SANOFI SA.
XX
XX PI Caput D, Ferrara P, Laurent P, Vita N;
XX
XX DR WPI; 1997-319773/29.
XX
XX N-PSDB; AAT85827.
XX
XX PS Claim 8; Page 46-47; 83pp; French.
XX
XX CC This sequence represents interleukin-13 (IL-13) alpha receptor. The
XX CC invention relates to new purified peptides comprising 380 or 427 amino
XX CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380
XX CC and 427 aa proteins are designated IL-13R beta and alpha respectively.
XX CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
XX CC affinity, but acquires high affinity when associated with the IL-4
XX CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as
XX CC diagnostic probes to identify aberrant synthesis or genetic anomalies
XX CC such as loss of heterozygosity and rearrangements, or chromosomal
XX CC anomalies. They are also used for production of recombinant IL-13R beta
XX CC and alpha which can be used as IL-13 antagonists, specifically to
XX CC regulate IL-13-induced responses for treatment of inflammation and
XX CC allergy. IL-13 receptors are also useful as antisense molecules for gene
XX CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
XX CC immunoassays) to diagnose diseases associated with abnormal expression of
XX CC IL-13 receptors; when coupled to a toxin also for treatment of
XX CC overproduction of IL-13R. Cells that express IL-13R at the surface are
XX CC used to identify ligands and modulators of IL-13R
XX
XX SQ Sequence 427 AA;
XX
XX Query Match 99.5%; Score 2309.5; DB 2; Length 427;
XX Best Local Similarity 99.8%; Pred. No. 4, 7e-211;
XX Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX QY 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNLVSVENLCTVIMTNPPGASN 59
XX Db 1 MEMPARLCGIMALLLTCAGGGGGGGAAPTETQPPVNLVSVENLCTVIMTNPPGASN 60
XX
XX QY 60 NCSLWYFSHFQDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 119
XX Db 61 NCSLWYFSHFQDKODKKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCISPP 120
XX
XX QY 120 PEGDPESAVTELOCIWHNLSTYKCSWLPGRNTSPDTNNTLYYHRSLEKIHQENIFREG 179
XX Db 121 PEGDPESAVTELOCIWHNLSTYKCSWLPGRNTSPDTNNTLYYHRSLEKIHQENIFREG 180
XX
XX QY 180 QYFGCSFDLTQVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 239
XX Db 181 QYFGCSFDLTQVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHN 240
XX
XX QY 240 DDLVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYVQAKCENPEFERNVENTSCFMVPG 299
XX Db 241 DDLVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYVQAKCENPEFERNVENTSCFMVPG 300
XX
XX QY 300 GVLVPLTNTVIRIKRKNKLCYEDDKLMSNSQEMSIGKRRNSTLYITMLLIVPIVAGAI 359
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Db      301 GVLPDITNTVIRIKTKTKLCEYEDDKLMSNMSOEMSIGKKNSTLYITMLLIVPIYVAGAI 360
QY      360 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETSVDLIE 419
Db      361 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETSVDLIE 420
QY      420 NLKKSQ 426
Db      421 NLKKSQ 427

RESULT 3
AAB19807
ID      AAB19807 standard; protein; 427 AA.
AC      AAB19807;
XX      XX
DT      05-MAR-2001 (first entry)
XX      XX
DE      Human interleukin-13 receptor alpha-1.
XX      XX
KM      Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KM      atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KM      dermatological; antiasthmatic; antiallergic; therapy; diagnosis.
XX      OS
XX      Homo sapiens.
FH      Key
FH      Peptide
FT      1..26
FT      /label= Sig_peptide
FT      27..347
FT      /label= Extracellular_domain
FT      28..427
FT      /label= Mature_protein
FT      327..331
FT      /note= "MSXWS motif conserved in the type-I cytokine
FT      receptor superfamily"
FT      348..367
FT      /label= Transmembrane_domain
FT      368..427
FT      /label= Cytoplasmic_domain
FT      405..408
FT      /note= "YXXQ motif, consensus for STAT binding"
XX      XX
PN      US6143871-A.
XX      XX
PD      07-NOV-2000.
XX      XX
PF      12-NOV-1997; 97US-00969125.
XX      XX
PR      13-DEC-1996; 96GB-00025899.
XX      XX
PA      (GAUC/) GAUCHAT J.
PA      (BONN/) BONNEFOY J.
XX      XX
PI      Gauchat J, Bonnefoy J;
XX      XX
DR      WPI; 2001-006445/01.
DR      N-PSDB; AAA88907.
XX      XX
PT      Novel polypeptide capable of binding interleukin-13 or interleukin-4
PT      useful for treating atopy, atopic dermatitis, allergies, rhinitis,
PT      eczema, asthma or AIDS.
XX      XX
PS      Claim 2; Fig 1A; 26pp; English.
XX      XX
CC      The present sequence is that of a protein capable of binding human
CC      interleukin-13 (IL-13) and/or human interleukin-4 (IL-4) in the presence
CC      of IL-4 receptor alpha. It was deduced from cDNA (see AAA88907) isolated
CC      from a human activated tonsillar cDNA library. This IL-13 receptor alpha-1
CC      polypeptide can be used to inhibit IL-13 or IL-4 induced IGE synthesis in
CC      B cells, useful in the treatment of diseases in which IGE or Th2

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CC      differentiation plays a role, e.g. atopy, atopic dermatitis, allergy,
CC      rhinitis, eczema, asthma or AIDS. Antibodies raised against the
CC      polypeptide are useful for detecting IL-13 and IL-4 receptor or parts of
CC      them which have been shed from cells as a result of disease, e.g. cancer,
CC      leukaemia, atopy, atopic dermatitis, allergies, rhinitis, eczema, asthma,
CC      lupus erythematosus, AIDS, thyroiditis, diabetes, uveitis, dermatitis,
CC      psoriasis, urticaria, nephrotic syndrome, inflammatory bowel disease,
CC      glomerulonephritis, ulcerative colitis, Crohn's disease, Sjogren's
CC      syndrome and toxoplasmosis
XX      XX
SQ      Sequence 427 AA;
XX      XX
Query Match      99.5%; Score 2309.5; DB 4; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 MEMPARLCIGMALILCGGGGGGGG-APTEOPPYTNLSVENVLCYITWNPPEGASS 59
Db      1 MEMPARLCIGMALILCGGGGGGGGAPTEOPPYTNLSVENVLCYITWNPPEGASS 60
QY      60 NCSLWYSHFGDKODKKIAPETRRSIEVPLNERICLVGSOCSTNESKPSILVEKCTSP 119
Db      61 NCSLWYSHFGDKODKKIAPETRRSIEVPLNERICLVGSOCSTNESKPSILVEKCTSP 120
QY      120 PEGDPESAATVLELCIMWNLISYMKCSWLPGRNTSPDTVITYWHRSLKIHQCENIPREG 179
Db      121 PEGDPESAATVLELCIMWNLISYMKCSWLPGRNTSPDTVITYWHRSLKIHQCENIPREG 180
QY      180 QYRGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSNIVPLTSRVKPDPHIKNLSFHN 239
Db      181 QYRGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSNIVPLTSRVKPDPHIKNLSFHN 240
QY      240 DDLVYQWENPONFISRLCFYEVEVNNSTHNVFYQOEKCEPFEERNVEMSCFVP 299
Db      241 DDLVYQWENPONFISRLCFYEVEVNNSTHNVFYQOEKCEPFEERNVEMSCFVP 300
QY      300 GVLPDITNTVIRIKTKTKLCEYEDDKLMSNMSOEMSIGKKNSTLYITMLLIVPIYVAGAI 359
Db      301 GVLPDITNTVIRIKTKTKLCEYEDDKLMSNMSOEMSIGKKNSTLYITMLLIVPIYVAGAI 360
QY      360 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETSVDLIE 419
Db      361 IVLLLYLKRLLKIIIFPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETSVDLIE 420
QY      420 NLKKSQ 426
Db      421 NLKKSQ 427

RESULT 4
ADL71812
ID      ADL71812 standard; protein; 427 AA.
XX      XX
AC      ADL71812;
XX      XX
DT      20-MAY-2004 (first entry)
XX      XX
DE      Human interleukin-13 receptor alpha (IL-13 R) protein.
XX      XX
KM      Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;
KM      eczema; asthma; AIDS; gene therapy; interleukin; receptor.
XX      XX
OS      Homo sapiens.
FH      Key
FH      Peptide
FT      1..26
FT      /label= Signal_peptide
FT      27..427
FT      /note= "Human mature IL-13 R protein"
FT      27..347
FT      /note= Extracellular domain
FT      327..331
FT      /note= MSXWS motif

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FT Domain 368..427
FT /note = Cytoplasmic domain
XX
XX US2004043921-A1.
XX
XX PD 04-MAR-2004.
XX
XX PF 29-SEP-2003; 2003US-00671697.
XX
XX PR 13-DEC-1996; 96GB-00025899.
XX PR 12-NOV-1997; 97US-00969125.
XX PR 06-APR-2000; 2000US-00545002.
XX
XX PA (BONN/) BONNEFOY J.
XX PA (GAUC/) GAUCHAT J.
XX PI Bonnefoy J, Gauchat J;
XX
XX DR WPI, 2004-225726/21.
XX DR N-PSDB; ADL71811.
XX
XX PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse
XX PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma
XX PT or AIDS, comprises administering a polypeptide or soluble polypeptide.
XX
XX PS Claim 1; SEQ ID NO 9; 27bp; English.
XX
XX CC The invention relates to polypeptides capable of binding human
XX CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The
XX CC invention also relates to a method of treatment of a disease in which
XX CC IL13 and IL4 cause adverse effects. The method is useful for treating a
XX CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic
XX CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides
XX CC of the invention are useful in raising antibodies. It is also useful in
XX CC gene therapy. The present sequence is human interleukin-13 receptor alpha
XX CC (IL-13 Ralpha) protein.
XX
XX SQ Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVNLISVVENLCTVIWTWNPREGASS 59
DB 1 MEMPARLCGLMALLLCAGGGGGGGGAAPTETQPPVNLISVVENLCTVIWTWNPREGASS 60
QY 60 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLQVSGQSTNSEKPSILVEKCISP 119
DB 61 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLQVSGQSTNSEKPSILVEKCISP 120
QY 120 PEGDPSAYATELQCIWHNLSYMKCSWLPGRNTPDNTYLYWHRSLKTHOCENLFRG 179
DB 121 PEGDPSAYATELQCIWHNLSYMKCSWLPGRNTPDNTYLYWHRSLKTHOCENLFRG 180
QY 180 QYFGCSFDLTLYKVDSSFEQHSVQIMWKDAGAKIKPSFNIVPLTSRYKPDPEPHIKNSFHN 239
DB 181 QYFGCSFDLTLYKVDSSFEQHSVQIMWKDAGAKIKPSFNIVPLTSRYKPDPEPHIKNSFHN 240
QY 240 DDLVYQWENPQNFISRLCFYEVEVNNNSQETHNANFYVOEAKCENPEFERNVENTSCFMPV 299
DB 241 DDLVYQWENPQNFISRLCFYEVEVNNNSQETHNANFYVOEAKCENPEFERNVENTSCFMPV 300
QY 300 GVLPTDLNLTVRIRVKTNNKLCYEDDKLMSNMKSQEMSGTKRNSLTLYTMTLLIVPVIAGAI 359
DB 301 GVLPTDLNLTVRIRVKTNNKLCYEDDKLMSNMKSQEMSGTKRNSLTLYTMTLLIVPVIAGAI 360
QY 360 IVLLILYLRKLKIIIFPPIPDGKIFKEMFGDQNDDTLHMKKYDIYEKOTKEEDSVLIE 419
DB 361 IVLLILYLRKLKIIIFPPIPDGKIFKEMFGDQNDDTLHMKKYDIYEKOTKEEDSVLIE 420
QY 420 NTKKASQ 426
DB 420 NTKKASQ 426

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DB 421 NTKKASQ 427

RESULT 5
ADL82843
ID ADL82843 standard; protein; 427 AA.
XX
XX ADL82843;
XX
XX AC ADL82843;
XX
XX DT 17-JUN-2004 (first entry)
XX
XX DE Human PRO2537, SEQ ID 45.
XX
XX KW Immunosuppressive; Cystostatic; Antiarthritic; Antirheumatic; Antianemic;
XX KW Antiallergic; Muscular; Neutroprotective; Nephrotoxic; Antiinflammatory;
XX KW Gene Therapy; PRO; B cell related disorder; cancer;
XX KW immune-mediated inflammatory disease; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004024097-A2.
XX
XX PD 25-MAR-2004.
XX
XX PF 15-SEP-2003; 2003WO-US029097.
XX
XX PR 16-SEP-2002; 2002US-0411392P.
XX
XX PA (GENTH ) GENENTECH INC.
XX
XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
XX PI Wu TD;
XX
XX DR WPI; 2004-329389/30.
XX DR N-PSDB; ADL82842.
XX
XX PT New PRO polypeptide, useful for diagnosing and treating a B cell related
XX PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
XX PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX PS Claim 10; Fig 45; 695bp; English.
XX
XX CC The present invention relates to PRO proteins and their coding sequences.
XX CC The PRO proteins are useful for diagnosing and treating a B cell related
XX CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
XX CC antigen unresponsiveness, selective IgA deficiency, selective IgM
XX CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
XX CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
XX CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX CC myasthenia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
XX CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
XX CC medicament for treating a condition that is responsive to the PRO
XX CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
XX CC coding sequences are useful as hybridization probes in chromosome and
XX CC gene mapping, in preparing PRO proteins, or in generating transgenic
XX CC animals or knockout animals, which in turn are useful in the development
XX CC and screening of therapeutically useful reagents.
XX
XX SQ Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 8; Length 427;
Best Local Similarity 99.8%; Pred. No. 4.7e-211;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVNLISVVENLCTVIWTWNPREGASS 59
DB 1 MEMPARLCGLMALLLCAGGGGGGGGAAPTETQPPVNLISVVENLCTVIWTWNPREGASS 60
QY 60 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLQVSGQSTNSEKPSILVEKCISP 119
DB 61 NCSLWFSHFQKODKKIAPETRRSIEVPLNERICLQVSGQSTNSEKPSILVEKCISP 120

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|    |     |   |     |
|----|-----|---|-----|
| QY | 120 | PEGDESAVTELOQIMHNLSYKCSWLPBRTNSPDTNYTLTYWHRLEKIHOCENIFRFG   | 179 |
| Db | 121 | PEGDESAVTELOQIMHNLSYKCSWLPBRTNSPDTNYTLTYWHRLEKIHOCENIFRFG   | 180 |
| QY | 180 | QYFGCSFDLTAKVXSSFEQHSVOIMWKDAGIKPSFNIVPLTSRYKPDPRHINKLSFHN  | 239 |
| Db | 181 | QYFGCSFDLTAKVXSSFEQHSVOIMWKDAGIKPSFNIVPLTSRYKPDPRHINKLSFHN  | 240 |
| QY | 240 | DDLIVQWENPQNFISRCLEFYEVEVNNNSQTEHNVFVQEAECENPEFERVENTSCFMPV | 299 |
| Db | 241 | DDLIVQWENPQNFISRCLEFYEVEVNNNSQTEHNVFVQEAECENPEFERVENTSCFMPV | 300 |
| QY | 300 | GVLPTLTMTVRIRVXTNKLCEYDDKXLSWMSQMSIGKKRNSTLYTMTLLIYVIVAAGAI | 359 |
| Db | 301 | GVLPTLTMTVRIRVXTNKLCEYDDKXLSWMSQMSIGKKRNSTLYTMTLLIYVIVAAGAI | 360 |
| QY | 360 | IVLLLYLRLKIIIFRPIDPEKIKPREMGDONDOTLHWKKYDIYEKQTEETDSVLLIE   | 419 |
| Db | 361 | IVLLLYLRLKIIIFRPIDPEKIKPREMGDONDOTLHWKKYDIYEKQTEETDSVLLIE   | 420 |
| QY | 420 | NLKRSQ 426  |     |
| Db | 421 | NLKRSQ 427  |     |

|    |  |     |
|----|--|-----|
| QY | MEMPRILGIMALLILCAGGGGGGGG-APETQTPVTNLISVSENLCTVIMWNPREGASS         | 59  |
| Db | 1 MEMPRILGIMALLILCAGGGGGGGGAPEIQTPTVNLISVSENLCTVIMWNPREGASS        | 60  |
| QY | 60 NCSLWYFSHFGBDKODKIKIAPETRRSIEVPLNERICLVQVGSQSTNESEKPSILVEKCIAP  | 119 |
| Db | 61 NCSLWYFSHFGBDKODKIKIAPETRRSIEVPLNERICLVQVGSQSTNESEKPSILVEKCIAP  | 120 |
| QY | 120 PEGDEESAVTELQCIWMHLSYMKCGMLPBRNRSPTNTYLYYWHRSLEKIHOCENIFREG    | 179 |
| Db | 121 PEGDEESAVTELQCIWMHLSYMKCGMLPBRNRSPTNTYLYYWHRSLEKIHOCENIFREG    | 180 |
| QY | 180 QYFGCSFDLTUKKQKSSFEQSHSVQIWMKNAGKIKESFNIVPLTSRYKPDPPHINKLSFHN  | 239 |
| Db | 181 QYFGCSFDLTUKKQKSSFEQSHSVQIWMKNAGKIKESFNIVPLTSRYKPDPPHINKLSFHN  | 240 |
| QY | 240 DDLYIQMENPQNFISRCLEFYEVEVNNSSQTEHTNVFVYQAKCENPEFERNVENTSCFMPVP | 299 |
| Db | 241 DDLYIQMENPQNFISRCLEFYEVEVNNSSQTEHTNVFVYQAKCENPEFERNVENTSCFMPVP | 300 |
| QY | 300 GVLPTLTVTRVRYVTNKLCTCEDDKLMSWQSQEMSIGKGRNSTLYYTMLLIVPVIYAAGAI  | 359 |
| Db | 301 GVLPTLTVTRVRYVTNKLCTCEDDKLMSWQSQEMSIGKGRNSTLYYTMLLIVPVIYAAGAI  | 360 |
| QY | 360 IVLLIYLKRLKIIIFPPIPDPEKIKFKEMFGDONDDTLHWKKYDIYEKQTEETDSVYLIE   | 419 |
| Db | 361 IVLLIYLKRLKIIIFPPIPDPEKIKFKEMFGDONDDTLHWKKYDIYEKQTEETDSVYLIE   | 420 |
| QY | 420 NLKKRASQ 426   |     |
| Db | 421 NLKKRASQ 427   |     |

DR WPI; 2004-409324/38.  
DR N-PSDB; ADN62574.  
XX  
PT New isolated nucleic acid molecule encoding a polypeptide capable of  
PT binding human IL-13 and/or binding human IL-4, useful in medicine, in  
PT diagnostics or for producing antibodies.  
XX  
PS Claim 1; SEQ ID NO 9; 24pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (ADN62574),  
CC which encodes the mature form of a polypeptide capable of binding human  
CC IL-13 (interleukin 13, a cytokine) and/or binding human IL-4 (designated  
CC IL-13 receptor alpha 1 subunit) appearing as ADN62575. Also included are  
CC a vector comprising the nucleic acid molecule and a host cell comprising  
CC the vector. The nucleic acids are useful as probes or primers or in the  
CC analysis of allelic variation. The polypeptides are useful for binding  
CC human IL-13 and/or binding human IL-4 and act as inhibitors by  
CC interfering with the interaction between human IL-13 or IL-4 and their  
CC natural receptors. They can also be used in medicine, e.g. for treatment  
CC of diseases such as atopy, atopic dermatitis, allergy, rhinitis, eczema,  
CC asthma, AIDS, cancer, inflammatory disease (e.g. rheumatoid arthritis and  
CC inflammatory bowel disease), multiple sclerosis, Alzheimer's disease,  
CC lupus erythematosus, thyroiditis, diabetes, uveitis, psoriasis,  
CC urticaria, nephrotic syndrome, glomerulonephritis, ulcerative colitis,  
CC Crohn's disease, Sjogren's syndrome, toxoplasmosis, listeriosis, leprosy,  
CC Lyme disease, tuberculosis, malaria and leishmaniasis. They can also be  
CC used for producing antibodies, which can be used for diagnosing diseases.  
CC The present sequence represents IL-13 receptor alpha 1 subunit.  
XX  
XX  
SQ Sequence 427 AA;  
Query Match 99.5%; Score 2309.5; DB 8; Length 427;  
Best Local Similarity 99.8%; Pred. No. 4.7e-211;  
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MEMPARLCGLMALLCAGGGGGGGG-APTETOPPVNTLSVSVENLCVITWNNPPRGASS 59  
DB 1 MEMPARLCGLMALLCAGGGGGGGGGAAPTETOPPVNTLSVSVENLCVITWNNPPRGASS 60  
QY 60 NCSLWYFSHFGRKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 119  
DB 61 NCSLWYFSHFGRKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 120  
QY 120 PGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLEKIHOCENIFREG 179  
DB 121 PGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLEKIHOCENIFREG 180  
QY 180 QYFGCSFDLTXYKDSFEGHSVOIMKDNAGKIKPSFNIVPLTSRYKDPDPHAIKNLSFHN 239  
DB 181 QYFGCSFDLTXYKDSFEGHSVOIMKDNAGKIKPSFNIVPLTSRYKDPDPHAIKNLSFHN 240  
QY 240 DDLVYOMENPONFISRCLEFYEVEVNNISQETTHNVFVQAEKCNPEREVENVENTSCFMP 299  
DB 241 DDLVYOMENPONFISRCLEFYEVEVNNISQETTHNVFVQAEKCNPEREVENVENTSCFMP 300  
QY 300 GVLPTLNTVTRIRVKTNKLCEYEDDKLMSWNSQEMSIGKKNSTLYITMLIIVIVAGAI 359  
DB 301 GVLPTLNTVTRIRVKTNKLCEYEDDKLMSWNSQEMSIGKKNSTLYITMLIIVIVAGAI 360  
QY 360 IVLLVLRKLTIIIPPIPDGKIFKEMRGDQNDPTLHMKKXIVYERKQTEERTDSVLLIE 419  
DB 361 IVLLVLRKLTIIIPPIPDGKIFKEMRGDQNDPTLHMKKXIVYERKQTEERTDSVLLIE 420  
QY 420 NLKASQ 426  
DB 421 NLKASQ 427  
RESULT 8  
ABM82441  
ID ABM82441 standard; protein; 427 AA.  
XX  
AC ABM82441;

XX 18-NOV-2004 (first entry)  
XX  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2537, SEQ:6271.  
XX  
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic.  
XX  
OS Homo sapiens.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
XX  
XX 29-SEP-2003; 2003MO-US028547.  
PF 02-OCT-2002; 2002US-0414971P.  
XX  
PA (GENTH ) GENTENTECH INC.  
XX  
PI Wu TD, Zhang Z, Zhou Y;  
XX  
DR WPI; 2004-347921/32.  
DR N-PSDB; ACN41073.  
XX  
PT New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.  
XX  
PS Claim 12; SEQ ID NO 6271; 7273pp; English.  
XX  
CC The invention relates to human tumour-associated antigenic target (TAT)  
CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention  
XX  
SQ Sequence 427 AA;  
Query Match 99.5%; Score 2309.5; DB 8; Length 427;  
Best Local Similarity 99.8%; Pred. No. 4.7e-211;  
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MEMPARLCGLMALLCAGGGGGGGG-APTETOPPVNTLSVSVENLCVITWNNPPRGASS 59  
DB 1 MEMPARLCGLMALLCAGGGGGGGGGAAPTETOPPVNTLSVSVENLCVITWNNPPRGASS 60  
QY 60 NCSLWYFSHFGRKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 119  
DB 61 NCSLWYFSHFGRKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 120  
QY 120 PGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDTNVTLYYHRSLEKIHOCENIFREG 179

Db 121 PEEDPSAVTELOCIMHNLSYMKCSWLPGRNTSPDITVTLTYWHRSLKTHQENIFREG 180  
 QY 180 QYFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239  
 Db 181 QYFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240  
 QY 240 DDLYVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYQAKCENPEFERVENTSCMPV 299  
 Db 241 DDLYVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYQAKCENPEFERVENTSCMPV 300  
 QY 300 GVLPTLNTVIRIRKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYTMTLLIVPIVAGAI 359  
 Db 301 GVLPTLNTVIRIRKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYTMTLLIVPIVAGAI 360  
 QY 360 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDSVLLIE 419  
 Db 361 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDSVLLIE 420  
 QY 420 NLKKAQ 426  
 Db 421 NLKKAQ 427

RESULT 9  
 AEC31473  
 ID AEC31473 standard; protein; 427 AA.  
 XX  
 AEC31473;

DT 03-NOV-2005 (first entry)  
 XX  
 DE Human IL-13 receptor alpha-1 SEQ ID NO:3.

XX interleukin-13 receptor; fusion protein; therapeutic; antisthmatic;  
 KM anti-allergic; dermatological; anti-inflammatory; immunosuppressive;  
 KM cytotoxic; hepatotropic; anti-HIV; virucide; gastrointestinal-gen;  
 KM antihistaminic; fungicide; antiparasitic; antitumor; antithyroid;  
 KM nephrotropic.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT Domain 27..343  
 FT /label = extracellular domain

PN US2005191730-A1.

XX 01-SEP-2005.

PF 25-FEB-2005; 2005US-00067251.

PR 27-FEB-2004; 2004US-0548541P.

PR 17-AUG-2004; 2004US-0602139P.

PR 16-NOV-2004; 2004US-0628343P.

XX (REG- ) REGENERON PHARM INC.

PI Karow M, Fairhurst J;

DR WPI; 2005-590777/60.

XX New nucleic acid molecules encoding polypeptides capable of binding  
 PT interleukin-4 and interleukin-13, useful for diagnosing and/or treating  
 PT asthma, lupus, Grave's disease, hepatic fibrosis, HIV infection, cancer  
 PT and infections.

XX Claim 1; SEQ ID NO 3; 35pp; English.

XX The invention relates to a novel nucleic acid molecule encoding a fusion  
 CC polypeptide. The fusion polypeptide consists (R1)-(R2)-Y-F, where R1 is 1  
 CC -231 and 24-231 of a fully defined sequence of 231 amino acids  
 CC (AEC31472), which sequences may comprise 1-10 modifications, R2 is a

CC fully defined sequence of 427 or 380 bp (AEC31473+AEC31474), which  
 CC sequences may comprise one to three modifications. F is a fusion  
 CC component, and x and y are each independently a positive integer 1. The F  
 CC is a multimerizing component, a serum protein, or a molecule capable of  
 CC binding a serum protein, where the multimerizing component is an  
 CC immunoglobulin-derived domain, a cleavable region (C-region), an amino  
 CC acid sequence between 1-500 amino acids in length, optionally comprising  
 CC at least one cysteine residue, a leucine zipper, a helix loop motif, or a  
 CC coil-coil motif. The immunoglobulin-derived domain is the Fc domain of  
 CC IgG or the heavy chain of IgG. A fusion protein of the invention has  
 CC antisthmatic, anti-allergic, dermatological, anti-inflammatory,  
 CC immunosuppressive, cytotoxic, hepatotropic, anti-HIV, virucide,  
 CC gastrointestinal-gen, antibacterial, fungicide, antiparasitic, antitumor,  
 CC antithyroid, and nephrotropic activity. The protein has a use in gene  
 CC therapy, and acts as an interleukin-antagonist. The methods and  
 CC compositions of the invention are useful for the diagnosis, prevention  
 CC and/or treatment of diseases or conditions associated with aberrant  
 CC expression or activity of IL-4 and/or IL-13, such as asthma, atopic  
 CC dermatitis, lupus, nephritis, Grave's disease, hepatic fibrosis, HIV  
 CC infection, ulcerative colitis, cancer, and viral, parasitic, bacterial  
 CC and fungal infections. The present sequence represents human IL-13  
 CC receptor alpha-1.

XX Sequence 427 AA;

Query Match 99.5%; Score 2309.5; DB 9; Length 427;  
 Best Local Similarity 99.8%; Pred. No. 4.7e-211;  
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARICGLMALLLCAGGGGGGGG-APTETOPVNTLSVSVENLCVITWNPPEGASS 59  
 Db 1 MEMPARICGLMALLLCAGGGGGGGGAPETQPPVNTLSVSVENLCVITWNPPEGASS 60

QY 60 NCSLWTFSHRGDKQDKKIAETRRSIFVPLNERICLOVSGQCSSTNESEKSIIVEKICIS 119  
 Db 61 NCSLWTFSHRGDKQDKKIAETRRSIEVPLNERICLOVSGQCSSTNESEKSIIVEKICIS 120

QY 120 PEEDPSAVTELOCIMHNLSYMKCSWLPGRNTSPDITVTLTYWHRSLKTHQENIFREG 179  
 Db 121 PEEDPSAVTELOCIMHNLSYMKCSWLPGRNTSPDITVTLTYWHRSLKTHQENIFREG 180

QY 180 QYFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 239  
 Db 181 QYFGCSFDLTKVXDSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKPDPPHINKLSFHN 240

QY 240 DDLYVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYQAKCENPEFERVENTSCMPV 299  
 Db 241 DDLYVQWENPQNFISRCIFYEVEVNNQSOTETHNVFYQAKCENPEFERVENTSCMPV 300

QY 300 GVLPTLNTVIRIRKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYTMTLLIVPIVAGAI 359  
 Db 301 GVLPTLNTVIRIRKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYTMTLLIVPIVAGAI 360

QY 360 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDSVLLIE 419  
 Db 361 IVLLLYLKRLLKIIFFPIPDGKIFKEMFGDQNDTLHMKKYDIYERQTEEDSVLLIE 420

QY 420 NLKKAQ 426  
 Db 421 NLKKAQ 427

RESULT 10  
 AEE93788  
 ID AEE93788 standard; protein; 427 AA.

XX AEE93788;

XX 23-FEB-2006 (first entry)

XX Human interleukin-13 alpha receptor.

XX Monoclonal antibody; IL-13 alpha receptor; cytokine;

|    |   |
|----|---|
| KW | protein;co-ordinate data; protein structure; crystallography;               |
| KW | Anticardiac; Antiallergic; Cytostatic; Respiratory-Gen.;                    |
| KW | Antiinflammatory; Immunosuppressive; Dermatological;                        |
| KW | Gastrointestinal-Gen.; Vasostrictic; CNS-Gen.; Hepatotropic; asthma;        |
| KW | cancer; eosinophilia; fibrosis; inflammation; autoimmune disease;           |
| KW | chronic obstructive pulmonary disease; cystic fibrosis;                     |
| KW | pulmonary fibrosis; allergic rhinitis; atopic dermatitis;                   |
| KW | inflammatory bowel disease; Crohns disease; cirrhosis; scleroderma;         |
| KW | Hodgkins disease.   |
| XX |   |
| XX | Homo sapiens.   |
| XX |   |
| FT | Key   |
| FT | Binding-site  |
| FT | 76  |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 77  |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 78  |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 79  |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 254   |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 255   |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 256   |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 318   |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 320   |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| FT | 321   |
| FT | /note= "Residue interacting with IL-13, specifically                        |
| FT | claimed in claim 61"  |
| XX |   |
| XX | WO2005121177-A2.  |
| XX |   |
| PD | 22-DEC-2005.  |
| XX |   |
| PF | 09-JUN-2005; 2005WO-US020334.   |
| XX |   |
| XX | 09-JUN-2004; 2004US-0578473P.   |
| PR | 09-JUN-2004; 2004US-0578736P.   |
| PR | 22-JUN-2004; 2004US-0581375P.   |
| XX |   |
| PA | (AMHP ) WYETH.  |
| XX |   |
| XX | Lin IL, Parris KD, Tam ASP, Tan X, Shane T, Wilhelm CW,                     |
| PI | Stahl M, Mosyak L, Hu Z;  |
| XX |   |
| XX | WPI; 2006-067089/07.  |
| DR | SWISSPROT; P78552.  |
| XX |   |
| XX | Crystalaline antibody useful for designing agent that interacts with IL-13  |
| PT | polypeptide, comprises anti-IL-13 antibody capable of binding site of IL-13 |
| PT | 13 polypeptide to which IL-4R polypeptide binds in vivo.                    |
| XX |   |
| PS | Claim 58; SEQ ID NO 12; 318pp; English.                                     |
| CC |   |
| CC | The invention relates to a crystalaline antibody (I), where the antibody    |
| CC | comprises an anti-interleukin (IL)-13 antibody or its Fab fragment, and     |
| CC | is capable of binding a site of an IL-13 polypeptide to which an IL-4R      |
| CC | (interleukin-4 receptor) polypeptide binds in vivo. Also included are a     |
| CC | crystalline composition/complexes that comprises an antibody (where the     |

| Query Match           | 99.5%   | Score 2309.5   | DB 10    | Length 427 |
|-----------------------|---|--|----------|------------|
| Best Local Similarity | 99.8%   | Pred. No. 4.7e-211   |          |            |
| Matches 426           | Conservative 0  | Mismatches 0   | Indels 1 | Gaps 1     |
| QY                    | 1   | MEMPARLCGMALLLCAGGGGGGGG-APTETOPVTNLVSVENLCYIMTMNPEGASS          | 59       |            |
| Db                    | 1   | MEMPARLCGMALLLCAGGGGGGGGAAPTETOPVTNLVSVENLCYIMTMNPEGASS          | 60       |            |
| QY                    | 60  | NCSLMYFSPHDKODKKAIPETRRSIEVPLNERICLCQVSGCSTNSESKEPSILVEKCTSP     | 119      |            |
| Db                    | 61  | NCSLMYFSPHDKODKKAIPETRRSIEVPLNERICLCQVSGCSTNSESKEPSILVEKCTSP     | 120      |            |
| QY                    | 120   | PEGDESAVTELOCIMHNL SYMKCSWLPGRNTSPDNTYLLYMRSLSEKIHQCENIPREG      | 179      |            |
| Db                    | 121   | PEGDESAVTELOCIMHNL SYMKCSWLPGRNTSPDNTYLLYMRSLSEKIHQCENIPREG      | 180      |            |
| QY                    | 180   | QYFGCSPLUTKYKXSSPFQHSVOQLMYKDNACKIKPSFNIVPLTSRYKDPHILKXLSFHN     | 239      |            |
| Db                    | 181   | QYFGCSPLUTKYKXSSPFQHSVOQLMYKDNACKIKPSFNIVPLTSRYKDPHILKXLSFHN     | 240      |            |
| QY                    | 240   | DDL YQWQNPONPFI SRCLFYEVEVNNSSOTETGHNFYVOEACENDEPERFENENTS CFNVP | 299      |            |
| Db                    | 241   | DDL YQWQNPONPFI SRCLFYEVEVNNSSOTETGHNFYVOEACENDEPERFENENTS CFNVP | 300      |            |
| QY                    | 300   | GVLDPDLTNTVIRVKTNKL CYEDDKLXSNMSQEMSIGKRNSLTYITMLLI VPIVAGAI     | 359      |            |
| Db                    | 301   | GVLDPDLTNTVIRVKTNKL CYEDDKLXSNMSQEMSIGKRNSLTYITMLLI VPIVAGAI     | 360      |            |
| QY                    | 360   | IVLLIYLRKLIKIIFPPPI PDPGKIFKEMFGQONDTLHWKKYDIYEKOTKSEETSVLIE     | 419      |            |
| Db                    | 361   | IVLLIYLRKLIKIIFPPPI PDPGKIFKEMFGQONDTLHWKKYDIYEKOTKSEETSVLIE     | 420      |            |
| QY                    | 420   | NLKKRASQ 426   |          |            |
| Db                    | 421   | NLKKRASQ 427   |          |            |
| RESULT 11             |   |  |          |            |
| AEF57817              |   |  |          |            |
| ID                    | AEF57817 standard; protein; 427 AA.                                 |  |          |            |
| XX                    | AEF57817;   |  |          |            |
| XX                    | 23-MAR-2006 (first entry)   |  |          |            |
| DT                    | Anti-IL-13 antibody associated polypeptide SEQ ID NO 37.            |  |          |            |
| XX                    | antiasthmatic; dermatological; respiratory-gen.; immunosuppressive; |  |          |            |



KM antiinflammatory; cytostatic; virucide; antiallergic;  
 KM gastrointestinal-gen.; vaccine; antibody; diagnosis; therapeutic; asthma;  
 KM antisthmatic; chronic obstructive pulmonary disease; respiratory-gen.;  
 KM infection; viral infection; virucide; autoimmune disorder;  
 KM immunosuppressive; immune disorder; inflammatory bowel disease;  
 KM antiinflammatory; gastrointestinal-gen.; gastrointestinal disease;  
 KM inflammation; allergic rhinitis; antiallergic; ear, nose, throat disease;  
 KM immune disorder; respiratory disease.  
 XX Homo sapiens.  
 OS  
 XX  
 XX MO2005123126-A2.  
 PD  
 XX 29-DEC-2005.  
 XX  
 XX 09-JUN-2005; 2005MO-US020160.  
 XX  
 XX 09-JUN-2004; 2004US-0578473P.  
 PR 09-JUN-2004; 2004US-0578736P.  
 PR 22-JUN-2004; 2004US-0581375P.  
 XX  
 XX (AMHP ) WYETH.  
 XX  
 XX Kasajan MT, Tchistiakova L, Veldman GM, Marquette KA, Tan X;  
 PI Donaldson DP, Lin LL, Shane T, Tam AS, Feyfant E, Wood NL, Fitz LJ;  
 PI Wadon AM, Parris KD, Goldman SJ;  
 XX  
 XX WPI; 2006-172770/18.  
 XX  
 XX New antibody against human interleukin-13, useful for diagnosing,  
 PT preventing, and/or treating a disorder, e.g. asthma, tumors, allergic  
 PT rhinitis, or inflammatory bowel disease.  
 XX  
 PS Disclosure; SEQ ID NO 37; 169pp; English.  
 XX  
 XX The invention describes an antibody, or its antigen-binding, that binds  
 CC to interleukin (IL)-13. Also described are: a pharmaceutical composition  
 CC comprising the antibody, or its antigen-binding fragment above and a  
 CC pharmaceutical carrier; a nucleic acid that comprises a sequence that  
 CC encodes a polypeptide that comprises a heavy chain immunoglobulin  
 CC variable region or a light chain immunoglobulin variable region described  
 CC above; a host cell comprising a nucleic acid sequence that encodes the  
 CC antibody, or its antigen-binding fragment, above; providing a recombinant  
 CC antibody; treating an IL-13-associated disorder; and detecting the  
 CC presence of IL-13 in a sample. The antibody, composition, and method are  
 CC useful for diagnosing, preventing, and/or treating IL-13 associated  
 CC disorder, e.g. asthmatic disorders, atopic disorders, chronic obstructive  
 CC pulmonary disease (COPD), conditions involving airway inflammation,  
 CC eosinophilia, fibrosis and excess mucus production, inflammatory  
 CC conditions, autoimmune conditions, tumors or cancers, viral infection,  
 CC suppression of expression of protective type 1 immune responses, allergic  
 CC rhinitis, or inflammatory bowel disease. This is the amino acid sequence  
 CC of a polypeptide associated with anti-IL-13-antibodies of the invention.  
 XX  
 SQ Sequence 427 AA:  
 Query Match 99.5%; Score 2309.5; DB 10; Length 427;  
 Best Local Similarity 99.8%; Pred. No. 4,7e-211;  
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 MEMPARLCGLMALLCAGGGGGGGG-APTETOPVTNLVSVERNLCTVITWMPPEGASS 59  
 Db 1 MEMPARLCGLMALLCAGGGGGGGGAPTETOPVTNLVSVERNLCTVITWMPPEGASS 60  
 QY 60 NCSLWTFSHFGDQKXIAPETRRSIVPINERICLOVSGQCSSTNESEKSPILVEKCI 119  
 Db 61 NCSLWTFSHFGDQKXIAPETRRSIVPINERICLOVSGQCSSTNESEKSPILVEKCI 120  
 QY 120 PEGDPSAATVETLCCIMHNTLSYMKCSMLPGNTSPDNTVYTYWHRSLKTHOCENIFREG 179  
 Db 121 PEGDPSAATVETLCCIMHNTLSYMKCSMLPGNTSPDNTVYTYWHRSLKTHOCENIFREG 180  
 QY 180 QYFGCSFDLTAKVDSFEQHSVOIMVKNAGKIKPSFNIIVPLTSRVKPDPPHIKNLSFHN 239

Db 181 QYFGCSFDLTAKVDSFEQHSVOIMVKNAGKIKPSFNIIVPLTSRVKPDPPHIKNLSFHN 240  
 QY 240 DDLYVQWENQNFISRLCFEVEVNNQSTETHANVFYQVAKCENPEPRNVENTNSCFVNP 299  
 Db 241 DDLYVQWENQNFISRLCFEVEVNNQSTETHANVFYQVAKCENPEPRNVENTNSCFVNP 300  
 QY 300 GVLPTDINTVIRIKTNKLCYEDDKLMSNMQSEMSIGKKNSTLYITMLLIVPIVAGAI 359  
 Db 301 GVLPTDINTVIRIKTNKLCYEDDKLMSNMQSEMSIGKKNSTLYITMLLIVPIVAGAI 360  
 QY 360 IVLLLYKRLKIIFPPIPPGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLIE 419  
 Db 361 IVLLLYKRLKIIFPPIPPGKIFKEMFGDQNDTLHMKKYDIYEKQTEEDSVLIE 420  
 QY 420 NLKKASQ 426  
 Db 421 NLKKASQ 427  
 RESULT 12  
 ADL71813  
 ID ADL71813 standard; protein; 427 AA.  
 AC  
 AC ADL71813;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, T130I.  
 XX  
 KM Human, IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;  
 KM eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;  
 KM mutcin.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 130 /note="Wild-type Thr is substituted with Ile"  
 FT  
 XX US2004043921-A1.  
 PN  
 XX 04-MAR-2004.  
 PD  
 XX 29-SEP-2003; 2003US-00671697.  
 PF  
 XX 13-DEC-1996; 96GB-00025899.  
 PR 12-NOV-1997; 97US-00969125.  
 PR 06-APR-2000; 2000US-00545002.  
 XX  
 XX (BONN/) BONNEFOY J.  
 PA (GAUC/) GAUCHAT J.  
 PA  
 XX  
 PI Bonnefoy J, Gauchat J;  
 DR WPI; 2004-225726/21.  
 XX  
 XX Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse  
 PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma  
 PT or AIDS, comprises administering a polypeptide or soluble polypeptide.  
 PT  
 XX Claim 14; Page; 27pp; English.  
 PS  
 XX The invention relates to polypeptides capable of binding human  
 CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The  
 CC invention also relates to a method of treatment of a disease in which a  
 CC IL13 and IL4 cause adverse effects. The method is useful for treating a  
 CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic  
 CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides  
 CC of the invention are useful in raising antibodies. It is also useful in  
 CC gene therapy. The present sequence is human interleukin-13 receptor alpha  
 CC (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the

CC specification, however it is constructed based on human IL-13 Ralpha  
CC protein shown as SEQ ID NO:9 in the specification.

XX  
XX  
SQ Sequence 427 AA;

Query Match 99.3%; Score 2303.5; DB 8; Length 427;  
Best Local Similarity 99.5%; Pred. No. 1,7e-210;  
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
OY 1 MEMPARLCGLMALLLCAGGGGGGGG--APTETOPVTNLSVSVNLCVITWTNMPBGASS 59
   |||||
DB 1 MEMPARLCGLMALLLCAGGGGGGGGGAAPTETOPVTNLSVSVNLCVITWTNMPBGASS 60
   |||||
OY 60 NCSLWYFSHFGDKQDKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 119
   |||||
DB 61 NCSLWYFSHFGDKQDKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 120
   |||||
OY 120 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYWHRSLKTHOCENIFREG 179
   |||||
DB 121 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYWHRSLKTHOCENIFREG 180
   |||||
OY 180 OYFGCSFDLTKVDSFEQHSVOIMVKDNAGTKPSFNIVPLTSRYKPPDPHINKLSFHN 239
   |||||
DB 181 OYFGCSFDLTKVDSFEQHSVOIMVKDNAGTKPSFNIVPLTSRYKPPDPHINKLSFHN 240
   |||||
OY 240 DDLVYQWENPQNFISRCLFYEVEVNNSSQETETNHFVYQEAKECNPEFERNVENTSCFMVP 239
   |||||
DB 241 DDLVYQWENPQNFISRCLFYEVEVNNSSQETETNHFVYQEAKECNPEFERNVENTSCFMVP 300
   |||||
OY 300 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYITMLIIVPIVAGAI 359
   |||||
DB 301 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYITMLIIVPIVAGAI 360
   |||||
OY 360 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLIE 419
   |||||
DB 361 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLIE 420
   |||||
OY 420 NLKKAQ 426
   |||||
DB 421 NLKKAQ 427
```

RESULT 13  
ADL71835  
ID ADL71835 standard; protein; 427 AA.

XX  
XX  
AC ADL71835;

DT 12-FEB-2004 (first entry)

DE Human IL-13 alpha 1 receptor (IL-13R) protein.

XX  
XX  
KW IL-13R; human; receptor; anaphylaxis; hay fever; asthma;  
KW antiinflammatory; cyostatic; antitumor; dermatological; antiasthmatic;  
KW antitumor; fibrosis; Hodgkin's disease; ulcerative colitis;  
KW scleroderma; allergic rhinitis; oncological;  
KW chronic obstructive pulmonary disease.

OS Homo sapiens.

PN WO2003080675-A2.

PD 02-OCT-2003.

PF 21-MAR-2003; 2003WO-AU000352.

PR 22-MAR-2002; 2002AU-00001301.

PR 03-FEB-2003; 2003AU-00900437.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

PA Dunlop FM, Baca M, Nash AD, Fabri LJ;

XX

DR WPI; 2003-876912/81.  
DR N-PSDB; ADL71834.

XX  
XX  
PT New monoclonal antibodies against interleukin-13 receptor alpha, useful  
PT for treating fibrosis, Hodgkin's disease, ulcerative colitis,  
PT scleroderma, allergic rhinitis, oncological conditions, asthma or an  
PT inflammatory disorder.

PS Disclosure; SEQ ID NO 4; 99pp; English.

CC This invention relates to a novel antibodies that function as interleukin  
CC -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used  
CC for treating certain conditions induced by IL-13. Specifically, it refers  
CC to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13  
CC and IL-4 induced signaling. IL-13 is a mediator in the immunostimulatory  
CC system, such that it is involved in the induction of IgE, IgG4 and T-  
CC helper cells and accordingly is implicated in conditions from anaphylaxis  
CC to hay fever and asthma. As such, the present invention describes these  
CC novel antibodies as antiinflammatory, cyostatic, antitumor,  
CC dermatological, antiallergic and antiasthmatic. The methods and  
CC compositions are useful for treating various disorders including  
CC fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic  
CC rhinitis, oncological conditions and chronic obstructive pulmonary  
CC disease. This polypeptide sequence is the human IL-13 alpha 1 receptor  
CC protein of the invention.

XX  
SQ Sequence 427 AA;

Query Match 99.2%; Score 2302.5; DB 7; Length 427;  
Best Local Similarity 99.5%; Pred. No. 2,2e-210;  
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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OY 1 MEMPARLCGLMALLLCAGGGGGGGG--APTETOPVTNLSVSVNLCVITWTNMPBGASS 59
   |||||
DB 1 MEMPARLCGLMALLLCAGGGGGGGGGAAPTETOPVTNLSVSVNLCVITWTNMPBGASS 60
   |||||
OY 60 NCSLWYFSHFGDKQDKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 119
   |||||
DB 61 NCSLWYFSHFGDKQDKKIAETRRSIEVPLNERICLQVGSQCSTNSEKRSILVEKCISP 120
   |||||
OY 120 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYWHRSLKTHOCENIFREG 179
   |||||
DB 121 PEGDPSAATTELQCTIWHNLSYMKCSWLPGRNTSPDNTNLTLYWHRSLKTHOCENIFREG 180
   |||||
OY 180 OYFGCSFDLTKVDSFEQHSVOIMVKDNAGTKPSFNIVPLTSRYKPPDPHINKLSFHN 239
   |||||
DB 181 OYFGCSFDLTKVDSFEQHSVOIMVKDNAGTKPSFNIVPLTSRYKPPDPHINKLSFHN 240
   |||||
OY 240 DDLVYQWENPQNFISRCLFYEVEVNNSSQETETNHFVYQEAKECNPEFERNVENTSCFMVP 239
   |||||
DB 241 DDLVYQWENPQNFISRCLFYEVEVNNSSQETETNHFVYQEAKECNPEFERNVENTSCFMVP 300
   |||||
OY 300 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYITMLIIVPIVAGAI 359
   |||||
DB 301 GVLPDTLNTVIRIRVKTNKLCEYDDKLSWNSQEMSIGKGRNSTLYITMLIIVPIVAGAI 360
   |||||
OY 360 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLIE 419
   |||||
DB 361 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQNDTLHMKKYDIYEKQTEETDSVLLIE 420
   |||||
OY 420 NLKKAQ 426
   |||||
DB 421 NLKKAQ 427
```

RESULT 14  
ADL71814  
ID ADL71814 standard; protein; 427 AA.

XX ADL71814;

DT 20-MAY-2004 (first entry)

XX

DE Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.  
 KW Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;  
 KW eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;  
 KW mutant.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 358 /note= "Wild-type Gly is substituted with Asp"  
 XX  
 XX US2004043921-A1.  
 XX  
 XX 04-MAR-2004.  
 XX  
 XX 29-SEP-2003; 2003US-00671697.  
 XX  
 XX 13-DEC-1996; 96GB-00025899.  
 PR 12-NOV-1997; 97US-00969125.  
 PR 06-APR-2000; 2000US-00545002.  
 XX  
 XX (BONN/) BONNEFOY J.  
 PA (GAUC/) GAUCHAT J.  
 XX  
 XX Bonnefoy J, Gauchat J;  
 DR WPI; 2004-225726/21.  
 XX  
 PT Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse  
 PT effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma  
 PT or AIDS, comprises administering a polypeptide or soluble polypeptide.  
 XX  
 PS Claim 14; Page; 27pp; English.  
 XX  
 CC The invention relates to polypeptides capable of binding human  
 CC interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The  
 CC invention also relates to a method of treatment of a disease in which  
 CC IL13 and IL4 cause adverse effects. The method is useful for treating a  
 CC disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic  
 CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides  
 CC of the invention are useful in raising antibodies. It is also useful in  
 CC gene therapy. The present sequence is human interleukin-13 receptor alpha  
 CC (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the  
 CC specification, however it is constructed based on human IL-13 Ralpha  
 CC protein shown as SEQ ID NO:9 in the specification.  
 CC  
 SQ Sequence 427 AA;

Query Match 99.2%; Score 2302.5; DB 8; Length 427;  
 Best Local Similarity 99.5%; Pred. No. 2.2e-210;  
 Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MEMPARLCGIMALLLCAGGGGGGGG-APTETOPVTNLSVSNLCVITWNPPEGASS 59  
 DB 1 MEMPARLCGIMALLLCAGGGGGGGGAAPTETOPVTNLSVSNLCVITWNPPEGASS 60  
 QY 60 NCSLMWFSHFGDKQDKKIAPETRRSTIEVPLNERICLOVSGQSTNSEKPSIIVEKCISP 119  
 DB 61 NCSLMWFSHFGDKQDKKIAPETRRSTIEVPLNERICLOVSGQSTNSEKPSIIVEKCISP 120  
 QY 120 PEGDPESAATVTELOCIMHNLSTYKCSMLPGRNTSPDNTLYYHRSLEKIHOCENIFREG 179  
 DB 121 PEGDPESAATVTELOCIMHNLSTYKCSMLPGRNTSPDNTLYYHRSLEKIHOCENIFREG 180  
 QY 180 QYFGCSFDLTKVDSFEGHSVQIMVKNAGKIKPSFNIVLTSRYKPPPHIKNLSFHN 239  
 DB 181 QYFGCSFDLTKVDSFEGHSVQIMVKNAGKIKPSFNIVLTSRYKPPPHIKNLSFHN 240  
 QY 240 DDLVYQWENPONTISCLFYEVEVNNSTQETHNVFYQAKCENPERERVNTSCFMPV 299  
 DB 241 DDLVYQWENPONTISCLFYEVEVNNSTQETHNVFYQAKCENPERERVNTSCFMPV 300

QY 300 GVLPDITNTVRIKYNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLIIVPIVAGAI 359  
 DB 301 GVLPDITNTVRIKYNKLCEYEDDKLMSNMSQEMSIGKRNSTLYITMLIIVPIVADAI 360  
 QY 360 IVLLLYKRLKIIIFPIPPGKIFKEMFGDQNDTLHWKKYDIYEKQTEKETSVDLIE 419  
 DB 361 IVLLLYKRLKIIIFPIPPGKIFKEMFGDQNDTLHWKKYDIYEKQTEKETSVDLIE 420  
 QY 420 NLKRSQ 426  
 DB 421 NLKRSQ 427

RESULT 15  
 AAB19808  
 ID AAB19808 standard; protein; 427 AA.  
 XX  
 XX AAB19808;  
 AC  
 XX  
 XX 05-MAR-2001 (first entry)  
 DT  
 XX  
 XX Human interleukin-13 receptor alpha-1 variant.  
 DE  
 XX  
 KW Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;  
 KW atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;  
 KW dermatological; antiasthmatic; antiallergic; therapy; diagnosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT FH  
 FT Peptide 1..26  
 FT /label= Sig\_peptide  
 FT Domain 27..347  
 FT /label= Extracellular\_domain  
 FT Protein 28..427  
 FT /label= Mature\_protein  
 FT Misc-difference 130  
 FT /note= "Gly in "  
 FT Peptide 327..331  
 FT /note= "MSXMS motif conserved in the type-I cytokine  
 FT receptor superfamily"  
 FT Domain 348..367  
 FT /label= Transmembrane\_domain  
 FT Domain 368..427  
 FT /label= Cytoplasmic\_domain  
 FT Binding-site 405..408  
 FT /note= "YXXQ motif, consensus for STAT binding"  
 FT  
 XX  
 PN US6143871-A.  
 XX  
 PD 07-NOV-2000.  
 XX  
 XX 12-NOV-1997; 97US-00969125.  
 PF  
 PR 13-DEC-1996; 96GB-00025899.  
 XX  
 XX (GAUC/) GAUCHAT J.  
 PA (BONN/) BONNEFOY J.  
 XX  
 XX Gauchat J, Bonnefoy J;  
 PI  
 XX  
 DR WPI; 2001-006445/01.  
 XX  
 XX Novel polypeptide capable of binding interleukin-13 or interleukin-4  
 PT useful for treating atopy, atopic dermatitis, allergies, rhinitis,  
 PT eczema, asthma or AIDS.  
 PT  
 XX  
 PS Claim 4; -: 26pp; English.  
 XX  
 CC The present sequence is that of a claimed isolated polypeptide which is  
 CC capable of binding human interleukin-13 (IL-13) and/or human interleukin-  
 CC 4 (IL-4) in the presence of IL-4 receptor alpha. It differs from a

CC sequence (see AAB19807) deduced from isolated cDNA by having residue 130  
 CC as Ile rather than Thr and residue 358 as Asp rather than Gly. This IL-13  
 CC receptor alpha-1 polypeptides can be used to inhibit IL-13 or IL-4  
 CC induced IgE synthesis in B cells, useful in the treatment of diseases in  
 CC which IgE or Th2 differentiation plays a role, e.g. atopy, atopic  
 CC dermatitis, allergy, rhinitis, eczema, asthma or AIDS. Antibodies raised  
 CC against the polypeptide are useful for detecting IL-13 and IL-4 receptor  
 CC or parts of them which have been shed from cells as a result of disease,  
 CC e.g. cancer, leukaemia, atopy, atopic dermatitis, allergies, rhinitis,  
 CC eczema, asthma, lupus erythematosus, AIDS, thyroiditis, diabetes,  
 CC uveitis, dermatitis, psoriasis, urticaria, nephrotic syndrome,  
 CC inflammatory bowel disease, glomerulonephritis, ulcerative colitis,  
 CC Crohn's disease, Sjogren's syndrome and toxoplasmosis. Note: The present  
 CC sequence is not shown in the specification but is derived from the IL-13  
 CC receptor alpha 1 sequence given in figure 1 (see AAB19807)

XX  
 SQ Sequence 427 AA:

Query Match 99.0%; Score 2296.5; DB 4; Length 427;  
 Best Local Similarity 99.3%; Pred. No. 8.1e-210;  
 Matches 424; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | MEMPARLCGLMALLCAGGGGGGGG-APETOPPVNTLSVSEVNTCTVITWNPPEGASS     | 59  |
| DB | 1   | MEMPARLCGLMALLCAGGGGGGGGAPETOPPVNTLSVSEVNTCTVITWNPPEGASS      | 60  |
| QY | 60  | NCSLWYFSHFGDKDKKIAPETRRSIEVPINERICLOVGSQCSSTNESEKPSILVEKCISP  | 119 |
| DB | 61  | NCSLWYFSHFGDKDKKIAPETRRSIEVPINERICLOVGSQCSSTNESEKPSILVEKCISP  | 120 |
| QY | 120 | PEGDPESAATLELCIWHNLSYMKCSWLPGRNTSPDNTYTLVYWHRSLEKIHQCENTIFREG | 179 |
| DB | 121 | PEGDPESAATLELCIWHNLSYMKCSWLPGRNTSPDNTYTLVYWHRSLEKIHQCENTIFREG | 180 |
| QY | 180 | QYEGCSFDLTKVDSSEFQHSVOIMVKNAGKIKPSFNIPLTSRVKDPDPHINKLSFHN     | 239 |
| DB | 181 | QYEGCSFDLTKVDSSEFQHSVOIMVKNAGKIKPSFNIPLTSRVKDPDPHINKLSFHN     | 240 |
| QY | 240 | DDLVOEMENPQNFISRLCFEVEVNNQSOTETHNVFYQEAKECENPEPERNVENTSCEMPV  | 299 |
| DB | 241 | DDLVOEMENPQNFISRLCFEVEVNNQSOTETHNVFYQEAKECENPEPERNVENTSCEMPV  | 300 |
| QY | 300 | GVLPTLNTVIRIKVTNKLCEYEDDKLMSNWSQEMSIGKKNSTLYITMLLIPVIYAGAI    | 359 |
| DB | 301 | GVLPTLNTVIRIKVTNKLCEYEDDKLMSNWSQEMSIGKKNSTLYITMLLIPVIYADAI    | 360 |
| QY | 360 | IYLLLYIKRLKIIIPPIPDPGKIFKEMFGDNDTLHMKKYDIYKQTKETDVSVLTIE      | 419 |
| DB | 361 | IYLLLYIKRLKIIIPPIPDPGKIFKEMFGDNDTLHMKKYDIYKQTKETDVSVLTIE      | 420 |
| QY | 420 | NLKKASQ 426   |     |
| DB | 421 | NLKKASQ 427   |     |

Search completed: July 8, 2006, 01:38:40  
 Job time : 197 secs

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:38:58 ; Search time 41 Seconds  
(without alignments)  
999.716 Million cell updates/sec

Title: US-09-051-843d-4

Perfect score: 2320  
Sequence: 1 MEMPARLCSGLMALLCAGG.....QTRKETDSVVLINLKASQ 426

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_80:\*\n1: p1r1:\*\n2: p1r2:\*\n3: p1r3:\*\n4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID     | Description        |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1          | 1653  | 71.2        | 426    | 2  | JC7773 | IL-13Ra1pha 1 prot |
| 2          | 318   | 13.7        | 415    | 2  | S12357 | interleukin-5 rece |
| 3          | 294.5 | 12.7        | 420    | 2  | S21052 | interleukin-5 rece |
| 4          | 269.5 | 11.6        | 348    | 2  | JC7907 | common cytokine re |
| 5          | 229   | 9.9         | 335    | 2  | A40267 | interleukin-5 rece |
| 6          | 228   | 9.8         | 400    | 2  | S06945 | granulocyte-macrop |
| 7          | 207   | 8.9         | 373    | 2  | A55718 | interleukin-2 rece |
| 8          | 205.5 | 8.9         | 369    | 2  | I49280 | interleukin-2 rece |
| 9          | 202   | 8.7         | 369    | 2  | A42565 | interleukin-2 rece |
| 10         | 197.5 | 8.5         | 610    | 2  | JQ1655 | prolactin receptor |
| 11         | 190   | 8.2         | 610    | 2  | A34631 | lactogen receptor  |
| 12         | 189   | 8.1         | 310    | 2  | A29884 | prolactin receptor |
| 13         | 189   | 8.1         | 412    | 2  | A41070 | prolactin receptor |
| 14         | 189   | 8.1         | 610    | 2  | A36116 | prolactin receptor |
| 15         | 186   | 8.0         | 581    | 2  | I45971 | prolactin receptor |
| 16         | 185   | 8.0         | 616    | 2  | A30304 | prolactin receptor |
| 17         | 183   | 7.9         | 292    | 2  | I77525 | prolactin receptor |
| 18         | 180   | 7.8         | 303    | 2  | I77524 | prolactin receptor |
| 19         | 180   | 7.8         | 608    | 2  | I53269 | prolactin receptor |
| 20         | 176   | 7.6         | 630    | 2  | I51086 | prolactin receptor |
| 21         | 173   | 7.5         | 918    | 2  | A36337 | membrane glycoprot |
| 22         | 172.5 | 7.4         | 288    | 2  | B59405 | prolactin receptor |
| 23         | 172.5 | 7.4         | 376    | 2  | A59405 | prolactin receptor |
| 24         | 172.5 | 7.4         | 622    | 2  | A40144 | prolactin receptor |
| 25         | 170   | 7.3         | 897    | 1  | A39255 | cytokine receptor  |
| 26         | 165   | 7.1         | 396    | 2  | S22909 | interleukin-3 rece |
| 27         | 163   | 7.0         | 830    | 2  | I50455 | prolactin receptor |
| 28         | 162.5 | 7.0         | 333    | 2  | S13684 | granulocyte-macrop |
| 29         | 161.5 | 7.0         | 1092   | 2  | JX0312 | differentiation-st |

|    |       |     |      |          |                    |
|----|-------|-----|------|----------|--------------------|
| 30 | 157   | 6.8 | 378  | 2 A40266 | interleukin-3 rece |
| 31 | 157   | 6.8 | 896  | 1 A35782 | cytokine receptor  |
| 32 | 156.5 | 6.7 | 378  | 2 S50040 | granulocyte-macrop |
| 33 | 154.5 | 6.7 | 896  | 2 I56563 | interleukin-3 rece |
| 34 | 149   | 6.4 | 878  | 1 A40091 | interleukin-3 rece |
| 35 | 146.5 | 6.3 | 608  | 2 S32823 | somatotropin recep |
| 36 | 145   | 6.2 | 638  | 2 A33991 | somatotropin recep |
| 37 | 144.5 | 6.2 | 1097 | 2 S17308 | leukemia inhibitor |
| 38 | 144   | 6.2 | 918  | 2 A44257 | interleukin-6 sign |
| 39 | 142.5 | 6.1 | 917  | 2 I49699 | glycoprotein 130 - |
| 40 | 141   | 6.1 | 638  | 2 S12136 | somatotropin recep |
| 41 | 140   | 6.0 | 638  | 2 B28176 | somatotropin recep |
| 42 | 139   | 6.0 | 508  | 1 ZUHUR  | erythropoietin rec |
| 43 | 139   | 6.0 | 634  | 2 S33339 | somatotropin recep |
| 44 | 135.5 | 5.8 | 286  | 2 S50039 | granulocyte-macrop |
| 45 | 134.5 | 5.8 | 557  | 2 A32654 | interferon alpha/b |

## ALIGNMENTS

RESULT 1  
JC7773  
IL-13Ralpha 1 protein - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
C/Accession: JC7773  
R/Protein: C.; Benigne; L.; Begue, A.; Khalife, J.  
Biochem. Biophys. Res. Commun. 287, 969-976, 2001  
A/Title: Expression of a functional IL-13Ralpha by rat B cells.  
A/Reference number: JC7773; PMID:11573960  
A/Accession: JC7773  
A/Molecule type: mRNA  
A/Residues: 1-426 <PIE>  
A/Cross-references: UNIPROT:Q8VHC2; UNIPARC:UPI000017CC49; GB:AY044251  
C/Comment: This protein is an functionally binding protein involved in B cell prolifera  
C/Genetics:  
A/Gene: il-13ralphal

| Query Match           | 71.2%           | Score 1653   | DB 2     | Length 426 |
|-----------------------|-----------------|--|----------|------------|
| Best Local Similarity | 73.3%           | Pred. No. 3e-121   |          |            |
| Matches 313           | Conservative 43 | Mismatches 67  | Indels 4 | Gaps 3     |
| QY                    | 1               | MEMPARLCSGLMALLCAGGSGGAGPTENQPTVNLVSVENCTVIMTNPEGASNN        | 60       |            |
| DB                    | 1               | MARPAMIGELLVLLPFAASLDQVALA-TEVQPPVTNLVSVENCTVIMTNPEGASPN     | 59       |            |
| QY                    | 61              | CSLMYFSHFQDKODKKIAPETRRSIEVPLNERICLQVGSOCSTNSESKEPSILYEKCTSP | 120      |            |
| DB                    | 60              | CSLRYSFHFDDQDKKIAPETRRKKEPLNEKICLQVGSOCSTNSESKEPSILYEKCTSP   | 119      |            |
| QY                    | 121             | EGDPESAVTELQCIWNLSTYMKCSWLPGRNTSPDNTYLYWHSLEKIHOCENIFREQ     | 180      |            |
| DB                    | 120             | RGSSESATVELQCIWNLSTYMKCSWLPGRNTSPDNTYLYWHSLEKIHOCENIFREQ     | 179      |            |
| QY                    | 181             | YFGCSFPLTVKXSSPEQHSVOIMVKNACKIRPSFIYVLTSTYKVDPPHIKLSFND      | 240      |            |
| DB                    | 180             | HIGCSFPLTV-ESNVEHNIQIMVKNACKIRPSFIYVLTSTYKVDPPHIKLPKNG       | 238      |            |
| QY                    | 241             | DLVYWMENPQNTSRCLFEVEVNSQTEH--NVFVQAKCENPEFEHNVETSCFMV        | 298      |            |
| DB                    | 239             | ALFVQWKNPQNTSRCLFEVEVNSQTEH--NVFVQAKCENPEFEHNVETSCFMV        | 298      |            |
| QY                    | 299             | PGVLPDLTAVTRVAVTKNLCYEDDKLMSWSQEMSGKKRNGTLYTMLLIYVYAGA       | 358      |            |
| DB                    | 299             | PGVLPDLTAVTRVAVTKNLCYEDDKLMSWSQEMSGKKRNGTLYTMLLIYVYAVV       | 358      |            |
| QY                    | 359             | IIVLLYLKRLKIIIPPIPKIFKEMGQNDNDITLHKKXYDIYEKQTRKETDSVLLI      | 418      |            |
| DB                    | 359             | IIVLLYLKRLKIIIPPIPKIFKEMGQNDNDITLHKKXYDIYEKQTRKETDSVLLI      | 418      |            |
| QY                    | 419             | ENLKAS 425   |          |            |

DB 419 ENLKKA 425

RESULT 2  
S12357  
interleukin-5 receptor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Nov-1993 #sequence revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S12357  
R:Takaki, S.; Tomimaga, A.; Hiroshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu, K.  
EMBO J. 9, 4367-4374, 1990  
A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.  
A:Reference number: S12357, MUID:91092260, PMID:2265612  
A:Accession: S12357  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-415 <TAK>  
A:Cross-references: UNIPROT:P21183; UNIPARC:UPI0000028472; GB:D90205; NID:9220465; PIDD:  
C:Keywords: cytokine receptor, transmembrane protein

Query Match 13.7%; Score 318; DB 2; Length 415;  
Best Local Similarity 23.9%; Pred. No. 4.2e-17;  
Matches 97; Conservative 74; Mismatches 179; Indels 56; Gaps 14;

QY 32 PPPTNLSSVENICTYIWTNRP-PEGASSNCSLMYFSHF-GDKQDKIAPEFRRSIEVPL 89  
DB 29 PPV-NEFKATGLAQLVLLHMDPNPDQEQRHVDLEHYKINAPQEDVDTRKTESKCVPL 87  
QY 90 NERICGLQVSGQSTNESEKPSILVEKCSIPREGPESAVTELQCIYHNL----- 138  
DB 88 HEGFAASVRIILKSSHTTLLASSWSAEIKAPGSGISVTNLTCTHTVSSHTLHPYQ 147  
QY 139 SYMKCSWLPGRNTPSDTNYTLYYHRSLEKIHOCENIFRE--GQYFGCSFDLTKYDSGF 196  
DB 148 VSLRCWLVWGKAPBEDQYLYRFGVLT--KQEYSRDALNRTACMPPTFINSKEF 205  
QY 197 EGHVSQIOMKDNAGKIKPSFNIVPLTSRVKDPDPRHINKLSFHNDDLQVQWENPN-Q-FISR 255  
DB 206 EQLAVHINSSSKRAAIKPFQDLFSLAIDQVNPNNVVEIESNLSLYQWEKPLSAFPDH 265  
QY 256 CLEFEVAVNNSSQFETHNVFFVQGEAKCENFEFERAVENTSCFNVPGVLEDTLVIRIVYT 315  
DB 266 CENYELEKINYTKNG---HIQKEKLANKFKISKIDVSTY-----SIOVRAAV 309  
QY 316 INKLCEYDDDKLMSWMSQMSIGKKRNSTLYTMLIVPPIVAGAILVLLYLRKLKI--- 372  
DB 310 SSPCRNPKGR-WGMSQPIYVGEKES-LVENHLIVLP--TRACVLLIFSLICRYCHLM 364  
QY 373 --IPPEIPDPGKIFKEMFGQNDDTLHKYDIYEKQTEEDTSVY 416  
DB 365 TRLFPVPAPAKSNIKDL-----PVTEYEKPESENKRIEVV 399

RESULT 3  
S21052  
interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored isoform 1  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S21052; S21050; S21053; A46175; S78106; S78107  
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.  
J. Exp. Med. 175, 341-351, 1992  
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.  
A:Reference number: S21050, MUID:92121815, PMID:1732409  
A:Accession: S21052  
A:Molecule type: DNA  
A:Residues: 1-420 <MUR>  
A:Cross-references: UNIPROT:Q14633; UNIPARC:UPI00000729EE; EMBL:X61176; NID:933843; PIDD:  
A:Experimental source: clone lambda h5R.12  
A:Accession: S21050  
A:Molecule type: DNA  
A:Residues: 1-395, 'T' <MUR>  
A:Cross-references: UNIPARC:UPI0000179A7F; EMBL:X61177; NID:933839; PIDD:CAA43484.1; PIDD:  
A:Experimental source: clone lambda h5R.27

[illegible]

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:35:33 ; Search time 299 Seconds  
(without alignments)  
1317.915 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 2320

Sequence: 1 MEMPARLCGLWALLCAGAG.....QTKETDSVLLENIKTASQ 426

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID             | Description        |
|------------|--------|-------------|--------|----------------|--------------------|
| 1          | 2309.5 | 99.5        | 427    | 1 I13R1_HUMAN  | P78552 homo sapien |
| 2          | 2309.5 | 99.5        | 427    | 05JSL4_HUMAN   | 05JSL4 homo sapien |
| 3          | 2296.5 | 99.0        | 427    | 096BB4_HUMAN   | 096BB4 homo sapien |
| 4          | 2291.5 | 98.8        | 426    | 059EG2_HUMAN   | 059EG2 homo sapien |
| 5          | 2140   | 92.2        | 409    | 07YRV5_MACCA   | 07YRV5 macaca fasc |
| 6          | 1939.5 | 83.6        | 423    | 0863Z6_PIG     | 0863Z6 sus scrofa  |
| 7          | 1927   | 83.1        | 401    | 06U6T1_SHEEP   | 06U6T1 ovis aries  |
| 8          | 1878   | 80.9        | 405    | 095LFL_CANFA   | 095LFL canis fami  |
| 9          | 1696   | 73.1        | 424    | 1 I13R1_MOUSE  | 095030 mus musculu |
| 10         | 1690   | 72.8        | 424    | 08C1Z3_MOUSE   | 08C1Z3 mus musculu |
| 11         | 1687   | 72.7        | 426    | 0561K3_RAT     | 0561K3 rattus norv |
| 12         | 1680   | 72.4        | 424    | 08BNM4_MOUSE   | 08BNM4 mus musculu |
| 13         | 1654   | 71.3        | 426    | 08VHC2_RAT     | 08VHC2 rattus norv |
| 14         | 1610   | 69.4        | 349    | 097597_BOVIN   | 097597 bos taurus  |
| 15         | 1533   | 66.1        | 399    | 03UPG9_MOUSE   | 03UPG9 mus musculu |
| 16         | 1524.5 | 65.7        | 279    | 09UDJ5_HUMAN   | 09UDJ5 homo sapien |
| 17         | 977.5  | 42.1        | 252    | 08VDJ7_MOUSE   | 08VDJ7 mus musculu |
| 18         | 463    | 20.0        | 226    | 06ZMW0_HUMAN   | 06ZMW0 homo sapien |
| 19         | 329    | 14.2        | 386    | 1 I13R2_CANFA  | 0951F0 canis fami  |
| 20         | 329    | 14.2        | 386    | 03HTU7_CANFA   | 03HTU7 canis fami  |
| 21         | 318    | 13.7        | 415    | 1 I15RA_MOUSE  | P21189 mus musculu |
| 22         | 296.5  | 12.8        | 420    | 1 I15RA_HUMAN  | Q01344 homo sapien |
| 23         | 294.5  | 12.7        | 380    | 1 I13R2_HUMAN  | Q14627 homo sapien |
| 24         | 287.5  | 12.4        | 383    | 088786_MOUSE   | 088786 mus musculu |
| 25         | 285.5  | 12.3        | 383    | 03VZV5_MOUSE   | 03VZV5 mus musculu |
| 26         | 282.5  | 12.2        | 396    | 2 I14631_HUMAN | 014631 homo sapien |
| 27         | 279.5  | 12.0        | 415    | 09ZOK4_CAVPO   | 09ZOK4 cavia porce |
| 28         | 277    | 11.9        | 385    | 2 08VHK6_RAT   | 08VHK6 rattus norv |
| 29         | 273.5  | 11.8        | 414    | 1 09ZOB8_RAT   | 09ZOB8 rattus norv |
| 30         | 272.5  | 11.7        | 414    | 2 099P53_RAT   | 099P53 rattus norv |

|    |       |      |     |                |                    |
|----|-------|------|-----|----------------|--------------------|
| 32 | 269.5 | 11.6 | 348 | 2 08AUP2_CHICK | 08AUP2 gallus gall |
| 33 | 263   | 11.3 | 391 | 2 06UAN8_TETNG | 06UAN8 tetradon n  |
| 34 | 262.5 | 11.3 | 374 | 2 08AV07_CHICK | 08AV07 gallus gall |
| 35 | 242.5 | 10.5 | 393 | 2 05U516_XENLA | 05U516 xenopus lae |
| 36 | 241.5 | 10.4 | 404 | 2 090XP8_ONCMY | 090XP8 oncomychnu  |
| 37 | 229   | 9.9  | 333 | 2 015469_HUMAN | 015469 homo sapien |
| 38 | 228   | 9.8  | 400 | 1 C5P2R_HUMAN  | P15509 homo sapien |
| 39 | 228   | 9.8  | 400 | 2 04V311_HUMAN | 04V311 homo sapien |
| 40 | 225   | 9.7  | 335 | 2 08NHV7_HUMAN | 08NHV7 homo sapien |
| 41 | 221.5 | 9.5  | 410 | 2 04V312_HUMAN | 04V312 homo sapien |
| 42 | 216.5 | 9.3  | 415 | 2 0661N1_XENLA | 0661N1 xenopus lae |
| 43 | 215   | 9.3  | 368 | 2 076KD0_PIG   | 076KD0 sus scrofa  |
| 44 | 215   | 9.3  | 368 | 2 08SOT1_PIG   | 08SOT1 sus scrofa  |
| 45 | 211   | 9.1  | 368 | 2 068F06_RAT   | 068F06 rattus norv |

## ALIGNMENTS

## RESULT 1

1 I13R1\_HUMAN STANDARD, PRT, 427 AA.  
AC P78552; 095646; 099656;  
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.  
DT 01-MAY-1997, sequence version 1.  
DT 07-MAR-2006, entry version 50.  
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen).  
GN Name=IL13RA1; Synonyms=IL13R, IL13RA;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RC TISSUE=Carcinoma;  
RX MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;  
RA Miloux B., Laurent P., Bonnin O., Luppker J., Caput D., Vitta N.,  
RA Ferrara P.;  
RT "Cloning of the human IL-13R alpha chain and reconstitution with the  
RT IL13R alpha of a functional IL-4/IL-13 receptor complex";  
RL FEBS Lett. 401:163-166(1997).  
[2]  
RN NUCLEOTIDE SEQUENCE [MRNA].  
RP TISSUE=B-cell;  
RC TISSUE=B-cell;  
RX Gauchat J.F.M., Schlagenhauf E., Feng N.P., Moser R., Yamage M.,  
RX Jeanman P., Alouani S., Elson G., Notarangelo L.D., Wells T.,  
RA Eugster H.P., Bonnefoy J.Y.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
[3]  
RN NUCLEOTIDE SEQUENCE [MRNA].  
RP TISSUE=T-cell;  
RC TISSUE=T-cell;  
RX MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;  
RX Amen M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;  
RT "cDNA cloning and characterization of the human interleukin 13  
RT receptor alpha chain";  
RL J. Biol. Chem. 271:29265-29270(1996).  
[4]  
RN NUCLEOTIDE SEQUENCE [MRNA].  
RP Wada M., Hisanu T., Kuwana M.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
[5]  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RP TISSUE=Pancreas;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RX Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RX Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RX Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,



RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schencher A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha  
 CC can form a functional receptor for IL13. Also serves as an  
 CC alternate accessory protein to the common cytokine receptor gamma  
 CC chain for IL4 signaling, but cannot replace the function of gamma  
 CC C in allowing enhanced IL2 binding activity.  
 CC -1- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RAL,  
 CC and possibly other components.  
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein.  
 CC -1- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,  
 CC skeletal muscle and ovary; lowest levels in brain, lung and  
 CC kidney. Also found in B-cells, T-cells and endothelial cells.  
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding.  
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation.  
 CC -1- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5  
 CC subfamily.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC distributed under the Creative Commons Attribution-NoDerivs license  
 CC -----  
 CC EMBL, Y10659; CAAT1669.1; -; mRNA.  
 CC EMBL, Y09328; CAAT70508.1; -; mRNA.  
 CC EMBL, U62858; AAB37127.1; -; mRNA.  
 CC EMBL, U81379; AAD00510.3; -; mRNA.  
 CC EMBL, BC009960; AAH09960.1; -; mRNA.  
 CC EMBL, ENSG00000131724; Homo sapiens.  
 CC H-InvDB: HIX0017008; -;  
 CC DR HGNC: HGNC:5974; IL13RAL.  
 CC DR MIM: 300119; gene.  
 CC DR GO: GO:0005898; C:interleukin-13 receptor complex; TAS.  
 CC DR GO: GO:0005886; C:plasma membrane; TAS.  
 CC DR GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.  
 CC DR InterPro: IPR002996; Cyt\_kin\_rcpt\_B/G.  
 CC DR InterPro: IPR003532; Hempt\_rcpt\_S\_F2.  
 CC DR PROSITE: PS01356; HEMATOPO REC\_S\_F2; 1.  
 CC DR GlycoProtet: Membrane; Receptor; Signal; Transmembrane.  
 CC KW SIGNL 1 21 Potential.  
 CC FT CHAIN 1 21 Interleukin-13 receptor alpha-1 chain.  
 CC FT 22 427 /FTId=PRO\_0000010939.  
 CC FT TOPO\_DOM 22 343 Extracellular (Potential).  
 CC FT TRANSMEM 344 367 Transmembrane.  
 CC FT TOPO\_DOM 368 427 Cytoplasmic (Potential).  
 CC FT MOTIF 327 331 WSXWS motif.  
 CC FT MOTIF 374 382 Box 1 motif.  
 CC FT CARBOHYD 37 37 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 61 61 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 105 105 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 138 138 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 157 157 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 235 235 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 265 265 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 293 293 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 329 329 N-linked (GlcNAc... ) (Potential).  
 CC FT CARBOHYD 341 341 N-linked (GlcNAc... ) (Potential).  
 CC FT DISULFID 46 95 Potential.  
 CC FT DISULFID 134 144 By similarity.  
 CC FT DISULFID 173 185 By similarity.

FT CONFLICT 130 130 T -> I (in Ref. 3).  
 FT CONFLICT 358 358 G -> D (in Ref. 3).  
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F554107B CRC64;  
 Query Match 99.5%; Score 2309.5; DB 1; Length 427;  
 Best Local Similarity 99.8%; Pred. No. 6; 5e-167;  
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPPVNTLSVSVENLCTVIWTVNPPGAS 59  
 DB 1 MEMPARLCGLMALLLCAGGGGGGGGGAAPTETOPPVNTLSVSVENLCTVIWTVNPPGAS 60  
 QY 60 NCSLWYFSPHGKQKXKIAPETRRSIEVPLNERICLQVSGQSTNSEKPSILVEKICSP 119  
 DB 61 NCSLWYFSPHGKQKXKIAPETRRSIEVPLNERICLQVSGQSTNSEKPSILVEKICSP 120  
 QY 120 PRSDPSAATLELOCIHNNLSYMKCSMLPERNTSPDNTYLLYWHRSLEKIHOCENIFRG 179  
 DB 121 PRSDPSAATLELOCIHNNLSYMKCSMLPERNTSPDNTYLLYWHRSLEKIHOCENIFRG 180  
 QY 180 QYFGCSFDLTKYVDSSEFQHSVQIMWKDNAGKIKPSFNIVPLTSRYKPPPHIKNLSFHN 239  
 DB 181 QYFGCSFDLTKYVDSSEFQHSVQIMWKDNAGKIKPSFNIVPLTSRYKPPPHIKNLSFHN 240  
 QY 240 DDLVYQWENPQNFISRCLEFYEVVNSQETETHNVFYQAKCENPEFEHVENTSCFMPV 299  
 DB 241 DDLVYQWENPQNFISRCLEFYEVVNSQETETHNVFYQAKCENPEFEHVENTSCFMPV 300  
 QY 300 GVLPTPLNTRVRIRVKNKLCYEDDKLMSWQSMGSKRRNSTLYTMTLLIVVYAGAI 359  
 DB 301 GVLPTPLNTRVRIRVKNKLCYEDDKLMSWQSMGSKRRNSTLYTMTLLIVVYAGAI 360  
 QY 360 IVLLLYLKRLKILIPPIPDGKIFKEMFGDONDDTLHMKKYDIYEKQTEETSIVLIE 419  
 DB 361 IVLLLYLKRLKILIPPIPDGKIFKEMFGDONDDTLHMKKYDIYEKQTEETSIVLIE 420  
 QY 420 NLKKSQ 426  
 DB 421 NLKKSQ 427  
 RESULT 2  
 Q5USL4\_HUMAN PRELIMINARY; PRT; 427 AA.  
 ID Q5USL4\_HUMAN  
 AC Q5USL4;  
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 21-FEB-2006, entry version 6.  
 DE Interleukin 13 receptor, alpha 1.  
 GN Name=IL13RAL; ORFNames=RP13-12804.2-001;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OC NCBI\_TaxID=9606;  
 RN NCBI\_TaxID=9606;  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lawlor S.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein (By similarity).  
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding (By similarity).  
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation (By similarity).  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC distributed under the Creative Commons Attribution-NoDerivs license  
 CC -----  
 CC EMBL, AL391280; CA141410.1; -; Genomic DNA.  
 CC EMBL, ENSG00000131724; Homo sapiens.  
 CC GO: GO:0016021; C:integral to membrane; IEA.

DR GO: 0016020; C:membrane; IEA.  
 DR GO: 0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO: 0004872; F:receptor activity; IEA.  
 DR InterPro: IPR002996; Cyt\_kin\_rcpt\_B/G.  
 DR InterPro: IPR003532; Hempt\_rcpt\_S\_F2.  
 DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; 1.  
 DR KEGG: Transmembrane.  
 SQ SEQUENCE 427 AA; 48760 MW; 5983B3B8F54107B CRC64;

Query Match 99.5%; Score 2309.5; DB 2; Length 427;  
 Best Local Similarity 99.8%; Pred. No. 6.5e-167;  
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPPVNTLSVENVLCVITWNPPEGASS 59  
 DB 1 MEMPARLCGLMALLLCAGGGGGGGGAPPTETOPPVNTLSVENVLCVITWNPPEGASS 60

QY 60 NCSLWYFSGDKQDKKIAPETRSIEVPLNERICLOVSGCSTNESEKPSILVEKICSP 119  
 DB 61 NCSLWYFSGDKQDKKIAPETRSIEVPLNERICLOVSGCSTNESEKPSILVEKICSP 120

QY 120 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQECNIFREG 179  
 DB 121 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQECNIFREG 180

QY 180 QYFGCSFDLTQVDSFEGHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 239  
 DB 181 QYFGCSFDLTQVDSFEGHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 240

QY 240 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEFERNVENTSCMPV 299  
 DB 241 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEFERNVENTSCMPV 300

QY 300 GVLPTLNTNTRIRVKTNKLCEYEDDKLMSNWSQEMSTGKNSTLYTLMILIVPIVAGAI 359  
 DB 301 GVLPTLNTNTRIRVKTNKLCEYEDDKLMSNWSQEMSTGKNSTLYTLMILIVPIVAGAI 360

QY 360 IVLLVLYKRLKIIIPPIPDGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 419  
 DB 361 IVLLVLYKRLKIIIPPIPDGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 420

QY 420 NLKKAQ 426  
 DB 421 NLKKAQ 427

RESULT 3  
 Q96BB4\_HUMAN PRELIMINARY; PRT; 427 AA.  
 AC Q96BB4; O8WX08;  
 DT 01-DEC-2001; Integrated into UniProtKB/TrEMBL.  
 DT 01-DEC-2001; sequence version 1.  
 DE 21-FEB-2006; entry version 23.  
 DE Interleukin 13 receptor, alpha 1.  
 GN Name=IL13RA1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCB1\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Colon;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausberg R.L., Feingold E.A., Grose L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.C., Krzyzanski M.I., Skalska U., Smallus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Colon;  
 RA Klausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein (By similarity).  
 CC -1- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding (By similarity).  
 CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation (By similarity).  
 CC -----  
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 CC Distributed under the Creative Commons Attribution-NonDerivs license  
 CC -----

DR EMBL, BC015768; AAH15768.1; -; mRNA.  
 DR Ensembl; ENSG00000131724; Homo sapiens.  
 DR GO: 0016021; C:integral to membrane; IEA.  
 DR GO: 0016020; C:membrane; IEA.  
 DR GO: 0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO: 0004872; F:receptor activity; IEA.  
 DR InterPro: IPR002996; Cyt\_kin\_rcpt\_B/G.  
 DR InterPro: IPR003532; Hempt\_rcpt\_S\_F2.  
 DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; 1.  
 DR KEGG: Transmembrane.  
 SQ SEQUENCE 427 AA; 48677 MW; E6A42F7466A39A09 CRC64;

Query Match 99.0%; Score 2296.5; DB 2; Length 427;  
 Best Local Similarity 99.5%; Pred. No. 6.3e-166;  
 Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETOPPVNTLSVENVLCVITWNPPEGASS 59  
 DB 1 MEMPARLCGLMALLLCAGGGGGGGGAPPTETOPPVNTLSVENVLCVITWNPPEGASS 60

QY 60 NCSLWYFSGDKQDKKIAPETRSIEVPLNERICLOVSGCSTNESEKPSILVEKICSP 119  
 DB 61 NCSLWYFSGDKQDKKIAPETRSIEVPLNERICLOVSGCSTNESEKPSILVEKICSP 120

QY 120 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQECNIFREG 179  
 DB 121 PEGDPESAATVTELOCIMHNLSYMKCSWLPGRNTSPDNTLYWHRSLKTHQECNIFREG 180

QY 180 QYFGCSFDLTQVDSFEGHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 239  
 DB 181 QYFGCSFDLTQVDSFEGHSVOIMVKDNAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 240

QY 240 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEFERNVENTSCMPV 299  
 DB 241 DDLVYQWENPONTISRLCFYEVEVNNSTQETHNVFYQAKCENPEFERNVENTSCMPV 300

QY 300 GVLPTLNTNTRIRVKTNKLCEYEDDKLMSNWSQEMSTGKNSTLYTLMILIVPIVAGAI 359  
 DB 301 GVLPTLNTNTRIRVKTNKLCEYEDDKLMSNWSQEMSTGKNSTLYTLMILIVPIVAGAI 360

QY 360 IVLLVLYKRLKIIIPPIPDGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 419  
 DB 361 IVLLVLYKRLKIIIPPIPDGKIFKEMFGDQNDTLHMKKVYDIYEKQTEEDTSVLLIE 420

QY 420 NLKKAQ 426  
 DB 421 NLKKAQ 427

Db 421 LKASQ 427

RESULT 4  
O59EG2\_HUMAN PRELIMINARY; PRT; 426 AA.  
AC O59EG2;  
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.  
DT 26-APR-2005, sequence version 1.  
DE Interleukin 13 receptor, entry version 4.  
DE Interleukin 13 receptor, alpha 1 variant (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Arterio endothelial cell;  
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,  
RA Ohara O., Nagase T., Kikuno F.R.;  
RT "None Title."  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB209849; BAD93086.1; -; mRNA.  
DR Ensembl; ENSG00000131724; Homo sapiens.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR002996; Cytok rcpt B/G.  
DR InterPro; IPR003532; Hempt rcpt S\_F2.  
DR PROSITE; PS01356; HEMATOPO\_REC\_S\_F2; 1.  
KM Receptor.  
FT NON\_TER  
SQ SEQUENCE 426 AA; 48555 MW; 342A3A6F7347261B CRC64;

Query Match 98.8%; Score 2291.5; DB 2; Length 426;  
Best Local Similarity 99.5%; Pred. No. 1.5e-165;  
Matches 444; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 2 EMPARLCGLMALLLCAGGGGGGGG-APTETQPPVNLVSVENLCTVIWTNPPGASNN 60  
DB 1 EMPARLCGLMALLLCAGGGGGGGGAPTEIQPVNLSVENLCTVIWTNPPGASNN 60  
QY 61 CSLWYSHFGDKODKKIAPETRSIEVPLNERICLOVGSQCSNSESKESSILVEKCI 120  
DB 61 CSLWYSHFGDKODKKIAPETRSIEVPLNERICLOVGSQCSNSESKESSILVEKCI 120  
QY 121 EGPDSAVTELOCIMHNLGYMKCSMLPGRNTSPDTNTLYYHRSLEKIHQCENIRREG 180  
DB 121 EGPDSAVTELOCIMHNLGYMKCSMLPGRNTSPDTNTLYYHRSLEKIHQCENIRREG 180  
QY 181 YFGCSFDLTKVDSFEQHSVQIMVNDNAKIKPSFNIVPLTSRVKPDPPHINKLSFND 240  
DB 181 YFGCSFDLTKVDSFEQHSVQIMVNDNAKIKPSFNIVPLTSRVKPDPPHINKLSFND 240  
QY 241 DLYVQWENQNFISRLCFYEVVNSQTEHNVFYVQAKCENPEFRNVENTSCFVMDG 300  
DB 241 DLYVQWENQNFISRLCFYEVVNSQTEHNVFYVQAKCENPEFRNVENTSCFVMDG 300  
QY 301 VLPDITNTYRIKTKKLCYEDDKLMSNNSQEMSIGKRNSTLYITMLLIVPIVAGAIL 360  
DB 301 VLPDITNTYRIKTKKLCYEDDKLMSNNSQEMSIGKRNSTLYITMLLIVPIVAGAIL 360  
QY 361 VLLLYLKRLLKIIIFPPIPDPGKIFKEMFGQNDTLHMKKYDIYEKQTEETDSVVLIN 420  
DB 361 VLLLYLKRLLKIIIFPPIPDPGKIFKEMFGQNDTLHMKKYDIYEKQTEETDSVVLIN 420  
QY 421 LKASQ 426  
|||||

Db 421 LKASQ 426

RESULT 5  
Q7YRV5\_MACFA PRELIMINARY; PRT; 409 AA.  
AC Q7YRV5;  
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2003, sequence version 1.  
DE Interleukin 13 receptor alpha 1 (Fragment).  
GN Name=IL13R1;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopitheciidae; Cercopitheciinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Maccarone P., Drinkwater C.C., Nash A.D.;  
RA "Cynomolgus monkey interleukin 13 receptor alpha 1."  
RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY312267; AAP78901.1; -; mRNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR002996; Cytok rcpt B/G.  
DR InterPro; IPR003532; Hempt rcpt S\_F2.  
DR PROSITE; PS01356; HEMATOPO\_REC\_S\_F2; 1.  
KM Receptor.  
FT CHAIN 9 409 interleukin 13 receptor alpha 1.  
FT NON\_TER  
SQ SEQUENCE 409 AA; 46695 MW; 9B98A52671686AF4 CRC64;

Query Match 92.2%; Score 2140; DB 2; Length 409;  
Best Local Similarity 96.6%; Pred. No. 4.7e-154;  
Matches 394; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 19 GGGGGGGAAPTETQPPVNLVSVENLCTVIWTNPPGASNNCSLWYFSHFQDKODKXIA 78  
DB 2 GGGGGGGAAPTETQPPVNLVSVENLCTVIWTNPPGASNNCSLWYFSHFQDKODKXIA 61  
QY 79 PETRSIEVPLNERICLOVGSQCSNSESKESSILVEKCSPEGPDESATVTELOCIMHNL 138  
DB 79 PETRSIEVPLNERICLOVGSQCSNSESKESSILVEKCSPEGPDESATVTELOCIMHNL 121  
QY 139 SYMKCSMLPGRNTSPDTNTLYYHRSLEKIHQCENIPREGQYFGCSFDLTKVDSFEQ 198  
DB 122 SYMKCSMLPGRNTSPDTNTLYYHRSLEKIHQCENIYREGQYFGCSFDLTKVDSFEQ 181  
QY 199 HSVQIMVNDNAKIKPSFNIVPLTSRVKPDPPHINKLSFNDLIVQWENQNFISRLCF 258  
DB 182 HSVQIMVNDNAKIKPSFNIVPLTSRVKPDPPHINKLSFNDLIVQWENQNFISRLCF 241  
QY 259 YEVEVNSQTEHNVFYVQAKCENPEFRNVENTSCFVMDG 300  
DB 242 YEVEVNSQTEHNVFYVQAKCENPEFRNVENTSCFVMDG 301  
QY 319 CYEDDKLMSNNSQEMSIGKRNSTLYITMLLIVPIVAGAILVLLLYLKRLLKIIIFPPI 378  
DB 302 CYEDDKLMSNNSQEMSIGKRNSTLYITMLLIVPIVAGAILVLLLYLKRLLKIIIFPPI 361  
QY 379 DPGLKIFKEMFGQNDTLHMKKYDIYEKQTEETDSVVLINLKASQ 426  
DB 362 DPGLKIFKEMFGQNDTLHMKKYDIYEKQTEETDSVVLINLKASQ 409  
|||||

RESULT 6  
Q863Z6\_PIG

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:44:03 ; Search time 50 Seconds  
(without alignments)  
745.761 Million cell updates/sec

Title: US-09-051-843D-4  
Perfect score: 2320  
Sequence: 1 MEMPARICGMALLICAGGCGGGGGGAGPTETQPPVTNLSVSVENICTVIWTPNPEGASNN 426

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Issued\_Patente\_AA:\*2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/5\_COMB.pep:\*3: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6\_COMB.pep:\*4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7\_COMB.pep:\*5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/H\_COMB.pep:\*6: /EMC\_Celerra\_SIDS3/prodata/2/iaa/PCTUS\_COMB.pep:\*7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | ID                   | Description        |
|------------|--------|-------------|--------|----------------------|--------------------|
| 1          | 2320   | 100.0       | 426    | 2 US-09-688-286D-4   | Sequence 4, Appli  |
| 2          | 2309.5 | 99.5        | 427    | 2 US-08-969-125-9    | Sequence 9, Appli  |
| 3          | 2309.5 | 99.5        | 427    | 2 US-09-545-002-9    | Sequence 9, Appli  |
| 4          | 2309.5 | 99.5        | 427    | 2 US-09-949-016-6094 | Sequence 6094, Ap  |
| 5          | 1878   | 80.9        | 405    | 2 US-08-828-995B-50  | Sequence 50, Appli |
| 6          | 1875.5 | 80.8        | 793    | 2 US-09-313-942-32   | Sequence 32, Appli |
| 7          | 1875.5 | 80.8        | 793    | 2 US-10-282-162-32   | Sequence 32, Appli |
| 8          | 1779.5 | 76.7        | 784    | 2 US-09-313-942-30   | Sequence 30, Appli |
| 9          | 1779.5 | 76.7        | 784    | 2 US-10-282-162-30   | Sequence 30, Appli |
| 10         | 1769   | 76.2        | 322    | 2 US-09-825-561A-82  | Sequence 82, Appli |
| 11         | 1696   | 73.1        | 424    | 2 US-09-688-286D-2   | Sequence 2, Appli  |
| 12         | 1265   | 54.5        | 233    | 2 US-09-949-016-8550 | Sequence 8550, Ap  |
| 13         | 329    | 14.2        | 386    | 2 US-09-828-995B-61  | Sequence 61, Appli |
| 14         | 318    | 13.7        | 398    | 1 US-07-757-390-6    | Sequence 6, Appli  |
| 15         | 318    | 13.7        | 398    | 1 US-08-442-282-6    | Sequence 6, Appli  |
| 16         | 318    | 13.7        | 398    | 1 US-08-442-281-6    | Sequence 6, Appli  |
| 17         | 318    | 13.7        | 398    | 1 US-08-939-727-6    | Sequence 6, Appli  |
| 18         | 318    | 13.7        | 415    | 1 US-07-757-390-5    | Sequence 5, Appli  |
| 19         | 318    | 13.7        | 415    | 1 US-08-442-282-5    | Sequence 5, Appli  |
| 20         | 318    | 13.7        | 415    | 1 US-08-442-281-5    | Sequence 5, Appli  |
| 21         | 318    | 13.7        | 415    | 1 US-08-939-727-5    | Sequence 5, Appli  |
| 22         | 318    | 13.7        | 415    | 2 US-09-886-319A-23  | Sequence 23, Appli |
| 23         | 310    | 13.4        | 365    | 2 US-09-828-995B-66  | Sequence 66, Appli |
| 24         | 304.5  | 13.1        | 561    | 2 US-09-828-995B-72  | Sequence 72, Appli |
| 25         | 303.5  | 13.1        | 561    | 2 US-09-828-995B-81  | Sequence 81, Appli |
| 26         | 297    | 12.8        | 565    | 2 US-09-828-995B-75  | Sequence 75, Appli |

|    |       |      |     |                      |                    |
|----|-------|------|-----|----------------------|--------------------|
| 27 | 296.5 | 12.8 | 420 | 2 US-09-886-319A-24  | Sequence 24, Appli |
| 28 | 296.5 | 12.8 | 420 | 2 US-09-949-016-5958 | Sequence 5958, Ap  |
| 29 | 296   | 12.8 | 318 | 2 US-09-828-995B-69  | Sequence 69, Appli |
| 30 | 296   | 12.8 | 563 | 2 US-09-828-995B-78  | Sequence 78, Appli |
| 31 | 294.5 | 12.7 | 380 | 1 US-08-609-572-4    | Sequence 4, Appli  |
| 32 | 294.5 | 12.7 | 380 | 2 US-08-841-751-4    | Sequence 4, Appli  |
| 33 | 294.5 | 12.7 | 380 | 2 US-08-846-340-4    | Sequence 4, Appli  |
| 34 | 294.5 | 12.7 | 380 | 2 US-08-846-344-4    | Sequence 4, Appli  |
| 35 | 294.5 | 12.7 | 380 | 2 US-09-301-808-4    | Sequence 4, Appli  |
| 36 | 294.5 | 12.7 | 420 | 1 US-07-757-380-13   | Sequence 13, Appli |
| 37 | 294.5 | 12.7 | 420 | 1 US-08-442-282-13   | Sequence 13, Appli |
| 38 | 294.5 | 12.7 | 420 | 1 US-08-442-281-13   | Sequence 13, Appli |
| 39 | 294.5 | 12.7 | 420 | 1 US-08-939-727-13   | Sequence 13, Appli |
| 40 | 293.5 | 12.7 | 427 | 2 US-09-949-016-8614 | Sequence 8614, Ap  |
| 41 | 293.5 | 12.7 | 427 | 2 US-09-949-016-8620 | Sequence 8620, Ap  |
| 42 | 287.5 | 12.4 | 383 | 1 US-08-609-572-2    | Sequence 2, Appli  |
| 43 | 287.5 | 12.4 | 383 | 2 US-08-841-751-2    | Sequence 2, Appli  |
| 44 | 287.5 | 12.4 | 383 | 2 US-08-846-340-2    | Sequence 2, Appli  |
| 45 | 287.5 | 12.4 | 383 | 2 US-08-846-344-2    | Sequence 2, Appli  |

ALIGNMENTS

RESULT 1  
US-09-688-286D-4  
Sequence 4, Application US/09688286D  
Patent No. 691530  
GENERAL INFORMATION:  
APPLICANT: Willson, Tracey  
APPLICANT: Nicola, Nicos  
APPLICANT: Hilton, Douglas  
APPLICANT: Metcalf, Donald  
APPLICANT: Zhang, Jian  
TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding san  
FILE REFERENCE: 23199-215  
CURRENT APPLICATION NUMBER: US/09/688,286D  
CURRENT FILING DATE: 2003-07-10  
PRIOR APPLICATION NUMBER: AU P6135  
PRIOR FILING DATE: 1995-10-23  
PRIOR APPLICATION NUMBER: AU P6135  
PRIOR FILING DATE: 1995-12-22  
PRIOR APPLICATION NUMBER: AU P6135  
PRIOR FILING DATE: 1995-12-22  
PRIOR APPLICATION NUMBER: AU P6135  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 426  
TYPE: PRT  
ORGANISM: human  
US-09-688-286D-4  
Query Match 100.0%; Score 2320; DB 2; Length 426;  
Best Local Similarity 100.0%; Pred. No. 5.7e-220;  
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MEMPARICGMALLICAGGCGGGGAGPTETQPPVTNLSVSVENICTVIWTPNPEGASNN 60  
1 MEMPARICGMALLICAGGCGGGGAGPTETQPPVTNLSVSVENICTVIWTPNPEGASNN 60  
CSLMYFSPGDKODKTAIPETRSIEVPLNERICLOVGSOCSTSEKSPSLVEKCTSP 120  
CSLMYFSPGDKODKTAIPETRSIEVPLNERICLOVGSOCSTSEKSPSLVEKCTSP 120  
EGDPESAATLQCIWNLSTYKSCWLPGRNTSPDTNLTLYWHRSLKIHOCENI 180  
EGDPESAATLQCIWNLSTYKSCWLPGRNTSPDTNLTLYWHRSLKIHOCENI 180  
EGDPESAATLQCIWNLSTYKSCWLPGRNTSPDTNLTLYWHRSLKIHOCENI 180  
YFGSFPITLVKXKSPFQSHVOIMVKNAGIKRSENFIVPLTSPVKRDPPIIKLSF 240  
YFGSFPITLVKXKSPFQSHVOIMVKNAGIKRSENFIVPLTSPVKRDPPIIKLSF 240  
YFGSFPITLVKXKSPFQSHVOIMVKNAGIKRSENFIVPLTSPVKRDPPIIKLSF 240  
DLVYQWENPONFISRLCFYEVENVNSOTETHNVFYQEAACENPEFERNVENTSCF 300  
DLVYQWENPONFISRLCFYEVENVNSOTETHNVFYQEAACENPEFERNVENTSCF 300

Db 241 DLVQWENPQNFISRLFEYEVVNNSTQETHNVFVQEAACENPEFERNNVENTSCFMWP 300  
QY 301 VLPDPLNTVRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRSSTLYITMLIIVPIVAGAI 360  
Db 301 VLPDPLNTVRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRSSTLYITMLIIVPIVAGAI 360  
QY 361 VLLLYLKRLLKIIIFPPIPDPGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLIEN 420  
Db 361 VLLLYLKRLLKIIIFPPIPDPGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLIEN 420  
QY 421 LKKSQ 426  
Db 421 LKKSQ 426  
RESULT 2  
US-08-969-125-9  
Sequence 9, Application US/08969125B  
Patent No. 6143871  
GENERAL INFORMATION:  
APPLICANT: BONNEFOY, JEAN-YVES  
GAUCHAT, JEAN-FRANCOIS  
TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/969,125B  
FILING DATE: 12-No. 6143871-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9625899.1  
FILING DATE: 13-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1430-179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 427 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-08-969-125-9  
Query Match 99.5%; Score 2309.5; DB 2; Length 427;  
Best Local Similarity 99.8%; Pred. No. 6,2e-219;  
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Db 1 MEMPARLGGMLALLCAGGGGGGGG--APETPTPTVNTLSVENVLCVITWNPPEGAS 59  
1 MEMPARLGGMLALLCAGGGGGGGGGAAPTPTPTPTVNTLSVENVLCVITWNPPEGAS 60  
QY 60 NCSLWFSHFGDKQDKKIAIPETRSIEVPLNERICLVQVSGQSTNSEKPSILVEKCI 119  
Db 61 NCSLWFSHFGDKQDKKIAIPETRSIEVPLNERICLVQVSGQSTNSEKPSILVEKCI 120  
QY 120 PEGDPESAVTEIQCIIWHNLSYMKCSWLPGRNTSPDTNNTLYVWHRSLKIHQCENIFREG 179

Db 121 PEGDPESAVTEIQCIIWHNLSYMKCSWLPGRNTSPDTNNTLYVWHRSLKIHQCENIFREG 180  
QY 180 QYFGCSFDLTLYKXDSSEFQHSVQIWKQDNAGIKESFNIVPLTSRYKPDPPHKNLSFHN 239  
Db 181 QYFGCSFDLTLYKXDSSEFQHSVQIWKQDNAGIKESFNIVPLTSRYKPDPPHKNLSFHN 240  
QY 240 DDLVQWENPQNFISRLFEYEVVNNSTQETHNVFVQEAACENPEFERNNVENTSCFMWP 299  
Db 241 DDLVQWENPQNFISRLFEYEVVNNSTQETHNVFVQEAACENPEFERNNVENTSCFMWP 300  
QY 300 GVLPDPLNTVRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRSSTLYITMLIIVPIVAGAI 359  
Db 301 GVLPDPLNTVRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRSSTLYITMLIIVPIVAGAI 360  
QY 360 IYLLLYLKRLLKIIIFPPIPDPGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLI 419  
Db 361 IYLLLYLKRLLKIIIFPPIPDPGKIFKEMFGDQNDDTLHMKKYDIYEKQTEETDSVLLI 420  
QY 420 NLKKSQ 426  
Db 421 NLKKSQ 427  
RESULT 3  
US-09-545-002-9  
Sequence 9, Application US/09545002  
Patent No. 6743604  
GENERAL INFORMATION:  
APPLICANT: BONNEFOY, JEAN-YVES  
GAUCHAT, JEAN-FRANCOIS  
TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/545,002  
FILING DATE: 12-No. 6743604-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/969,125  
FILING DATE: 12-No. 6743604-1997  
APPLICATION NUMBER: GB 9625899.1  
FILING DATE: 13-DEC-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: WILSON, MARY J.  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 1430-179  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 427 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-545-002-9  
Query Match 99.5%; Score 2309.5; DB 2; Length 427;  
Best Local Similarity 99.8%; Pred. No. 6,2e-219;  
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLGLWALLLCAGGGGGGGG -APETOPPVNTLSVENVLCVITWNPPEGASS 59  
DB 1 MEMPARLGLWALLLCAGGGGGGGGAPETOPPVNTLSVENVLCVITWNPPEGASS 60  
QY 60 NCSLMYSHFEDKODKXIAPETRSIEVPLNERICLVGSCCSTNESEKPSILVEKICSP 119  
DB 61 NCSLMYSHFEDKODKXIAPETRSIEVPLNERICLVGSCCSTNESEKPSILVEKICSP 120  
QY 120 PEGDESAVTELOCIWHLNLSYMKCSMLPGRNTSPDNTLYYWHRSLEKIHQCENIFREG 179  
DB 121 PEGDESAVTELOCIWHLNLSYMKCSMLPGRNTSPDNTLYYWHRSLEKIHQCENIFREG 180  
QY 180 QYFGCSFDLTRKVDKSSFEQSHVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 239  
DB 181 QYFGCSFDLTRKVDKSSFEQSHVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 240  
QY 240 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 299  
DB 241 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 300  
QY 300 GVLPTDNTVIRIRKYNKLCYEDDKLWSNNSQEMSIGKRNSTLYITMLLIVPIVAGAI 359  
DB 301 GVLPTDNTVIRIRKYNKLCYEDDKLWSNNSQEMSIGKRNSTLYITMLLIVPIVAGAI 360  
QY 360 IVLLLYLKRLLIIFPPIPDGKIFKEMFGQNDTLHWKXYDIYEKOTKEETDSVLAIE 419  
DB 361 IVLLLYLKRLLIIFPPIPDGKIFKEMFGQNDTLHWKXYDIYEKOTKEETDSVLAIE 420  
QY 420 NLKASQ 426  
DB 421 NLKASQ 427

RESULT 4  
US-09-949-016-6094  
Sequence 6094, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTNER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6094  
LENGTH: 427  
TYPE: PRF  
ORGANISM: Human  
US-09-949-016-6094

Query Match 99.5%; Score 2309.5; DB 2; Length 427;  
Best Local Similarity 99.8%; Pred. No. 6.2e-219;  
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MEMPARLGLWALLLCAGGGGGGGG -APETOPPVNTLSVENVLCVITWNPPEGASS 59  
DB 1 MEMPARLGLWALLLCAGGGGGGGGAPETOPPVNTLSVENVLCVITWNPPEGASS 60  
QY 60 NCSLMYSHFEDKODKXIAPETRSIEVPLNERICLVGSCCSTNESEKPSILVEKICSP 119  
DB 61 NCSLMYSHFEDKODKXIAPETRSIEVPLNERICLVGSCCSTNESEKPSILVEKICSP 120  
QY 120 PEGDESAVTELOCIWHLNLSYMKCSMLPGRNTSPDNTLYYWHRSLEKIHQCENIFREG 179  
DB 121 PEGDESAVTELOCIWHLNLSYMKCSMLPGRNTSPDNTLYYWHRSLEKIHQCENIFREG 180

DB 121 PEGDESAVTELOCIWHLNLSYMKCSMLPGRNTSPDNTLYYWHRSLEKIHQCENIFREG 180  
QY 180 QYFGCSFDLTRKVDKSSFEQSHVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 239  
DB 181 QYFGCSFDLTRKVDKSSFEQSHVOIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHN 240  
QY 240 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 299  
DB 241 DDLVYQWENPQNFISRCLEFEVEVNNQOTETHNVFYQEAACENPEFRNVENTSCFMPV 300  
QY 300 GVLPTDNTVIRIRKYNKLCYEDDKLWSNNSQEMSIGKRNSTLYITMLLIVPIVAGAI 359  
DB 301 GVLPTDNTVIRIRKYNKLCYEDDKLWSNNSQEMSIGKRNSTLYITMLLIVPIVAGAI 360  
QY 360 IVLLLYLKRLLIIFPPIPDGKIFKEMFGQNDTLHWKXYDIYEKOTKEETDSVLAIE 419  
DB 361 IVLLLYLKRLLIIFPPIPDGKIFKEMFGQNDTLHWKXYDIYEKOTKEETDSVLAIE 420  
QY 420 NLKASQ 426  
DB 421 NLKASQ 427

RESULT 5  
US-09-828-995B-50  
Sequence 50, Application US/09828995B  
Patent No. 6703360  
GENERAL INFORMATION:  
APPLICANT: Heska Corporation  
APPLICANT: McCall, Catherine A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13  
FILE REFERENCE: A1-7  
CURRENT APPLICATION NUMBER: US/09/828, 995B  
CURRENT FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 60/195,874  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/195,659  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 50  
LENGTH: 405  
TYPE: PRF  
ORGANISM: Canis familiaris  
US-09-828-995B-50

Query Match 80.9%; Score 1878; DB 2; Length 405;  
Best Local Similarity 85.2%; Pred. No. 2e-176;  
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;  
QY 22 GGGGAPETOPPVNTLSVENVLCVITWNPPEGASSNCSLMYSHFEDKODKXIAPET 81  
DB 1 GGGGAPETOPPVNTLSVENVLCVITWNPPEGASSNCSLMYSHFEDKODKXIAPET 60  
QY 82 RRSIEVPLNERICLVGSCCSTNESEKPSILVEKICSPPEGDESAVTELOCIWHLNLSY 141  
DB 81 RRSIEVPLNERICLVGSCCSTNESEKPSILVEKICSPPEGDESAVTELOCIWHLNLSY 120  
QY 142 KCSMLPGRNTSPDNTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTRKVDKSSFEQSHV 201  
DB 121 KCTWLPGRNTSPDNTLYYWHRSLEKIHQCENIFREGQYFGCSFDLTRKVDKSSFEQSHV 180  
QY 202 QIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHNDDLIVYQWENPQNFISRCLEFEV 261  
DB 181 QIMVKNACKIKPSFNIVPLTSRVKPDPHIKNLSFHNDDLIVYQWENPQNFISRCLEFEV 240  
QY 262 EVNNSQOTETHNVFYQEAACENPEFRNVENTSCFMPVGLPTDNTVIRIRKYNKLCYE 321  
DB 241 EVNNSQOTETHNVFYQEAACENPEFRNVENTSCFMPVGLPTDNTVIRIRKYNKLCYE 300  
QY 322 DDLKWSNNSQEMSIGKRNSTLYITMLLIVPIVAGAIIVLLLYLKRLLIIFPPIPDG 381  
DB 301 DDLKWSNNSQEMSIGKRNSTLYITMLLIVPIVAGAIIVLLLYLKRLLIIFPPIPDG 360

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Db      301 DDKLMSNWSQMSIGENTDPTFYITMLATQVIACAGIILLLYLKRIIIFPPIDBg 360
Qy      382 KIFKEMFGQNDPTLWKYDIYEKQKEETSDVLLENKKSQ 426
      361 KIFKEMFGQNDPTLWKYDIYEKQKEETSDVLLENKKSQ 405

RESULT 6
US-09-313-942-32
; Sequence 32, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32

Query Match      80.8%; Score 1875.5; DB 2; Length 793;
Best Local Similarity 99.4%; Pred. No. 1e-175;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      1 MEMPARLGLMALLLCAGGGGGGGG-APTETOPPVNTLSVSVENLCTVIWTNMPREGASS 59
      1 MWPARLGLMALLLCAGGGGGGGGAAPTETOPPVNTLSVSVENLCTVIWTNMPREGASS 60
Db      60 NCSLWFSHFQKODKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKCIAP 119
      61 NCSLWFSHFQKODKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKCIAP 120
Qy      120 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 179
      121 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 180
Db      180 QYFGCSFDLTKYKDSSEFQHSVOIMWKDAGKIKPSFNIVPLTSRYKPDPPHINKLSFHN 239
      181 QYFGCSFDLTKYKDSSEFQHSVOIMWKDAGKIKPSFNIVPLTSRYKPDPPHINKLSFHN 240
Qy      240 DDLVYOMENPQNFISRCLEFYEVVNSQETNHFVYVOAKCENPEFERNVENTSCFMPV 299
      241 DDLVYOMENPQNFISRCLEFYEVVNSQETNHFVYVOAKCENPEFERNVENTSCFMPV 300
Db      300 GVLPTLNTVRIKVTNKLCEYEDDKLMSNWSQMSIGKGRNST 342
      301 GVLPTLNTVRIKVTNKLCEYEDDKLMSNWSQMSIGKGRNST 343

RESULT 7
US-10-282-162-32
; Sequence 32, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
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; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-32

Query Match      80.8%; Score 1875.5; DB 2; Length 793;
Best Local Similarity 99.4%; Pred. No. 1e-175;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      1 MEMPARLGLMALLLCAGGGGGGGG-APTETOPPVNTLSVSVENLCTVIWTNMPREGASS 59
      1 MWPARLGLMALLLCAGGGGGGGGAAPTETOPPVNTLSVSVENLCTVIWTNMPREGASS 60
Db      60 NCSLWFSHFQKODKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKCIAP 119
      61 NCSLWFSHFQKODKIAPETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKCIAP 120
Qy      120 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 179
      121 PEGDPSAVTELOCIWHNLSYMKCSWLPGRNTSPDTNTLYYWHRSLEKIHOCENIFREG 180
Db      180 QYFGCSFDLTKYKDSSEFQHSVOIMWKDAGKIKPSFNIVPLTSRYKPDPPHINKLSFHN 239
      181 QYFGCSFDLTKYKDSSEFQHSVOIMWKDAGKIKPSFNIVPLTSRYKPDPPHINKLSFHN 240
Qy      240 DDLVYOMENPQNFISRCLEFYEVVNSQETNHFVYVOAKCENPEFERNVENTSCFMPV 299
      241 DDLVYOMENPQNFISRCLEFYEVVNSQETNHFVYVOAKCENPEFERNVENTSCFMPV 300
Db      300 GVLPTLNTVRIKVTNKLCEYEDDKLMSNWSQMSIGKGRNST 342
      301 GVLPTLNTVRIKVTNKLCEYEDDKLMSNWSQMSIGKGRNST 343

RESULT 8
US-09-313-942-30
; Sequence 30, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1999-05-19
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30

Query Match      76.7%; Score 1779.5; DB 2; Length 784;
Best Local Similarity 90.4%; Pred. No. 2.9e-166;
Matches 328; Conservative 5; Mismatches 15; Indels 15; Gaps 2;

Qy      20 GGGGGAAPETOPPVNTLSVSVENLCTVIWTNMPREGASSNCSLWFSHFQKODKIAPE 79
      233 GGGGGAAPETOPPVNTLSVSVENLCTVIWTNMPREGASSNCSLWFSHFQKODKIAPE 292
Db      80 ETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKCIAPPEGDPESAVTELOCIWHNS 139
      293 ETRRSIEVPLNERICLVQVSCSTNESEKPSILVEKCIAPPEGDPESAVTELOCIWHNS 352
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:44:48 / Search time 184 Seconds  
(without alignments)  
1072.443 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 2320  
Sequence: 1 MEMPARLCGIMALLICAGCG.....QTKRETDVLIENLKASQ 426

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database:

Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | ID                  | Description       |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1          | 2309.5 | 99.5        | 427    | 4 US-10-671-697-9   | Sequence 9, Appl  |
| 2          | 2309.5 | 99.5        | 427    | 6 US-11-067-251-3   | Sequence 3, Appl  |
| 3          | 2309.5 | 99.5        | 427    | 6 US-11-185-230-4   | Sequence 4, Appl  |
| 4          | 2309.5 | 99.5        | 427    | 6 US-11-182-384A-4  | Sequence 4, Appl  |
| 5          | 2309.5 | 99.5        | 427    | 6 US-11-183-599A-4  | Sequence 4, Appl  |
| 6          | 2309.5 | 99.5        | 427    | 6 US-11-149-309-37  | Sequence 3, Appl  |
| 7          | 2302.5 | 99.2        | 427    | 5 US-10-850-270-4   | Sequence 4, Appl  |
| 8          | 2302.5 | 99.2        | 427    | 6 US-10-036-568-4   | Sequence 4, Appl  |
| 9          | 2296.5 | 99.0        | 427    | 6 US-11-155-843-125 | Sequence 15, Appl |
| 10         | 1878   | 80.9        | 405    | 3 US-09-828-9958-50 | Sequence 50, Appl |
| 11         | 1878   | 80.9        | 405    | 4 US-10-753-159-50  | Sequence 50, Appl |
| 12         | 1875.5 | 80.8        | 780    | 3 US-09-935-868-34  | Sequence 34, Appl |
| 13         | 1875.5 | 80.8        | 793    | 3 US-09-313-942-32  | Sequence 32, Appl |
| 14         | 1875.5 | 80.8        | 793    | 3 US-09-935-868-32  | Sequence 32, Appl |
| 15         | 1875.5 | 80.8        | 793    | 4 US-10-287-035-32  | Sequence 32, Appl |
| 16         | 1875.5 | 80.8        | 793    | 4 US-10-282-162-32  | Sequence 32, Appl |
| 17         | 1875.5 | 80.8        | 793    | 6 US-11-134-114-32  | Sequence 32, Appl |
| 18         | 1866.5 | 80.5        | 780    | 3 US-09-935-868-42  | Sequence 42, Appl |
| 19         | 1866.5 | 80.5        | 780    | 3 US-09-935-868-48  | Sequence 48, Appl |
| 20         | 1865.5 | 80.4        | 782    | 3 US-09-935-868-38  | Sequence 38, Appl |
| 21         | 1865.5 | 80.4        | 782    | 3 US-09-935-868-52  | Sequence 52, Appl |
| 22         | 1862   | 80.3        | 780    | 4 US-10-287-035-34  | Sequence 34, Appl |
| 23         | 1853   | 79.9        | 782    | 4 US-10-287-035-42  | Sequence 42, Appl |
| 24         | 1853   | 79.9        | 782    | 4 US-10-287-035-48  | Sequence 48, Appl |
| 25         | 1853   | 79.9        | 782    | 4 US-10-287-035-54  | Sequence 54, Appl |
| 26         | 1852   | 79.8        | 780    | 4 US-10-287-035-38  | Sequence 38, Appl |
| 27         | 1852   | 79.8        | 782    | 4 US-10-287-035-52  | Sequence 52, Appl |

|    |        |      |     |                     |                   |
|----|--------|------|-----|---------------------|-------------------|
| 28 | 1852   | 79.8 | 782 | 4 US-10-287-035-58  | Sequence 58, Appl |
| 29 | 1784.5 | 76.9 | 664 | 5 US-10-850-270-10  | Sequence 10, Appl |
| 30 | 1779.5 | 76.7 | 784 | 3 US-09-313-942-30  | Sequence 30, Appl |
| 31 | 1779.5 | 76.7 | 784 | 3 US-09-935-868-30  | Sequence 30, Appl |
| 32 | 1779.5 | 76.7 | 784 | 4 US-10-287-035-30  | Sequence 30, Appl |
| 33 | 1779.5 | 76.7 | 784 | 4 US-10-282-162-30  | Sequence 30, Appl |
| 34 | 1779.5 | 76.7 | 784 | 6 US-11-134-114-30  | Sequence 30, Appl |
| 35 | 1769   | 76.2 | 322 | 3 US-09-825-561A-82 | Sequence 82, Appl |
| 36 | 1769   | 76.2 | 322 | 5 US-10-872-087-82  | Sequence 82, Appl |
| 37 | 1750   | 75.4 | 776 | 3 US-09-935-868-36  | Sequence 36, Appl |
| 38 | 1741   | 75.0 | 776 | 3 US-09-935-868-44  | Sequence 44, Appl |
| 39 | 1741   | 75.0 | 776 | 4 US-10-287-035-40  | Sequence 40, Appl |
| 40 | 1741   | 75.0 | 776 | 6 US-11-067-251-8   | Sequence 8, Appl  |
| 41 | 1741   | 75.0 | 776 | 6 US-11-067-251-10  | Sequence 10, Appl |
| 42 | 1741   | 75.0 | 776 | 6 US-11-067-251-12  | Sequence 12, Appl |
| 43 | 1741   | 75.0 | 776 | 6 US-11-067-251-14  | Sequence 14, Appl |
| 44 | 1741   | 75.0 | 776 | 6 US-11-067-251-16  | Sequence 16, Appl |
| 45 | 1740   | 75.0 | 776 | 3 US-09-935-868-40  | Sequence 40, Appl |

## ALIGNMENTS

RESULT 1  
US-10-671-697-9  
Sequence 9, Application US/10671697  
Publication No. US20040043921A1  
GENERAL INFORMATION:  
APPLICANT: BONNEFOY, JEAN-YVES  
TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE P. C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: MS Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/671.697  
FILING DATE: 29-Sep-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/545,002  
FILING DATE: 06-APR-2000  
APPLICATION NUMBER: US 08/969,125  
FILING DATE: 12-NOV-1997  
APPLICATION NUMBER: GB 9625899.1  
FILING DATE: 13-DEC-1996  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 427 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-10-671-697-9  
Query Match 99.5%; Score 2309.5; DB 4; Length 427;  
Best Local Similarity 99.8%; Pred. No. 2.9e-188;  
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MEMPARLCGIMALLICAGGGGGG-APETTOPVNTLSVSVNTCTVITWNPBEGASS 59  
DB 1 MEMPARLCGIMALLICAGGGGGGAPETTOPVNTLSVSVNTCTVITWNPBEGASS 60  
OY 60 NCSIMYSHFGKDDKKIAPETRRSIEVPINERICIVGSGCSTNESEKRSILVEKICSP 119

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Db      61 NCSLWFSHFHGDKODKKIAPETRRSIEVPLNERICLQVGSQCSTNSEKPSIIIVEKCI6P 120
Qy      120 PGDPSAATTELOCIMHNLSYMKCSMLPGRNTSPDTNYTLTYWHRSLKXIHOCENIFREG 179
Db      121 PGDPSAATTELOCIMHNLSYMKCSMLPGRNTSPDTNYTLTYWHRSLKXIHOCENIFREG 180
Qy      180 QYFGCSFDLTLYKXDSFEGHSVOIMWKDAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 239
Db      181 QYFGCSFDLTLYKXDSFEGHSVOIMWKDAGKIKPSFNIVPLTSRVKPDPPHKNLSFHN 240
Qy      240 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVPYVQAKCENPFERNVENTSCFMPV 299
Db      241 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVPYVQAKCENPFERNVENTSCFMPV 300
Qy      300 GVLPTLNTVTRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAI 359
Db      301 GVLPTLNTVTRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAI 360
Qy      360 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQNDDTLHWKXYDIYEKQTEETDSVLLIE 419
Db      361 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQNDDTLHWKXYDIYEKQTEETDSVLLIE 420
Qy      420 NLKKSQ 426
Db      421 NLKKSQ 427

RESULT 2
US-11-067-251-3
/ Sequence 3, Application US/11067251
/ Publication No. US20050191730A1
/ GENERAL INFORMATION:
/ APPLICANT: Karow, Margaret
/ APPLICANT: Faithurst, Jeanette
/ TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
/ FILE REFERENCE: 2020A
/ CURRENT APPLICATION NUMBER: US/11/067,251
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: 60/548,541
/ PRIOR FILING DATE: 2004-02-27
/ PRIOR APPLICATION NUMBER: 60/602,139
/ PRIOR FILING DATE: 2004-08-17
/ PRIOR APPLICATION NUMBER: 60/628,343
/ PRIOR FILING DATE: 2004-11-16
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-11-067-251-3

Query Match      99.5%; Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2,9e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Qy      240 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVPYVQAKCENPFERNVENTSCFMPV 299
Db      241 DDLVQWENPQNFISRCLEFYEVVNNNSQETHNVPYVQAKCENPFERNVENTSCFMPV 300
Qy      300 GVLPTLNTVTRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAI 359
Db      301 GVLPTLNTVTRIRVKTNKLCEYEDDKLMSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAI 360
Qy      360 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQNDDTLHWKXYDIYEKQTEETDSVLLIE 419
Db      361 IVLLYLKRLKIIIPPIPDGKIFKEMFGDQNDDTLHWKXYDIYEKQTEETDSVLLIE 420
Qy      420 NLKKSQ 426
Db      421 NLKKSQ 427

RESULT 3
US-11-185-230-4
/ Sequence 4, Application US/11185230
/ Publication No. US20050282216A1
/ GENERAL INFORMATION:
/ APPLICANT: Caput, Daniel
/ APPLICANT: Ferrara, Pascual
/ APPLICANT: Laurent, Patrick
/ APPLICANT: Vltz, Natalio
/ TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
/ FILE REFERENCE: IVD924 US CNT 1
/ CURRENT APPLICATION NUMBER: US/11/185,230
/ CURRENT FILING DATE: 2005-07-18
/ PRIOR APPLICATION NUMBER: PCT/FR96/01756
/ PRIOR FILING DATE: 1996-11-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 427
/ TYPE: PRT 3
/ ORGANISM: Homo sapiens
/ FEATURE:
US-11-185-230-4

Query Match      99.5%; Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2,9e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY 420 NLKASQ 426  
 Db 421 NLKASQ 427

# RESULT 4 US-11-182-384A-4

Sequence 4, Application US/11182384A  
 Publication No. US20060035855A1  
 GENERAL INFORMATION:  
 APPLICANT: Caput, Daniel  
 APPLICANT: Ferrata, Pascual  
 APPLICANT: Laurent, Patrick  
 APPLICANT: Valta, Natalio  
 TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity  
 FILE REFERENCE: IVD924 US Div 2  
 CURRENT APPLICATION NUMBER: US/11/182,384A  
 PRIOR FILING DATE: 2005-07-15  
 PRIOR APPLICATION NUMBER: 09/077,817  
 PRIOR FILING DATE: 1998-09-14  
 PRIOR APPLICATION NUMBER: PCT/FR96/01756  
 PRIOR FILING DATE: 1996-11-07  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 4  
 LENGTH: 427  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-182-384A-4

Query Match 99.5%; Score 2309.5; DB 6; Length 427;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-188;  
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVTNLVSVENLCTVIWTPNPEGASS 59  
 Db 1 MEMPARLCGLMALLLCAGGGGGGGGAPTETQPPVTNLVSVENLCTVIWTPNPEGASS 60  
 QY 60 NCSLMWFSHFQDKDKKIAETRRSIEVPLNERICLVGSGCSTNSESKEPSILVEKICSP 119  
 Db 61 NCSLMWFSHFQDKDKKIAETRRSIEVPLNERICLVGSGCSTNSESKEPSILVEKICSP 120  
 QY 120 PEGDPESAVTELOCIMWNL SYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 179  
 Db 121 PEGDPESAVTELOCIMWNL SYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 180  
 QY 180 QYFGCSFDLTRKVDSSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 239  
 Db 181 QYFGCSFDLTRKVDSSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 240  
 QY 240 DDLVQWENQNFISRLCFEVEVNNSTQETHNVFYQEA KCENPEERVENVENTSCFMP 299  
 Db 241 DDLVQWENQNFISRLCFEVEVNNSTQETHNVFYQEA KCENPEERVENVENTSCFMP 300  
 QY 300 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYITMLLIVPIYVAGAI 359  
 Db 301 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYITMLLIVPIYVAGAI 360  
 QY 360 IVLLLYLKRLLKIIIFPIIPDPGKIFKEMFGDQNDTLHMKKYDIYERKQTEETDSVLLIE 419  
 Db 361 IVLLLYLKRLLKIIIFPIIPDPGKIFKEMFGDQNDTLHMKKYDIYERKQTEETDSVLLIE 420  
 QY 420 NLKASQ 426  
 Db 421 NLKASQ 427

RESULT 5  
 US-11-183-599A-4  
 Sequence 4, Application US/11183599A  
 Publication No. US20060035855A1  
 GENERAL INFORMATION:  
 APPLICANT: Caput, Daniel

APPLICANT: Ferrata, Pascual  
 APPLICANT: Laurent, Patrick  
 APPLICANT: Valta, Natalio  
 TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity  
 FILE REFERENCE: IVD924 US Div 1  
 CURRENT APPLICATION NUMBER: US/11/183,599A  
 PRIOR FILING DATE: 2005-07-15  
 PRIOR APPLICATION NUMBER: 09/077,817  
 PRIOR FILING DATE: 1998-09-14  
 PRIOR APPLICATION NUMBER: PCT/FR96/01756  
 PRIOR FILING DATE: 1996-11-07  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 4  
 LENGTH: 427  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-183-599A-4

Query Match 99.5%; Score 2309.5; DB 6; Length 427;  
 Best Local Similarity 99.8%; Pred. No. 2.9e-188;  
 Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MEMPARLCGLMALLLCAGGGGGGGG-APTETQPPVTNLVSVENLCTVIWTPNPEGASS 59  
 Db 1 MEMPARLCGLMALLLCAGGGGGGGGAPTETQPPVTNLVSVENLCTVIWTPNPEGASS 60  
 QY 60 NCSLMWFSHFQDKDKKIAETRRSIEVPLNERICLVGSGCSTNSESKEPSILVEKICSP 119  
 Db 61 NCSLMWFSHFQDKDKKIAETRRSIEVPLNERICLVGSGCSTNSESKEPSILVEKICSP 120  
 QY 120 PEGDPESAVTELOCIMWNL SYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 179  
 Db 121 PEGDPESAVTELOCIMWNL SYMKCSWLPGRNTSPDTNTLYYWRSLSEKIHOCENIFREG 180  
 QY 180 QYFGCSFDLTRKVDSSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 239  
 Db 181 QYFGCSFDLTRKVDSSFEQHSVOIMVKNAGKIKPSFNIVPLTSRVKDPDPHINKLSFHN 240  
 QY 240 DDLVQWENQNFISRLCFEVEVNNSTQETHNVFYQEA KCENPEERVENVENTSCFMP 299  
 Db 241 DDLVQWENQNFISRLCFEVEVNNSTQETHNVFYQEA KCENPEERVENVENTSCFMP 300  
 QY 300 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYITMLLIVPIYVAGAI 359  
 Db 301 GVL PDTLNTVIRIKTNKLCYEDDKLMSNMSOEMSIGKKNSTLYITMLLIVPIYVAGAI 360  
 QY 360 IVLLLYLKRLLKIIIFPIIPDPGKIFKEMFGDQNDTLHMKKYDIYERKQTEETDSVLLIE 419  
 Db 361 IVLLLYLKRLLKIIIFPIIPDPGKIFKEMFGDQNDTLHMKKYDIYERKQTEETDSVLLIE 420  
 QY 420 NLKASQ 426  
 Db 421 NLKASQ 427

RESULT 6  
 US-11-149-309-37  
 Sequence 37, Application US/11149309  
 Publication No. US20060063228A1  
 GENERAL INFORMATION:  
 APPLICANT: Kasaian, Marion T.  
 APPLICANT: Tchistiakova, Lioudmila  
 APPLICANT: Veldman, Geetruida M.  
 APPLICANT: Marquette, Kimberly Ann  
 APPLICANT: Tan, Xiang-Yang  
 APPLICANT: Donaldson, Debra D.  
 APPLICANT: Lin, Laura Long  
 APPLICANT: Shane, Tania  
 APPLICANT: Tam, Amy Szepni  
 APPLICANT: Feyfiant, Eric  
 APPLICANT: Wood, Nancy L.  
 APPLICANT: Fitz, Lori J.

```
/ APPLICANT: widom, Angela M.
/ APPLICANT: Parits, Kevin D.
/ APPLICANT: Goldman, Samuel J.
/ TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor
/ FILE REFERENCE: 16158-048001 / AM01493
/ CURRENT APPLICATION NUMBER: US/11/149,309
/ PRIOR FILING DATE: 2005-06-09
/ PRIOR APPLICATION NUMBER: US 60/578,473
/ PRIOR FILING DATE: 2004-06-09
/ PRIOR APPLICATION NUMBER: US 60/581,375
/ PRIOR FILING DATE: 2004-06-22
/ PRIOR APPLICATION NUMBER: US 60/578,736
/ PRIOR FILING DATE: 2004-06-09
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 37
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-149-309-37
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```
Query Match          99.5%; Score 2309.5; DB 6; Length 427;
Best Local Similarity 99.8%; Pred. No. 2.9e-188;
Matches 426; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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QY      1 MEMPARLCGIMALLLCAGGGGGGGG-APTETQPPVTNLVSVENLCTVITWNPPEGASS 59
DB      1 MEMPARLCGIMALLLCAGGGGGGGGAAPTETQPPVTNLVSVENLCTVITWNPPEGASS 60
QY      60 NCSLWYFSGHGDQKDKKIAETRRSIEVPLNERICLQVSGQCSSTNESEKPSIIVEKCISP 119
DB      61 NCSLWYFSGHGDQKDKKIAETRRSIEVPLNERICLQVSGQCSSTNESEKPSIIVEKCISP 120
QY      120 PEGDPSAATTELQCIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 179
DB      121 PEGDPSAATTELQCIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 180
QY      180 QYFGCSFDLTKVDSFEGHSVOIMVKNAGKIKPSFNIIVPLTSRYKPDPPHKNLSFHN 239
DB      181 QYFGCSFDLTKVDSFEGHSVOIMVKNAGKIKPSFNIIVPLTSRYKPDPPHKNLSFHN 240
QY      240 DDLYVQWENPQNFISRCLEFYEVEVNNNSQETIHNVFYQAEKCNPEFERVENTSCFMVP 299
DB      241 DDLYVQWENPQNFISRCLEFYEVEVNNNSQETIHNVFYQAEKCNPEFERVENTSCFMVP 300
QY      300 GVLPTDLNTVRIKVTNKLCEYEDDKLMSNWSQEMSGKKRNSTLYITMLLIIVYIAGAI 359
DB      301 GVLPTDLNTVRIKVTNKLCEYEDDKLMSNWSQEMSGKKRNSTLYITMLLIIVYIAGAI 360
QY      360 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQDDTLHMKKYDIYEKQTEETDSVLLIE 419
DB      361 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQDDTLHMKKYDIYEKQTEETDSVLLIE 420
QY      420 NLKKSQ 426
DB      421 NLKKSQ 427
```

```
RESULT 7
US-10-850-270-4
/ Sequence 4, Application US/10850270
/ Publication No. US20050058645A1
/ GENERAL INFORMATION:
/ APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
/ APPLICANT: Dunlop, Felicity (US only)
/ APPLICANT: Baca, Manuel (US only)
/ APPLICANT: Nash, Andrew (US only)
/ APPLICANT: Fabri, Louis (US only)
/ TITLE OF INVENTION: Novel peptides
/ FILE REFERENCE: 12175890/BJH
/ CURRENT APPLICATION NUMBER: US/10/850,270
/ CURRENT FILING DATE: 2004-05-20
/ PRIOR APPLICATION NUMBER: AU PS1301
```

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/ PRIOR FILING DATE: 2002-03-22
/ PRIOR APPLICATION NUMBER: AU 2003900437
/ PRIOR FILING DATE: 2003-02-03
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: human
US-10-850-270-4
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```
Query Match          99.2%; Score 2302.5; DB 5; Length 427;
Best Local Similarity 99.5%; Pred. No. 1.2e-187;
Matches 425; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY      1 MEMPARLCGIMALLLCAGGGGGGGG-APTETQPPVTNLVSVENLCTVITWNPPEGASS 59
DB      1 MEMPARLCGIMALLLCAGGGGGGGGAAPTETQPPVTNLVSVENLCTVITWNPPEGASS 60
QY      60 NCSLWYFSGHGDQKDKKIAETRRSIEVPLNERICLQVSGQCSSTNESEKPSIIVEKCISP 119
DB      61 NCSLWYFSGHGDQKDKKIAETRRSIEVPLNERICLQVSGQCSSTNESEKPSIIVEKCISP 120
QY      120 PEGDPSAATTELQCIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 179
DB      121 PEGDPSAATTELQCIWHNLSYMKCSWLPGRNTSPDNTYTLTYWHRSLKTHOCENIFREG 180
QY      180 QYFGCSFDLTKVDSFEGHSVOIMVKNAGKIKPSFNIIVPLTSRYKPDPPHKNLSFHN 239
DB      181 QYFGCSFDLTKVDSFEGHSVOIMVKNAGKIKPSFNIIVPLTSRYKPDPPHKNLSFHN 240
QY      240 DDLYVQWENPQNFISRCLEFYEVEVNNNSQETIHNVFYQAEKCNPEFERVENTSCFMVP 299
DB      241 DDLYVQWENPQNFISRCLEFYEVEVNNNSQETIHNVFYQAEKCNPEFERVENTSCFMVP 300
QY      300 GVLPTDLNTVRIKVTNKLCEYEDDKLMSNWSQEMSGKKRNSTLYITMLLIIVYIAGAI 359
DB      301 GVLPTDLNTVRIKVTNKLCEYEDDKLMSNWSQEMSGKKRNSTLYITMLLIIVYIAGAI 360
QY      360 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQDDTLHMKKYDIYEKQTEETDSVLLIE 419
DB      361 IYLLLYLKRLLKIIIPPIPDGKIFKEMFGDQDDTLHMKKYDIYEKQTEETDSVLLIE 420
QY      420 NLKKSQ 426
DB      421 NLKKSQ 427
```

```
RESULT 8
US-10-036-568-4
/ Sequence 4, Application US/10036568
/ Publication No. US20020090682A1
/ GENERAL INFORMATION:
/ APPLICANT: Willson, Tracy
/ APPLICANT: Nicola, Nicos A.
/ APPLICANT: Hilton, Douglas J.
/ APPLICANT: Metcalf, Donald
/ APPLICANT: Zhang, Jian G.
/ TITLE OF INVENTION: NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
/ FILE REFERENCE: ENCODING SAME
/ CURRENT APPLICATION NUMBER: US/10/036,568
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: US/09/051,843
/ PRIOR FILING DATE: 1998-06-29
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 426
/ TYPE: PRT
/ ORGANISM: Human IL-13 receptor alpha-chain
US-10-036-568-4
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Query Match 99.2%; Score 2302; DB 4; Length 426;  
Best Local Similarity 99.3%; Pred. No. 1,3e-187;  
Matches 423; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 MEMPARLCGIMALLLCAGGGGGGGAAPTEPTOPPTVNLSSVENLCTVITWNNPPEGASSN 60
DB 1 MEMPARLCGIMALLLCAGGGGGGGAAPTEPTOPPTVNLSSVENLCTVITWNNPPEGASSN 60
QY 61 CSLMYFHFSGDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PP 120
DB 61 CSLMYFHFSGDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PP 120
QY 121 EGPESAVTELOCIWNLHLSYMKCSMLPGRNTSPDTNTLYYHRSLEKIHOCENIFR6Q 180
DB 121 EGPESAVTELOCIWNLHLSYMKCSMLPGRNTSPDTNTLYYHRSLEKIHOCENIFR6Q 180
QY 181 YFGCSFDLTGVKOSSEFQHSVQIMVKNAGKIKPSFNIIVPLTSRVKDPPIIKNLSFHN 240
DB 181 YFGCSFDLTGVKOSSEFQHSVQIMVKNAGKIKPSFNIIVPLTSRVKDPPIIKNLSFHN 240
QY 241 DLVYOMENPONFISRCIFYEVENNSQTEHNVFYOEAKCENPEFRNVENTSCFVWP 300
DB 241 DLVYOMENPONFISRCIFYEVENNSQTEHNVFYOEAKCENPEFRNVENTSCFVWP 300
QY 301 VLPDNTLVIRIRVKTNKLCEYEDDKLMSNMSQMSIGKRNSTLYITMLLIVPIVAGAI 360
DB 301 VLPDNTLVIRIRVKTNKLCEYEDDKLMSNMSQMSIGKRNSTLYITMLLIVPIVAGAI 360
QY 361 VLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLIEN 420
DB 361 VLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLIEN 420
QY 421 LKKASQ 426
DB 421 LKKASQ 426
```

## RESULT 9

US-11-155-843-125  
Sequence 125, Application US/11155843  
Publication No. US20060073148A1  
GENERAL INFORMATION:  
APPLICANT: Tchiastakova, Lioudmila  
APPLICANT: Kasalan, Marion T.  
APPLICANT: Donaldson, Debra D.  
APPLICANT: Tan, Xiang-Yang  
APPLICANT: Gill, Davinder  
APPLICANT: Jin, Macy X.  
APPLICANT: Jacobson, Bruce  
APPLICANT: Goldman, Samuel J.  
APPLICANT: Knopf, John  
APPLICANT: Widom, Angela M.  
TITLE OF INVENTION: IL-13 BINDING AGENTS  
FILE REFERENCE: 16158-020001  
CURRENT APPLICATION NUMBER: US/11/155,843  
PRIOR FILING DATE: 2005-06-17  
PRIOR APPLICATION NUMBER: US 60/581,078  
PRIOR FILING DATE: 2004-06-17  
PRIOR APPLICATION NUMBER: US 11/149,025  
NUMBER OF SEQ ID NOS: 192  
SOFTWARE: FastSeq for Windows Version 4.0  
SEO ID NO 125  
LENGTH: 427  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-155-843-125

Query Match 99.0%; Score 2296.5; DB 6; Length 427;  
Best Local Similarity 99.3%; Pred. No. 3.8e-187;  
Matches 424; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1 MEMPARLCGIMALLLCAGGGGGGGAAPTEPTOPPTVNLSSVENLCTVITWNNPPEGASS 59

```
DB 1 MEMPARLCGIMALLLCAGGGGGGGAAPTEPTOPPTVNLSSVENLCTVITWNNPPEGASS 60
QY 60 NCSLMYFHFSGDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3P 119
DB 61 NCSLMYFHFSGDKODKXIAPETRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3P 120
QY 120 EGPESAVTELOCIWNLHLSYMKCSMLPGRNTSPDTNTLYYHRSLEKIHOCENIFR6 179
DB 121 EGPESAVTELOCIWNLHLSYMKCSMLPGRNTSPDTNTLYYHRSLEKIHOCENIFR6 180
QY 180 QYFGCSFDLTGVKOSSEFQHSVQIMVKNAGKIKPSFNIIVPLTSRVKDPPIIKNLSFHN 239
DB 181 QYFGCSFDLTGVKOSSEFQHSVQIMVKNAGKIKPSFNIIVPLTSRVKDPPIIKNLSFHN 240
QY 240 DDLVYOMENPONFISRCIFYEVENNSQTEHNVFYOEAKCENPEFRNVENTSCFVWP 299
DB 241 DDLVYOMENPONFISRCIFYEVENNSQTEHNVFYOEAKCENPEFRNVENTSCFVWP 300
QY 300 GVLDPDNTLVIRIRVKTNKLCEYEDDKLMSNMSQMSIGKRNSTLYITMLLIVPIVAGAI 359
DB 301 GVLDPDNTLVIRIRVKTNKLCEYEDDKLMSNMSQMSIGKRNSTLYITMLLIVPIVAGAI 360
QY 360 IVLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLI 419
DB 361 IVLLLYLKRKLIIIFPPIPDGKIFKEMFGQNDTLMKKYDIYEKOTKEETDSVLI 420
QY 420 NLKASQ 426
DB 421 NLKASQ 427
```

## RESULT 10

US-09-828-995B-50  
Sequence 50, Application US/09828995B  
Patent No. US20020165135A1  
GENERAL INFORMATION:  
APPLICANT: Heeka Corporation  
APPLICANT: McCall, Catherine A.  
APPLICANT: Tang, Liang A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13  
FILE REFERENCE: AL-7  
CURRENT APPLICATION NUMBER: US/09/828,995B  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 60/195,874  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/195,659  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.1  
SEO ID NO 50  
LENGTH: 405  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-828-995B-50

Query Match 80.9%; Score 1878; DB 3; Length 405;  
Best Local Similarity 85.2%; Pred. No. 1.9e-151;  
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

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QY 22 GGGGAPTEPTOPPTVNLSSVENLCTVITWNNPPEGASSNCSLMYFHFSGDKODKXIAPET 81
DB 1 GGGGAPTEPTOPPTVNLSSVENLCTVITWNNPPEGASSNCSLMYFHFSGDKODKXIAPET 60
QY 82 RRSIEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PPGDPESAVTELOCIWNLHLSY 141
DB 61 HRSKEVPLNERICLOVGSOCSTNESEKPSILVEKCI3PPGDPESAVTELOCIWNLHLSY 120
QY 142 KCSMLPGRNTSPDTNTLYYHRSLEKIHOCENIFR6QYFGCSFDLTGVKOSSEFQHSV 201
DB 121 KCTWLPGRNTSPDTNTLYYHRSLEKIHOCENIFR6QYFGCSFDLTGVKOSSEFQHSV 180
QY 202 QIMVKNAGKIKPSFNIIVPLTSRVKDPPIIKNLSFHNDDL VYOMENPONFISRCIFYEV 261
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```
Db      181 QIMVKNARKIRSFNIVPLTSHVKPDPPHKKLFQONGLYQWKNPQMFYSRCLSYQV 240
Qy      262 EVNNSQTEHTHNVYVOEAKCENPEFERNVENTSCFMVPGVLPDTLTVIRVTKNLKCYE 321
Db      241 EVNNSQTEHTNDIFYVEAKCQNSEFEGNLEGTICFMVPGVLPDTLTVIRVTKNLKCYE 300
Qy      322 DDKLMSNWSQEMSIGKRNSTLYTMLIVPAIVAGAIIVLLYLKRLKIIFPPIDPG 361
Db      301 DDKLMSNWSQAMSIGENTDPTFYITMLLATQVIVAGAIITLLYLKRLKIIFPPIDPG 360
Qy      362 KIFKEMFGQNDDTLHMKKYDIYEKOTKETSDSVLIENLKASQ 426
Db      361 KIFKEMFGQNDDTLHMKKYDIYEKOTKETSDSVLIENLKASQ 405
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```
RESULT 11
US-10-753-159-50
; Sequence 50, Application US/10753159
; Publication No. US20040142372A1
; GENERAL INFORMATION:
; APPLICANT: Heska Corporation
; APPLICANT: McCall, Catherine A.
; APPLICANT: Tang, Liang A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R
; FILE REFERENCE: AL-7
; CURRENT APPLICATION NUMBER: US/10/753,159
; PRIOR FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: 60/195,874
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/195,659
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-753-159-50
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Query Match      80.9%; Score 1878; DB 4; Length 405;
Best Local Similarity 85.2%; Pred. No. 1.9e-151;
Matches 345; Conservative 24; Mismatches 36; Indels 0; Gaps 0;

Qy      22 GGGGAPTEPTOPPYTNLSVSVENLCTVIWTNPPREGASSNCSLWYFSHFGDKODKIAPET 81
Db      1 GGAAPATEPTOPPYTNLSVSVENLCTVIWTNPPREGASSNCSLWYFSHFGDKODKIAPET 60
Qy      82 RRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCTSPPEGDPESAVTELOCIWMHLSYM 141
Db      61 HRSKEVPLNERICLOVGSQCSSTNESDNPSILVEKCTPPPEGDPESAVTELOCIWMHLSYM 120
Qy      142 KCSWLGRNTPPTNTVTLVYWHRSLEKIHOCENIFREGQVFGSGPDLTKYKDSFPGHSV 201
Db      121 KCIWPLGRNTPPTNTVTLVYWHRSLEKIHOCENIFREGQVFGSGPDLTKYKDSFPGHSV 180
Qy      202 QIMVKNACKIKESFNIVPLTSRVKDPPIIKNLSPHNDLVLYQWENPQNFISRCLEFYEY 261
Db      181 QIMVKNACKIRSFNIVPLTSRVKDPPIIKRLLFQONGLYQWKNPQMFYSRCLSYQV 240
Qy      262 EVNNSQTEHTHNVYVOEAKCENPEFERNVENTSCFMVPGVLPDTLTVIRVTKNLKCYE 321
Db      241 EVNNSQTEHTNDIFYVEAKCQNSEFEGNLEGTICFMVPGVLPDTLTVIRVTKNLKCYE 300
Qy      322 DDKLMSNWSQEMSIGKRNSTLYTMLIVPAIVAGAIIVLLYLKRLKIIFPPIDPG 361
Db      301 DDKLMSNWSQAMSIGENTDPTFYITMLLATQVIVAGAIITLLYLKRLKIIFPPIDPG 360
Qy      362 KIFKEMFGQNDDTLHMKKYDIYEKOTKETSDSVLIENLKASQ 426
Db      361 KIFKEMFGQNDDTLHMKKYDIYEKOTKETSDSVLIENLKASQ 405
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RESULT 12
US-09-935-868-34
; Sequence 34, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203d
; CURRENT APPLICATION NUMBER: US/09/935,868
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-09-935-868-34
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Query Match      80.8%; Score 1875.5; DB 3; Length 780;
Best Local Similarity 99.4%; Pred. No. 7.5e-151;
Matches 341; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy      1 MEMPARLCGLMALLCAGGGGGGGC-APTETOPPYTNLSVSVENLCTVIWTNPPREGASS 59
Db      1 MWPAPRLCGIMALLCAGGGGGGGGAAPTETOPPYTNLSVSVENLCTVIWTNPPREGASS 60
Qy      60 NCSLWFSHFGDKODKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCTSP 119
Db      61 NCSLWFSHFGDKODKIAPETRRSIEVPLNERICLOVGSQCSSTNESEKPSILVEKCTSP 120
Qy      120 PEGDPESAVTELOCIWMHLSYMKCSWLPGRNTPSDTNTVTLVYWHRSLEKIHOCENIFREG 179
Db      121 PEGDPESAVTELOCIWMHLSYMKCSWLPGRNTPSDTNTVTLVYWHRSLEKIHOCENIFREG 180
Qy      180 QYFGCSFDLTKYKDSSEFEGHSQVQIMVKNACKIKESFNIVPLTSRVKDPPIIKNLISFHN 239
Db      181 QYFGCSFDLTKYKDSSEFEGHSQVQIMVKNACKIKESFNIVPLTSRVKDPPIIKNLISFHN 240
Qy      240 DDLVYQWENPQNFISRCLEFYEVEVNNNSQTEHTHNVYVOEAKCENPEFERNVENTSCFMV 299
Db      241 DDLVYQWENPQNFISRCLEFYEVEVNNNSQTEHTHNVYVOEAKCENPEFERNVENTSCFMV 300
Qy      300 GVLPTLNTVIRIRVKTNLKCYEDDKLMSNWSQEMSIGKRNST 342
Db      301 GVLPTLNTVIRIRVKTNLKCYEDDKLMSNWSQEMSIGKRNST 343
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RESULT 13
US-09-313-942-32
; Sequence 32, Application US/09313942
; Publication No. US20020012962A1
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-32
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Query Match 80.8%; Score 1875.5; DB 3; Length 793;

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2006, 01:45:43 ; Search time 21 Seconds  
(without alignments)  
544,307 Million cell updates/sec

Title: US-09-051-843d-4

Perfect score: 2320  
Sequence: 1 MEMPARLCGMALILCAGGG.....QTKETDSVLIENIKKASQ 426

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA\_New:\*

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3: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US07\_NEW\_PUB.pgp:\*  
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8: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US60\_NEW\_PUB.pgp:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 302   | 13.0        | 372    | US-11-331-993-7     | Sequence 7, Appli  |
| 2          | 294.5 | 12.7        | 380    | US-11-220-888-4     | Sequence 4, Appli  |
| 3          | 294.5 | 12.7        | 380    | US-11-331-993-2     | Sequence 2, Appli  |
| 4          | 293.5 | 12.7        | 380    | US-11-331-993-4     | Sequence 4, Appli  |
| 5          | 284   | 12.2        | 310    | US-11-220-888-1     | Sequence 1, Appli  |
| 6          | 202   | 8.7         | 369    | US-10-511-937-2966  | Sequence 2966, Ap  |
| 7          | 167.5 | 7.2         | 422    | US-11-296-092-32    | Sequence 32, Appli |
| 8          | 167.5 | 7.2         | 422    | US-11-296-155-32    | Sequence 32, Appli |
| 9          | 162.5 | 7.0         | 371    | US-11-297-957-4     | Sequence 4, Appli  |
| 10         | 142.5 | 6.1         | 662    | US-11-301-764-5     | Sequence 5, Appli  |
| 11         | 142.5 | 6.1         | 764    | US-11-301-764-39    | Sequence 39, Appli |
| 12         | 139   | 6.0         | 508    | US-10-511-937-2426  | Sequence 2426, Ap  |
| 13         | 137   | 5.9         | 519    | US-11-301-764-71    | Sequence 71, Appli |
| 14         | 125   | 5.4         | 825    | US-10-505-928-650   | Sequence 650, App  |
| 15         | 125   | 5.4         | 825    | US-10-511-937-3001  | Sequence 3001, App |
| 16         | 123.5 | 5.3         | 547    | US-11-301-764-114   | Sequence 114, App  |
| 17         | 123.5 | 5.3         | 662    | US-11-301-764-112   | Sequence 112, App  |
| 18         | 112   | 4.8         | 336    | US-10-953-349-18546 | Sequence 18546, A  |
| 19         | 112   | 4.8         | 372    | US-10-953-349-18545 | Sequence 18545, A  |
| 20         | 111.5 | 4.8         | 979    | US-11-301-764-7     | Sequence 7, Appli  |
| 21         | 106   | 4.6         | 635    | US-10-511-937-2424  | Sequence 2424, Ap  |
| 22         | 104.5 | 4.5         | 530    | US-10-449-902-36140 | Sequence 36140, A  |
| 23         | 104   | 4.5         | 970    | US-11-301-764-120   | Sequence 120, App  |
| 24         | 103.5 | 4.5         | 459    | US-10-511-937-2465  | Sequence 2465, Ap  |
| 25         | 102.5 | 4.4         | 459    | US-11-297-957-2     | Sequence 2, Appli  |

|    |      |     |      |                     |                    |
|----|------|-----|------|---------------------|--------------------|
| 26 | 102  | 4.4 | 17   | US-11-134-871-727   | Sequence 727, App  |
| 27 | 98.5 | 4.2 | 731  | US-11-155-444-6     | Sequence 6, Appli  |
| 28 | 98.5 | 4.2 | 731  | US-11-156-109-6     | Sequence 6, Appli  |
| 29 | 98.5 | 4.2 | 735  | US-11-155-444-10    | Sequence 10, Appli |
| 30 | 98.5 | 4.2 | 735  | US-11-156-109-10    | Sequence 10, Appli |
| 31 | 97.5 | 4.2 | 984  | US-11-259-133-22    | Sequence 22, Appli |
| 32 | 96   | 4.1 | 384  | US-11-293-697-2595  | Sequence 2595, Ap  |
| 33 | 96   | 4.1 | 996  | US-11-285-738-2     | Sequence 2, Appli  |
| 34 | 94.5 | 4.1 | 1259 | US-10-561-015-5     | Sequence 5, Appli  |
| 35 | 93.5 | 4.0 | 836  | US-10-511-937-2988  | Sequence 2988, Ap  |
| 36 | 93   | 4.0 | 531  | US-10-449-902-43013 | Sequence 43013, A  |
| 37 | 92.5 | 4.0 | 287  | US-10-953-349-18547 | Sequence 18547, A  |
| 38 | 92.5 | 4.0 | 983  | US-11-302-678-2     | Sequence 2, Appli  |
| 39 | 92.5 | 4.0 | 983  | US-11-259-133-6     | Sequence 6, Appli  |
| 40 | 92   | 4.0 | 353  | US-10-953-349-12271 | Sequence 32271, A  |
| 41 | 90.5 | 3.9 | 739  | US-11-301-764-69    | Sequence 69, Appli |
| 42 | 89.5 | 3.9 | 337  | US-11-274-375-2     | Sequence 2, Appli  |
| 43 | 89.5 | 3.9 | 428  | US-11-274-375-4     | Sequence 4, Appli  |
| 44 | 89.5 | 3.9 | 629  | US-11-274-375-6     | Sequence 6, Appli  |
| 45 | 89.5 | 3.9 | 1204 | US-11-289-102-236   | Sequence 236, App  |

## ALIGNMENTS

RESULT 1  
US-11-331-993-7  
Sequence 7, Application US/11331993  
Publication No. US20060110800A1  
GENERAL INFORMATION:  
APPLICANT: Baumgartner, James W.  
Foster, Theresa M.  
Foster, Donald C.  
Grant, Frank J.  
O'Hara, Patrick J.  
TITLE OF INVENTION: Testis-Specific Receptor  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/331,993  
FILING DATE: 04-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/090,867  
FILING DATE: 04-Jun-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, Gary E.  
REGISTRATION NUMBER: 31,648  
REFERENCE/DOCKET NUMBER: 95-33  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6673  
TELEFAX: 206-442-6678  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 372 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-11-331-993-7  
Query Match 13.0%; Score 302; DB 7; Length 372;



Best Local Similarity 27.5%; Pred. No. 3.2e-18;  
Matches 95; Conservative 60; Mismatches 127; Indels 64; Gaps 19;  
QY 51 WNPPEBASS--NCSLMYFSHFQDKODKTLAPETRRSI-----EVLNERICQVGS 99  
DB 53 WQPPSLDHFKECTVEY-----ELKRYNIGSETWTKIITKNLHYKQGFPLNGKIEAKIHT 107  
QY 100 ---OCSTNESEKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSP 153  
DB 108 LILPMQC-TNGSEVQSSMAETTWIS--PQGIPEFTKVQDMCVYNNWQYLCSMKRPGIGVLL 165  
QY 154 DNNYTLTYWHRSLSEKTHOCENIR-EGQYFGCSFDLTQVDSSEFGHSAVQIMKDNAGKI 212  
DB 166 DNNYTLFYWYEGIDRALQCVDIYIKADQNGICRFPY--LESSDYKOFYICVNGSSETKPI 223  
QY 213 KPSFNIVPLTSRYKPPPHIKNLSFHNDDLY---VQWENQNTL-SRCLFEYEVANNST 268  
DB 224 RSYFFPQOLNIYKPLPPVC--LTCTQESLYEIKLTKMIDPLGFIAPRCFYIEIREDDT 281  
QY 269 ETHNVEYVOEAKCENEFERNVENTS---CFWVPGVLPDLTNTVRIRVKTNKLCEYDDKL 325  
DB 282 T-----LVTTVENETVTLKITNETRQCFVY-----RSKNVNYC-SDDGI 321  
QY 326 WSNWSQEM--SICKKRNSTLYITMLLIVPIYVAGAILVLLYKRL 369  
DB 322 WSEMSDKOCWEGBELLKTL--LFLLPF---GFLILVIFVGTG 361

RESULT 2  
US-11-220-888-4

/ Sequence 4, Application US/11220888  
/ Publication No. US2006009652A1  
/ GENERAL INFORMATION:  
/ APPLICANT: GATELY, Stephen C.  
/ APPLICANT: MANASKI, Stephen P.  
/ TITLE OF INVENTION: IL 13 RECEPTOR ALPHA 2 ANTIBODY AND METHODS OF USE  
/ FILE REFERENCE: 238603  
/ CURRENT APPLICATION NUMBER: US/11/220,888  
/ PRIOR FILING DATE: 2005-09-07  
/ PRIOR APPLICATION NUMBER: PCT/US2004/009354  
/ PRIOR FILING DATE: 2003-03-26  
/ PRIOR APPLICATION NUMBER: US 60/457,898  
/ PRIOR FILING DATE: 2003-03-26  
/ NUMBER OF SEQ ID NOS: 4  
/ SOFTWARE: PatentIn version 3.3  
/ SEQ ID NO 4  
/ LENGTH: 380  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: MISC FEATURE  
/ OTHER INFORMATION: Interleukin 13 receptor, alpha 2  
US-11-220-888-4

Query Match 12.7%; Score 294.5; DB 7; Length 380;  
Best Local Similarity 27.0%; Pred. No. 1.4e-17;  
Matches 100; Conservative 59; Mismatches 138; Indels 73; Gaps 20;

QY 51 WNPPEBASS--SNCSLMYFSHFQDKODKTLAPETRRSI-----EVLNERICQVGS 99  
DB 53 WQPPSLDHFKECTVEY-----ELKRYNIGSETWTKIITKNLHYKQGFPLNGKIEAKIHT 107  
QY 100 ---OCSTNESEKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSP 153  
DB 108 LILPMQC-TNGSEVQSSMAETTWIS--PQGIPEFTKVQDMCVYNNWQYLCSMKRPGIGVLL 165  
QY 154 DNNYTLTYWHRSLSEKTHOC-ENIFREGQYFGCSFDLTQVDSSEFGHSAVQIMKDNAGKI 212  
DB 166 DNNYTLFYWYEGIDRALQCVDIYIKADQNGICRFPYLEASD--YKDFYICVNGSSENKPI 223  
QY 213 KPSFNIVPLTSRYKPPPHIKNLSFHNDDLY---VQWENQNTL-SRCLFEYEVANNST 268  
DB 224 RSYFFPQOLNIYKPLPP--VYLTFTRESSCEIKLKMISIPLGPIPARCFDYIEIREDDT 281

QY 269 ETHNVEYVOEAKCENEFERNVENTS---CFWVPGVLPDLTNTVRIRVKTNKLCEYDDKL 325  
DB 282 T-----LVATAVENETVTLKITNETRQCFVY-----RSKNVNYC-SDDGI 321  
QY 326 WSNWSQEM--SICKKRNSTLYITMLLIVPIYVAGAILVLLYKRLKIIIFPPIPD 360  
DB 322 WSEMSDKOCWEGBEDLSKTLIRFWLPF-----GFLILVIFVGTG--LIRKNTY 370  
QY 381 GKIFKEMFGD 390  
DB 371 -KMIFEFCD 379

RESULT 3  
US-11-331-993-2

/ Sequence 2, Application US/11331993  
/ Publication No. US20060110800A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Baumgartner, James W.  
/ Farrah, Theresa M.  
/ Foster, Donald C.  
/ Grant, Frank J.  
/ O'Hara, Patrick J.  
/ TITLE OF INVENTION: Testis-Specific Receptor  
/ NUMBER OF SEQUENCES: 33  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Zymogenetics, Inc.  
/ STREET: 1201 Eastlake Avenue East  
/ CITY: Seattle  
/ STATE: WA  
/ COUNTRY: USA  
/ ZIP: 98102  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/11/331,993  
/ FILING DATE: 04-Jun-1998  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/090,867  
/ FILING DATE: 04-Jun-1998  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Parker, Gary E.  
/ REGISTRATION NUMBER: 31,648  
/ REFERENCE/DOCKET NUMBER: 95-33  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 206-442-6673  
/ TELEFAX: 206-442-6678  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 380 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-11-331-993-2

Query Match 12.7%; Score 294.5; DB 7; Length 380;  
Best Local Similarity 27.0%; Pred. No. 1.4e-17;  
Matches 100; Conservative 59; Mismatches 138; Indels 73; Gaps 20;

QY 51 WNPPEBASS--SNCSLMYFSHFQDKODKTLAPETRRSI-----EVLNERICQVGS 99  
DB 53 WQPPSLDHFKECTVEY-----ELKRYNIGSETWTKIITKNLHYKQGFPLNGKIEAKIHT 107  
QY 100 ---OCSTNESEKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSMLPGRNTSP 153  
DB 108 LILPMQC-TNGSEVQSSMAETTWIS--PQGIPEFTKVQDMCVYNNWQYLCSMKRPGIGVLL 165

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2006, 01:21:03 ; Search time 195 Seconds  
(without alignments)  
998.842 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 426  
Sequence: 1 MEMPARICGMALLCAGGG.....QTKETDSVVLIENTKKASQ 426

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
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| 2          | 401   | 94.1        | 414    | 8     | ADX97531 Pandreati  |
| 3          | 401   | 94.1        | 427    | 2     | AAW24973 Human int  |
| 4          | 401   | 94.1        | 427    | 4     | AAAB19807 Human int |
| 5          | 401   | 94.1        | 427    | 8     | ADL17812 Human int  |
| 6          | 401   | 94.1        | 427    | 8     | ADL82843 Human PRO  |
| 7          | 401   | 94.1        | 427    | 8     | ADN04504 Antipsori  |
| 8          | 401   | 94.1        | 427    | 8     | ADN62575 Human int  |
| 9          | 401   | 94.1        | 427    | 8     | ADN82441 Tumour-as  |
| 10         | 401   | 94.1        | 427    | 9     | AEC31473 Human IL-  |
| 11         | 401   | 94.1        | 427    | 10    | AEE93788 Human nt   |
| 12         | 401   | 94.1        | 427    | 10    | AEE93788 Human nt   |
| 13         | 401   | 94.1        | 427    | 10    | AEE93788 Human nt   |
| 14         | 331   | 77.7        | 427    | 7     | ADL17812 Human int  |
| 15         | 331   | 77.7        | 427    | 7     | ADL17812 Human int  |
| 16         | 317   | 74.4        | 322    | 5     | AAE13745 Human sol  |
| 17         | 317   | 74.4        | 322    | 5     | AAE13745 Human sol  |
| 18         | 317   | 74.4        | 784    | 3     | AAW02180 Human IL-  |
| 19         | 317   | 74.4        | 793    | 3     | AAW02180 Human IL-  |
| 20         | 300   | 70.4        | 427    | 7     | ADL17812 Human int  |
| 21         | 297   | 69.7        | 776    | 8     | AEC31482 Human IL-  |
| 22         | 297   | 69.7        | 776    | 9     | AEC31482 Human IL-  |
| 23         | 297   | 69.7        | 776    | 9     | AEC31484 Human IL-  |

## ALIGNMENTS

|          |   |
|----------|---|
| RESULT 1 |   |
| AAW09822 | AAW09822 standard; protein; 426 AA.                                   |
| ID       | AAW09822;   |
| AC       | AAW09822;   |
| XX       |   |
| DT       | 15-JUL-1997 (first entry)   |
| XX       |   |
| DE       | Human interleukin-12 receptor alpha chain NR4.                        |
| XX       |   |
| KM       | NR4; haemopoietin receptor; interleukin-13 receptor; IL-13; cytokine; |
| KW       | allergy; asthma; therapy.   |
| XX       |   |
| OS       | Homo sapiens.   |
| XX       |   |
| PH       | Key   |
| FT       | peptide   |
| FT       | 1..27   |
| FT       | /label= Sig_peptide   |
| FT       | 28..426   |
| FT       | /label= Mat_protein   |
| FT       | 28..118   |
| FT       | /label= Extracellular domain  |
| FT       | /note= "Ig-like domain"   |
| FT       | 36  |
| FT       | /label= N-glycosylation site  |
| FT       | 104   |
| FT       | /label= N-glycosylation site  |
| FT       | 119..342  |
| FT       | /label= Hemoreceptor_receptor-domain                                  |
| FT       | 137   |
| FT       | /label= N-glycosylation site  |
| FT       | 326..330  |
| FT       | /label= WSDWS_motif   |
| FT       | 343..366  |
| FT       | /label= Transmembrane_domain  |
| FT       | 367..426  |
| FT       | /label= Cytoplasmic_tail  |
| XX       |   |
| XX       | WC9715663-A1.   |
| XX       |   |
| XX       | 01-MAY-1997.  |
| XX       |   |
| PF       | 23-OCT-1996; 96MO-AU000668.   |
| XX       |   |
| XX       | 23-OCT-1995; 95AU-00006135.   |
| PR       | 22-DEC-1995; 95AU-00007276.   |

PR 09-SEP-1996; 96AU-00002208.  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
XX Willson T, Nicola NA, Hilton DJ, Metcalf D, Zhang JG;  
XX MPI, 1997-259018/23.  
XX N-PSDB; AAT6165.  
XX  
XX DNA encoding animal haemopoietin receptor which interacts with  
XX interleukin-13 - useful to treat asthma, allergy or condition exacerbated  
XX by IGE production.  
XX  
XX Claim 5; Page 52-54; 93pp; English.  
XX  
XX Novel mouse and human haemoprotein receptors (AAW09821 and AAW09822),  
XX designated NR4, comprise the interleukin-13 (IL-13) receptor alpha-chain.  
XX The human NR4 amino acid sequence was deduced from a composite DNA  
XX sequence (AAT6165) derived from bone marrow cDNA clones. Recombinant  
XX NR4, or fusion proteins including NR4, can be produced in transformed  
XX host cells. The receptor molecules and their components are useful in the  
XX development of a range of agonists, antagonists, therapeutics and  
XX diagnostic reagents based on ligand interaction with its receptor. esp.  
XX for the development of cpds. capable of modulating the activity of IL-13  
XX and related cytokines such as interleukin-4 for the treatment of allergy,  
XX asthma and other conditions relating to IGE  
XX  
XX Sequence 426 AA;

Query Match 100.0%; Score 426; DB 2; Length 426;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEMPARLCGIMALLLCAGGGGGGGAPTERTQPVNTLSVENVLCYIWTWNPPEGASSN 60  
DB 1 MEMPARLCGIMALLLCAGGGGGGGAPTERTQPVNTLSVENVLCYIWTWNPPEGASSN 60  
QY 61 CSLMYFSHFQDKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 120  
DB 61 CSLMYFSHFQDKODKKIAPETRRSIEVPLNERICLOVSGQCSSTNESEKPSILVEKCI 120  
QY 121 EGDPEBAVTELQCIWHNLSTYMKCSWLPGRNTSPDNTYTLTYMHRSLKTHQCNIRFEGQ 180  
DB 121 EGDPEBAVTELQCIWHNLSTYMKCSWLPGRNTSPDNTYTLTYMHRSLKTHQCNIRFEGQ 180  
QY 121 YFGCSFDLTKVKQSSFEQHSVOIMVKNDAKIRPSFNIVPLTSRVKDPPIHNLSPHND 240  
DB 121 YFGCSFDLTKVKQSSFEQHSVOIMVKNDAKIRPSFNIVPLTSRVKDPPIHNLSPHND 240  
QY 181 YFGCSFDLTKVKQSSFEQHSVOIMVKNDAKIRPSFNIVPLTSRVKDPPIHNLSPHND 240  
DB 181 YFGCSFDLTKVKQSSFEQHSVOIMVKNDAKIRPSFNIVPLTSRVKDPPIHNLSPHND 240  
QY 241 DLYVQWENPQNFISRLCFYEVEVNNSTETHNFYVOEAKCENDEPERNVENTSCFVPG 300  
DB 241 DLYVQWENPQNFISRLCFYEVEVNNSTETHNFYVOEAKCENDEPERNVENTSCFVPG 300  
QY 301 VLPDITNTYAIRKYTKMLCYEDDKLWMSNWSQEMSIGKRNSTYITMLLIVPIYAGAIT 360  
DB 301 VLPDITNTYAIRKYTKMLCYEDDKLWMSNWSQEMSIGKRNSTYITMLLIVPIYAGAIT 360  
QY 361 VLLLYLKRLKILFFPPIPDGKIFKEMFGPNDLTHMKYDYLYEKOTKEETOSVVLLEN 420  
DB 361 VLLLYLKRLKILFFPPIPDGKIFKEMFGPNDLTHMKYDYLYEKOTKEETOSVVLLEN 420  
QY 421 LKKASQ 426  
DB 421 LKKASQ 426

RESULT 2  
ADX97531  
ID ADX97531 standard; protein; 414 AA.  
XX AC ADX97531;  
XX  
XX 21-APR-2005 (first entry)

XX  
XX Pancreatic cancer associated human protein, SEQ ID 79.  
XX  
XX pancreas tumor; cytostatic.  
XX  
XX Homo sapiens.  
XX  
XX EPI471075-A2.  
XX  
XX 27-OCT-2004.  
XX  
XX 31-MAR-2004; 2004EP-00090124.  
XX  
XX 31-MAR-2003; 2003DE-01015834.  
XX  
XX (HINZ/) HINZMANN B.  
XX (ROSE/) ROSENTHAL A.  
XX (PILA/) PILARSKY C.  
XX (DAHL/) DAHL E.  
XX (SPEC/) SPECHT T.  
XX (LICH/) LICHTNER R.  
XX  
XX Rosenthal A, Pilarsky C, Dahl E, Specht T, Bruemendorf T;  
XX Lichten R, Straub E, Roepeke S, Li X;  
XX  
XX MPI; 2004-768082/76.  
XX N-PSDB; ADX97460.  
XX  
XX New nucleic acid differentially expressed in pancreatic tumor tissue, for  
XX use as diagnostic agents and in screening for therapeutic agents.  
XX  
XX Claim 2; SEQ ID NO 79; 28pp; German.  
XX

The invention relates to a novel human nucleic acid sequence of the  
pancreas and its encoded protein. The invention further comprises:  
proteins and peptides, preferably isolated, that contain a sequence  
encoded by the novel nucleic acid; and methods for diagnosis and  
treatment of pancreatic cancer, using a substance that inhibits or binds  
to the protein or its DNA, including: an antisense oligonucleotide, short  
interfering RNA or ribozyme directed against the pancreatic protein, an  
organic molecule, particularly having a molecular weight below 5000,  
especially 300, that binds to the pancreatic DNA, an aptamer or  
(monoclonal) antibody, preferably human or humanized, that binds to the  
pancreatic DNA, or an anti-idiotypic antibody raised against the  
monoclonal antibody, any of which may be derivatized with a reporter  
group, cytotoxic compound, immunostimulant and/or radioisotope. The novel  
human pancreatic proteins and their encoding DNA have cytostatic  
activity. The novel sequences are useful for inhibiting transcription  
and/or expression of genes and proteins associated with pancreatic  
cancer. This sequence represents one of the novel human pancreatic  
proteins of the invention. Note: This sequence is not shown in the  
specification, it has been electronically downloaded from a DVD-ROM  
provided with this specification by the European Patent Office.

Sequence 414 AA;

Query Match 94.1%; Score 401; DB 8; Length 414;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTERTQPVNTLSVENVLCYIWTWNPPEGASSNCSLMYFSHFQDKODKKIAPETRRSI 85  
DB 14 APTERTQPVNTLSVENVLCYIWTWNPPEGASSNCSLMYFSHFQDKODKKIAPETRRSI 73  
QY 86 EVDPLNERICLOVSGQCSSTNESEKPSILVEKCI 145  
DB 74 EVDPLNERICLOVSGQCSSTNESEKPSILVEKCI 133  
QY 146 LPERNTSPDNTYTLTYMHRSLKTHQCNIRFEGQYFGSGPDLTKYKQSSFEQHSVOIMV 205  
DB 134 LPERNTSPDNTYTLTYMHRSLKTHQCNIRFEGQYFGSGPDLTKYKQSSFEQHSVOIMV 193  
QY 206 KDNAGKIKPSFNIIVPLTSRVKDPPIHNLSPHNDLTVQWENPQNFISRLCFYEVEVNN 265

```

Db      194 KDAGKIKPSFNTVPLISRVKPDPPHKNLSFHNDDLYVOMENPNTSRCLFYEVEVNN 253
QY      266 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 325
Db      254 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 313
QY      326 MSNWSQMSIGKRNSTLYITMLLIVPVIAGAIIVLLYLKRLKIIIFPPIPDGKIFK 385
Db      314 MSNWSQMSIGKRNSTLYITMLLIVPVIAGAIIVLLYLKRLKIIIFPPIPDGKIFK 373
QY      386 EMFGDQNDPTLHMKKYDIYEKQTEETDSVVLINLKKASQ 426
Db      374 EMFGDQNDPTLHMKKYDIYEKQTEETDSVVLINLKKASQ 414

RESULT 3
AAW24973
ID      AAW24973 standard; protein; 427 AA.
AC      AAW24973;
XX
DT      22-JUN-1998 (first entry)
DE      Human interleukin-13 alpha receptor.
XX
KM      Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.
XX
OS      Homo sapiens.
XX
PN      MO9720926-A1.
PD      12-JUN-1997.
PF      07-NOV-1996; 96MO-FR001756.
PR      06-DEC-1995; 95FR-00014424.
PA      (SNFI ) SANOFI SA.
XX
PI      Caput D, Ferrara P, Laurent P, Vitta N;
XX      WPI; 1997-319773/29.
DR      N-PSDB; AAT85827.
XX
PT      New purified human interleukin-13 receptors - and related nucleic acids,
PT      useful for diagnosis and treatment of inflammation, allergy, etc.
XX
PS      Claim 8; Page 46-47; 83pp; French.
XX
CC      This sequence represents interleukin-13 (IL-13) alpha receptor. The
CC      invention relates to new purified peptides comprising 380 or 427 amino
CC      acid sequences, which are receptors for interleukin-13 (IL-13); the 380
CC      and 427 aa proteins are designated IL-13R beta and alpha respectively.
CC      The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low
CC      affinity, but acquires high affinity when associated with the IL-4
CC      receptor. Nucleic acids encoding IL-13R beta and alpha are used as
CC      diagnostic probes to identify aberrant synthesis or genetic anomalies
CC      such as loss of heterozygosity and rearrangements, or chromosomal
CC      anomalies. They are also used for production of recombinant IL-13R beta
CC      and alpha which can be used as IL-13 antagonists, specifically to
CC      regulate IL-13-induced responses for treatment of inflammation and
CC      allergy. IL-13 receptors are also useful as antisense molecules for gene
CC      therapy (blocking synthesis of IL-13R). Antibodies are used (in standard
CC      immunassays) to diagnose diseases associated with abnormal expression of
CC      IL-13 receptors; when coupled to a toxin also for treatment of
CC      overproduction of IL-13R. Cells that express IL-13R at the surface are
CC      used to identify ligands and modulators of IL-13R
XX
SQ      Sequence 427 AA:
Query Match      94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;

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Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      26 APTETOPVNTLSVSVENLCTVIMTNPPGASNCSLMWFSHRGDKODKXIABETRRI 85
Db      27 APTETOPVNTLSVSVENLCTVIMTNPPGASNCSLMWFSHRGDKODKXIABETRRI 86
QY      86 EVPLNERICQVGSQCSSTNESEKPSILVEKCSPEEGDPESAATVLOCIMHNLGYMKCSW 145
Db      87 EVPLNERICQVGSQCSSTNESEKPSILVEKCSPEEGDPESAATVLOCIMHNLGYMKCSW 146
QY      146 LPEGNTSPDTNNTLYVWHSLEKIHQCENTIFREGQYFGCSFDLTRKVSSEFGHSVOIMV 205
Db      147 LPEGNTSPDTNNTLYVWHSLEKIHQCENTIFREGQYFGCSFDLTRKVSSEFGHSVOIMV 206
QY      206 KDAGKIKPSFNTVPLISRVKPDPPHKNLSFHNDDLYVOMENPNTSRCLFYEVEVNN 265
Db      207 KDAGKIKPSFNTVPLISRVKPDPPHKNLSFHNDDLYVOMENPNTSRCLFYEVEVNN 266
QY      266 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 325
Db      267 SOTETHNVFYVOEAKCENPEPERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEYEDDKL 326
QY      326 MSNWSQMSIGKRNSTLYITMLLIVPVIAGAIIVLLYLKRLKIIIFPPIPDGKIFK 385
Db      327 MSNWSQMSIGKRNSTLYITMLLIVPVIAGAIIVLLYLKRLKIIIFPPIPDGKIFK 386
QY      386 EMFGDQNDPTLHMKKYDIYEKQTEETDSVVLINLKKASQ 426
Db      387 EMFGDQNDPTLHMKKYDIYEKQTEETDSVVLINLKKASQ 427

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RESULT 4
AAB19807
ID      AAB19807 standard; protein; 427 AA.
AC      AAB19807;
XX
DT      05-MAR-2001 (first entry)
DE      Human interleukin-13 receptor alpha-1.
XX
KM      Interleukin-13 receptor alpha-1; interleukin-4; human; atopy;
KM      atopic dermatitis; allergy; rhinitis; eczema; asthma; AIDS;
KM      dermatological; antiaesthetic; antiallergic; therapy; diagnosis.
XX
OS      Homo sapiens.
XX
PS      Key      Location/Qualifiers
PS      Key      1..26
PS      Peptide  /label= Sig_Peptide
PS      FT      27..347
PS      FT      /label= Extracellular_domain
PS      FT      28..427
PS      FT      /label= Mature_protein
PS      FT      327..331
PS      FT      /note="MSXMS motif conserved in the type-1 cytokine
PS      FT      receptor superfamily"
PS      FT      Domain 348..367
PS      FT      /label= Transmembrane_domain
PS      FT      Domain 368..427
PS      FT      /label= Cytoplasmic_domain
PS      FT      Binding-site 405..408
PS      FT      /note="YXXQ motif, consensus for STAT binding"
XX
PN      US6143871-A.
PD      07-NOV-2000.
PF      12-NOV-1997; 97US-00969125.
PR      13-DEC-1996; 96GB-00025899.
PA      (GAUC/) GAUCHAR J.

```



QY 266 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNLCYEDDKL 325  
| | | | |  
DB 267 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNLCYEDDKL 326  
| | | | |  
QY 326 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 385  
| | | | |  
DB 327 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 386  
| | | | |  
QY 386 EMFGDQNDPDLHWKKYDIYEKQTEETDSVLIENLKASQ 426  
| | | | |  
DB 387 EMFGDQNDPDLHWKKYDIYEKQTEETDSVLIENLKASQ 427  
| | | | |  
RESULT 6  
ADL82843  
ID ADL82843 standard; protein: 427 AA.  
XX  
AC ADL82843;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human PRO2537, SEQ ID 45.  
XX  
KM Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;  
KW Antiallergic; Muscular; Neuroprotective; Nephrotoxic; Antiinflammatory;  
KW Gene Therapy; PRO; B cell related disorder; cancer;  
KM Immune-mediated inflammatory disease; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024097-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 15-SEP-2003; 2003MO-US029097.  
XX  
PR 16-SEP-2002; 2002US-0411392P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WT;  
PI Wu TD;  
XX  
DR MPI; 2004-329389/30.  
XX  
DR N-PSDB; ADL82842.  
XX  
PT New PRO polypeptide, useful for diagnosing and treating a B cell related  
PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune  
PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.  
XX  
PS Claim 10; Fig 45; 695pp; English.  
XX  
CC The present invention relates to PRO proteins and their coding sequences.  
CC The PRO proteins are useful for diagnosing and treating a B cell related  
CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polyclonal  
CC antigen unresponsiveness, selective IgM deficiency, selective IgM  
CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with  
CC hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's  
CC lymphoma, intermediate lymphoma, follicular lymphoma, type II  
CC hypersensitivity, rheumatoid arthritis, autoimmune mediated hemolytic  
CC anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or  
CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
CC medicament for treating a condition that is responsive to the PRO  
CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO  
CC coding sequences are useful as hybridization probes in chromosome and  
CC gene mapping, in preparing PRO proteins, or in generating transgenic  
CC animals or knockout animals, which in turn are useful in the development  
CC and screening of therapeutically useful reagents.  
XX  
SQ Sequence 427 AA;  
Query Match 94.1%; Score 401; DB 8; Length 427;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 APTEOPVNLISVSENLCTVITWNPBPASSNCSIMVSHHGDKQDKXIAPETRSI 85  
| | | | |  
DB 27 APTEOPVNLISVSENLCTVITWNPBPASSNCSIMVSHHGDKQDKXIAPETRSI 86  
| | | | |  
QY 86 EVPLNERICLVQSGCSTNSESEKPSILVEKISPPEDPESAVTELOCIMNLSYMKCSW 145  
| | | | |  
DB 87 EVPLNERICLVQSGCSTNSESEKPSILVEKISPPEDPESAVTELOCIMNLSYMKCSW 146  
| | | | |  
QY 146 LPGRNTSPDNTNYLYYHRSLEKIHQCCENIFREGQYFGCSFDLTKVDSSEQHSVOIMV 205  
| | | | |  
DB 147 LPGRNTSPDNTNYLYYHRSLEKIHQCCENIFREGQYFGCSFDLTKVDSSEQHSVOIMV 206  
| | | | |  
QY 206 KDNAGKIKPSFNIVPLLSRVKPPDPHILKNLSFNHDDLVOEMENPQNFISRLCFYEVEVNN 265  
| | | | |  
DB 207 KDNAGKIKPSFNIVPLLSRVKPPDPHILKNLSFNHDDLVOEMENPQNFISRLCFYEVEVNN 266  
| | | | |  
QY 266 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNLCYEDDKL 325  
| | | | |  
DB 267 SQTETHAVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKVTKNLCYEDDKL 326  
| | | | |  
QY 326 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 385  
| | | | |  
DB 327 WSNWSQMSIGKKRNSTLYITMLLIVPIVAGAIIVLLVYKRLKIIIFPPIPDGKIFK 386  
| | | | |  
QY 386 EMFGDQNDPDLHWKKYDIYEKQTEETDSVLIENLKASQ 426  
| | | | |  
DB 387 EMFGDQNDPDLHWKKYDIYEKQTEETDSVLIENLKASQ 427  
| | | | |  
RESULT 7  
ADN04504  
ID ADN04504 standard; protein: 427 AA.  
XX  
AC ADN04504;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Antipsoriatic protein sequence #445.  
XX  
KW antipsoriatic; gene therapy; psoriasis; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2004028479-A2.  
XX  
PD 08-APR-2004.  
XX  
PF 25-SEP-2003; 2003MO-US030907.  
XX  
PR 25-SEP-2002; 2002US-0414006P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;  
PI Wu TD;  
XX  
DR MPI; 2004-305105/28.  
XX  
DR N-PSDB; ADN04503.  
XX  
PT New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.  
XX  
XX Claim 9; SEQ ID NO 898; 3069pp; English.  
XX  
CC The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polypeptides of the invention.





| Query Match           | 94.1%  | Score 401   | DB 8         | Length 427 |
|-----------------------|--|-------------|--------------|------------|
| Beet Local Similarity | 100.0%   | Pred. No. 0 |              |            |
| Matches 401           | Conservative   | 0           | Mismatches 0 | Indels 0   |
|                       |  |             | Gaps 0       |            |
| 26                    | APTEOPVNTLMSVENVLCYIMWNPBEGASSNCSLWYFSPGDKDKKIAPEFRSI        | 85          |              |            |
| 27                    | APTEOPVNTLMSVENVLCYIMWNPBEGASSNCSLWYFSPGDKDKKIAPEFRSI        | 86          |              |            |
| 86                    | EVPLNERICLOVGSQCSSTNESEKPSILVEKCSIPBEGPDESAVTELOCIWHLSTYKCSW | 145         |              |            |
| 87                    | EVPLNERICLOVGSQCSSTNESEKPSILVEKCSIPBEGPDESAVTELOCIWHLSTYKCSW | 146         |              |            |
| 146                   | LGNTSPTDNTVTLVYMRSLKTHOCENIPREGQVFGCSPLTTRYKXSSFECHSVQIMV    | 205         |              |            |

| Db        | 147  | PGRNTSDPTNVTLYVMHRSLEKIHQCENI | PREGQVFGGS                       | PDLTYKXDSSEQHSQIWM | 206 |
|-----------|--|-------------------------------|----------------------------------|--------------------|-----|
| QY        | 206  | KDNAGKIRPSFNIVPLTSRKVDP       | PHIKLSTHNDLLYQWENPQNFISCLFYEEVNN | 265                |     |
| Db        | 207  | KDNAGKIRPSFNIVPLTSRKVDP       | PHIKLSTHNDLLYQWENPQNFISCLFYEEVNN | 266                |     |
| QY        | 266  | SQTEHNHFVYQEAACENDEPERNVENTS  | CFWVPGVLPDLTVLRIRVKTNKL          | CYEDDKL            | 325 |
| Db        | 267  | SQTEHNHFVYQEAACENDEPERNVENTS  | CFWVPGVLPDLTVLRIRVKTNKL          | CYEDDKL            | 326 |
| QY        | 326  | MSNMSEQMSIGKRNSTLYITMLLV      | PVACAIIVLLLYLKRKLII              | FPPIPDGKIFK        | 365 |
| Db        | 327  | MSNMSEQMSIGKRNSTLYITMLLV      | PVACAIIVLLLYLKRKLII              | FPPIPDGKIFK        | 366 |
| QY        | 386  | EMFGDQNDPTLHMKKYDIYEKQTEKETS  | SVLIENIKKASQ                     | 426                |     |
| Db        | 387  | EMFGDQNDPTLHMKKYDIYEKQTEKETS  | SVLIENIKKASQ                     | 427                |     |
| RESULT 10 |  |                               |                                  |                    |     |
| ID        | AEC31473   | standard; protein; 427 AA.    |                                  |                    |     |
| XX        | AC   | AEC31473;                     |                                  |                    |     |
| XX        | AC   | AEC31473;                     |                                  |                    |     |
| DT        | 03-NOV-2005  | (first entry)                 |                                  |                    |     |
| DE        | Human IL-13 receptor alpha-1   | SEQ ID NO:3.                  |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| KW        | interleukin-13 receptor; fusion protein; therapeutic; antiasthmatic; antiallergic; dermatological; anti-inflammatory; immunosuppressive; cyostatic; hepatotropic; anti-HIV; virulide; gastrointestinal-gen; antibacterial; fungicide; antiparasitic; antitumor; antithyroid; nephrotropic. |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| OS        | Homo sapiens.  |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| FT        | Key  | Location/Qualifiers           |                                  |                    |     |
| FT        | Domain   | 27..343                       |                                  |                    |     |
| FT        |  | /label = extracellular domain |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| EN        | US2005191730-A1.   |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| PD        | 01-SEP-2005.   |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| PF        | 25-FEB-2005; 2005US-00067251.  |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| PR        | 27-FEB-2004; 2004US-0548541P.  |                               |                                  |                    |     |
| PR        | 17-AUG-2004; 2004US-0602139P.  |                               |                                  |                    |     |
| PR        | 16-NOV-2004; 2004US-0628343P.  |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| PA        | (REGE-) REGENERON PHARM INC.   |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| FI        | Karow M, Fairhurst J;  |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| DR        | WPI; 2005-590777/60.   |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| PT        | New nucleic acid molecules encoding polypeptides capable of binding interleukin-4 and interleukin-13, useful for diagnosing and/or treating asthma, lupus, Grave's disease, hepatic fibrosis, HIV infection, cancer and infections.  |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| PS        | Claim 1; SEQ ID NO 3; 35pp; English.   |                               |                                  |                    |     |
| XX        | XX   |                               |                                  |                    |     |
| CC        | The invention relates to a novel nucleic acid molecule encoding a fusion polypeptide. The fusion polypeptide consists of 231 amino acids   |                               |                                  |                    |     |
| CC        | -231 and 24-231 of a fully defined sequence of 231 amino acids   |                               |                                  |                    |     |
| CC        | (AEC31472), which sequences may comprise 1-10 modifications, R2 is a fully defined sequence of 427 or 380 bp (AEC31473/AEC31474), which  |                               |                                  |                    |     |
| CC        | sequences may comprise one to three modifications, F is a fusion component, and x and y are each independently a positive integer 1. The F   |                               |                                  |                    |     |
| CC        | is a multimerizing component, a serum protein, or a molecule capable of binding a serum protein, where the multimerizing component is an   |                               |                                  |                    |     |

|           |                           |  |
|-----------|---------------------------|--|
| CC        |                           | immunoglobulin-derived domain, a cleavable region (C-region), an antio     |
| CC        |                           | acid sequence between 1-500 amino acids in length, optionally comprising   |
| CC        |                           | at least one cysteine residue, a leucine zipper, a helix loop motif, or a  |
| CC        |                           | coil-coil motif. The immunoglobulin-derived domain is the Fc domain of     |
| CC        |                           | IGG or the heavy chain of IGG. A fusion protein of the invention has       |
| CC        |                           | antiasthmatic, anti-allergic, dermatological, anti-inflammatory,           |
| CC        |                           | immunosuppressive, cytostatic, hepatotropic, anti-HIV, virocidic,          |
| CC        |                           | gastrointestinal-gen, antibacterial, fungicide, antiparasitic, anti-ulcer, |
| CC        |                           | anti-thyroid, and nephrotropic activity. The protein has a use in gene     |
| CC        |                           | therapy, and acts as an interleukin-antagonist. The methods and            |
| CC        |                           | compositions of the invention are useful for the diagnosis, prevention     |
| CC        |                           | and/or treatment of diseases or conditions associated with aberrant        |
| CC        |                           | expression or activity of IL-4 and/or IL-13, such as asthma, atopic        |
| CC        |                           | dermatitis, lupus, nephritis, Grave's disease, hepatic fibrosis, HIV       |
| CC        |                           | infection, ulcerative colitis, cancer, and viral, parasitic, bacterial     |
| CC        |                           | and fungal infections. The present sequence represents human IL-13         |
| CC        |                           | receptor alpha-1.  |
| XX        |                           |  |
| SQ        | Sequence 427 AA;          |  |
|           | Query Match               | 94.1%; Score 401; DB 9; Length 427;  |
|           | Best Local Similarity     | 100.0%; Pred. No. 0;   |
|           | Matches 401; Conservative | 0; Mismatches 0; Indels 0; Gaps 0;   |
| OY        | 26                        | APTETQPVTNLSVSEVENLCTVIWTWNPBEGASSNCISMYSFHFDKDKKIAPTETRSI 85              |
| Dd        | 27                        | APETTOPPVTNLSVSEVENLCTVIWTWNPBEGASSNCISMYSFHFDKDKKIAPTETRSI 86             |
| OY        | 86                        | EVLINERTCLGVSGCSTNESKEPSILVEKCISPESGPDESAVTELOCIMHNLGYMKCSW 145            |
| Dd        | 87                        | EVLINERTCLGVSGCSTNESKEPSILVEKCISPESGPDESAVTELOCIMHNLGYMKCSW 146            |
| OY        | 146                       | LPGRNTSPDITVTLTYMHRSLLEKIHQCENIFREGQYFGCSFDLTRYKXDSFEOSHVOJMV 205          |
| Dd        | 147                       | LPGRNTSPDITVTLTYMHRSLLEKIHQCENIFREGQYFGCSFDLTRYKXDSFEOSHVOJMV 206          |
| OY        | 206                       | KDNAGKIPESFNIVPLTSRVKPDPRPHIKNLSFHNDLYVQWENPONTISRCLFYEEVANN 265           |
| Dd        | 207                       | KDNAGKIPESFNIVPLTSRVKPDPRPHIKNLSFHNDLYVQWENPONTISRCLFYEEVANN 266           |
| OY        | 266                       | SOTETHNFVYOEAACENPEPERNNENTSCFNVPCVLPDTLTNTVAIRKYNLCEYEDKL 325             |
| Dd        | 267                       | SOTETHNFVYOEAACENPEPERNNENTSCFNVPCVLPDTLTNTVAIRKYNLCEYEDKL 326             |
| OY        | 326                       | WSNNSQEMSIKKRNSTLYITMLLTVPIYVAGAIIVLLLYEKRLIIFFPIPDGKITFK 385              |
| Dd        | 327                       | WSNNSQEMSIKKRNSTLYITMLLTVPIYVAGAIIVLLLYEKRLIIFFPIPDGKITFK 386              |
| OY        | 386                       | EMFGDQDDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 426                                 |
| Dd        | 387                       | EMFGDQDDTLHWKKYDIYEKQTKETSDSVLIENLKASQ 427                                 |
| RESULT 11 |                           |  |
| AAE93788  | ID                        | AAE93788 standard; protein; 427 AA.  |
| XX        | AAE93788;                 |  |
| XX        | 23-FEB-2006               | (first entry)  |
| XX        |                           | Human interleukin-13 alpha receptor.                                       |
| XX        |                           |  |
| KW        |                           | Monoclonal antibody, IL-13 alpha receptor; cytokine;                       |
| KW        |                           | protein co-ordinate data; protein structure; crystallography;              |
| KW        |                           | Antiaesthetic; Anti-allergic; Cytostatic; Respiratory-Gen.;                |
| KW        |                           | Antiinflammatory; Immunosuppressive; Dermatological;                       |
| KW        |                           | Gastrointestinal-Gen.; Vasodilator; CNS-Gen.; Hepatotrophic; asthma;       |
| KW        |                           | cancer; eosinophilia; fibrosis; inflammation; autoimmune disease;          |
| KW        |                           | chronic obstructive pulmonary disease; cystic fibrosis;                    |
| KW        |                           | pulmonary fibrosis; allergic rhinitis; atopic dermatitis;                  |
| KW        |                           | inflammatory bowel disease; Crohn's disease; cirrhosis; scleroderma;       |
| KW        |                           | Hodgkins disease.  |

|    |              |   |  |
|----|--------------|---|--|
| XX | OS           | Homo sapiens.   |  |
| XX | PH           | Location/Qualifiers   |  |
| XX | Key          | 76  |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 77  |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 78  |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 79  |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 254   |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 255   |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 256   |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 318   |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 320   |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| FT | Binding-site | 321   |  |
| FT | Binding-site | /note= "Residue interacting with IL-13, specifically claimed in claim 61"   |  |
| XX | PN           | WO2005121177-A2.  |  |
| XX | PD           | 22-DEC-2005.  |  |
| XX | PE           | 09-JUN-2005; 2005WO-US020334.   |  |
| XX | PR           | 09-JUN-2004; 2004US-0578473P.   |  |
| XX | PR           | 09-JUN-2004; 2004US-0578736P.   |  |
| XX | PR           | 22-JUN-2004; 2004US-0581375P.   |  |
| XX | PA           | (AMHP ) MYETH.  |  |
| XX | XX           | Lin Li, Parris KD, Tam ASD, Tan X, Shane T, Dumas J, Wilhelm JM,  |  |
| XX | P1           | Stehl M, Mosyak L, Hu Z;  |  |
| XX | XX           | WPI: 2006-067089/07.  |  |
| XX | DR           | SWISSPROT; P78552.  |  |
| XX | PS           | Claim 58; SEQ ID NO 12; 31bpb, English.   |  |
| XX | XX           | The invention relates to a crystalline antibody (1), where the antibody comprises an anti-interleukin (IL)-13 antibody or its Fab fragment, and is capable of binding a site of an IL-13 polypeptide to which an IL-4R (interleukin-4 receptor) polypeptide binds in vivo. Also included are a crystalline composition/complexes that comprises an antibody (where the antibody comprises an anti-IL-13 antibody or a Fab fragment of an anti-IL-13 antibody in complex with IL-13 or IL-13 alpha receptor), use of a three-dimensional model of an antibody to design an agent that interacts with an IL-13, a software system/computer for storing/analyzing information relating to a structure of an IL-13 polypeptide bound to an antibody, modulating IL-13 activity in a subject, treating a subject having a condition associated with IL-13 activity, a method of having a condition associated with IL-13 activity, a method of prophylactically treating a subject susceptible to a condition associated with IL-13 activity, and the use of an agent (A1) designed or selected by |  |

CC the methods above in the manufacture of a medicament for the prophylaxis  
CC or treatment of a condition associated with IL-13 activity. The antibody  
CC crystal and methods are useful for designing an agent that interacts with  
CC an IL-13 polypeptide. The agent is useful for treating an IL-13 condition  
CC chosen from allergic asthma or nonallergic asthma, cancer, airway  
CC inflammation, eosinophilia, fibrosis, excess mucus production,  
CC inflammatory condition of the skin, gastrointestinal organs, blood  
CC vessels or connective tissue, and an autoimmune condition of the skin,  
CC gastrointestinal organs, blood vessels, or connective tissue, chronic  
CC obstructive pulmonary disorder, cystic fibrosis, pulmonary fibrosis,  
CC allergic rhinitis, atopic dermatitis, inflammatory bowel disease, Crohn's  
CC disease, cirrhosis, scleroderma, or Hodgkin's lymphoma. The present  
CC sequence is the human IL-13 alpha receptor protein.

SQ Sequence 427 AA;

Query Match 94.1%; Score 401; DB 10; Length 427;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVTNLSVSVENLCTVIWTNPPGASNSCLMYFSHFQDKKIAPETRRSI 85  
DB 27 APTETQPPVTNLSVSVENLCTVIWTNPPGASNSCLMYFSHFQDKKIAPETRRSI 86  
QY 86 EVPLNERICLVQVSGQSTNESEKPSILVEKICISPPGDPBSAVTELCIWHNLSYMKCSW 145  
DB 87 EVPLNERICLVQVSGQSTNESEKPSILVEKICISPPGDPBSAVTELCIWHNLSYMKCSW 146  
QY 146 LPRNTSPDNTNLTLYWHSLEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVQIMV 205  
DB 147 LPRNTSPDNTNLTLYWHSLEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVQIMV 206  
QY 206 KDNAGKIKPSFNIPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISCLFYEVEVNN 265  
DB 207 KDNAGKIKPSFNIPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISCLFYEVEVNN 266  
QY 266 SQETTHNVFYVOAKCENPEFERNVENTSCFWPGVLPDLTNTVRIRVKTNKLCEYEDDKL 326  
DB 267 SQETTHNVFYVOAKCENPEFERNVENTSCFWPGVLPDLTNTVRIRVKTNKLCEYEDDKL 326  
QY 326 WSNWSQEMSIGKKRNSTLYITMLIVPVYVAGAIYVLLLYLKRKLTIIIPPDPGKIFK 385  
DB 327 WSNWSQEMSIGKKRNSTLYITMLIVPVYVAGAIYVLLLYLKRKLTIIIPPDPGKIFK 386  
QY 386 EMFGQNDPTLHWKXYDIYEKOTKEETDSVVLLENLKKASQ 426  
DB 387 EMFGQNDPTLHWKXYDIYEKOTKEETDSVVLLENLKKASQ 427

RESULT 12

ID AEF57817 standard; protein; 427 AA.

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

XX AEF57817;

| DB                    | 367   | EMFGQNDPDTLHWKXYDIYEKQTKERTSDSVLIENLKASQ                      | 427               |
|-----------------------|---|---|-------------------|
| DB                    | RESULT 13   |   |                   |
| ADFI7835              | ID  | ADFI7835  |                   |
| XX                    | ADFI7835  | standard; protein; 427 AA.                                    |                   |
| XX                    | ADFI7835;   |   |                   |
| XX                    | 12-FEB-2004   | (first entry)   |                   |
| DE                    | Human IL-13 alpha 1 receptor (IL-13R) protein.                            |   |                   |
| XX                    | IL-13R; human; receptor; anaphylaxis; hay fever; asthma;                  |   |                   |
| KW                    | antiinflammatory; cytosolic; antitumor; dermatological; antiallergic;     |   |                   |
| KW                    | antiallergic; fibrosis; Hodgkin's disease; ulcerative colitis;            |   |                   |
| KW                    | scleroderma; allergic rhinitis; oncological;                              |   |                   |
| KW                    | chronic obstructive pulmonary disease.                                    |   |                   |
| OS                    | Homo sapiens.   |   |                   |
| PN                    | WO2003080675-A2.  |   |                   |
| XX                    | 02-OCT-2003.  |   |                   |
| XX                    | 21-MAR-2003; 2003WO-AU000352.   |   |                   |
| XX                    | 22-MAR-2002; 2002AU-00001301.   |   |                   |
| PR                    | 03-FEB-2003; 2003AU-00900437.   |   |                   |
| XX                    | (AMRA-) AMRAD OPERATIONS PTY LTD.   |   |                   |
| PA                    | Dunlop FM, Baca M, Nash AD, Fabri LJ;                                     |   |                   |
| XX                    | WPI; 2003-876912/81.  |   |                   |
| DR                    | N-PSDB; ADFI7834.   |   |                   |
| XX                    | New monoclonal antibodies against interleukin-13 receptor alpha, useful   |   |                   |
| PT                    | for treating fibrosis, Hodgkin's disease, ulcerative colitis,             |   |                   |
| PT                    | scleroderma, allergic rhinitis, oncological conditions, asthma or an      |   |                   |
| PT                    | inflammatory disorder.  |   |                   |
| PS                    | Disclosure; SEQ ID NO 4; 99pp; English.                                   |   |                   |
| XX                    | This invention relates to a novel antibodies that function as interleukin |   |                   |
| CC                    | -13 receptor alpha-1 chain (IL-13R alpha-1) antagonists and can be used   |   |                   |
| CC                    | for treating certain conditions induced by IL-13. Specifically, it refers |   |                   |
| CC                    | to antibodies that bind to IL-13R alpha-1 and inhibit or modulate IL-13   |   |                   |
| CC                    | and IL-4 induced signalling. IL-13 is a mediator in the immunostimulatory |   |                   |
| CC                    | system, such that it is involved in the induction of IgE, IgG4 and T-     |   |                   |
| CC                    | helper cells and accordingly is implicated in conditions from anaphylaxis |   |                   |
| CC                    | to hay fever and asthma. As such, the present invention describes these   |   |                   |
| CC                    | novel antibodies as antiinflammatory, cytosolic, antitumor,               |   |                   |
| CC                    | dermatological, antiallergic and antiasthmatic. The methods and           |   |                   |
| CC                    | compositions are useful for treating various disorders including          |   |                   |
| CC                    | fibrosis, Hodgkin's disease, ulcerative colitis, scleroderma, allergic    |   |                   |
| CC                    | rhinitis, oncological conditions and chronic obstructive pulmonary        |   |                   |
| CC                    | disease. This polypeptide sequence is the human IL-13 alpha 1 receptor    |   |                   |
| CC                    | protein of the invention.   |   |                   |
| XX                    | Sequence 427 AA;  |   |                   |
| XX                    | Seq   |   |                   |
| Query Match           | 77.7%;  | Score 331;  | DB 7; Length 427; |
| Best Local Similarity | 100.0%;   | Pred. No. 0;  |                   |
| Matches 331;          | Conservative 0;   | Mismatches 0;   | Indels 0; Gaps 0  |
| 0Y                    | 26  | APTEQTPVNTLSVSVENICTVIWTVNPPGAGSNCSLMYFSHFQDKDKIAPETRRSI      | 85                |
| Db                    | 27  | APTEQTPVNTLSVSVENICTVIWTVNPPGAGSNCSLMYFSHFQDKDKIAPETRRSI      | 86                |
| 0Y                    | 86  | EVPINERICTQVSGSCSTNESEKPSILVVKCTISPPGDPESAVTELOCTIWHNLSYWKCSW | 145               |
| Db                    | 87  | EVPINERICTQVSGSCSTNESEKPSILVVKCTISPPGDPESAVTELOCTIWHNLSYWKCSW | 146               |

|           |          |   |                     |
|-----------|----------|---|---------------------|
| QY        | 146      | LPGRNTSPDNTNTLYYHMRSLFKIHQCENIPFEGQYFGCSFDLTXYKXDSFEDHSHQIMW              | 205                 |
| DB        | 147      | LPGRNTSPDNTNTLYYHMRSLFKIHQCENIPFEGQYFGCSFDLTXYKXDSFEDHSHQIMW              | 206                 |
| QY        | 206      | KDNAGKIKPSFNIIVPLTSRVKDPPEHIKNLSFHNDDLYYQWENPQNFISRCLEFYEVEVNN            | 265                 |
| DB        | 207      | KDNAGKIKPSFNIIVPLTSRVKDPPEHIKNLSFHNDDLYYQWENPQNFISRCLEFYEVEVNN            | 266                 |
| QY        | 266      | SQTEHNFFYYQAEACENPEFERNVENTSCFMPVGLPDTLNTVIRIVKTNKLCYEDDKL                | 325                 |
| DB        | 267      | SQTEHNFFYYQAEACENPEFERNVENTSCFMPVGLPDTLNTVIRIVKTNKLCYEDDKL                | 326                 |
| QY        | 326      | WSNMSQEMSIGKRNSTLYITMTLLIVPIYA  | 356                 |
| DB        | 327      | WSNMSQEMSIGKRNSTLYITMTLLIVPIYA  | 357                 |
| RESULT 14 |          |   |                     |
| ID        | ADL71814 | standard; protein; 427 AA.  |                     |
| XX        | AC       | ADL71814;   |                     |
| XX        | DT       | 20-MAY-2004 (first entry)   |                     |
| DE        | XX       | Human interleukin-13 receptor alpha (IL-13 Ralpha) mutant, G358D.         |                     |
| XX        | XX       | Human; IL-13; IL-4; IL-4 R; atopy; atopic dermatitis; allergy; rhinitis;  |                     |
| KW        | XX       | eczema; asthma; AIDS; gene therapy; interleukin; receptor; mutant;        |                     |
| XX        | XX       | muteln.   |                     |
| OS        | XX       | Homo sapiens.   |                     |
| OS        | XX       | Synthetic.  |                     |
| FH        | XX       | Key   | Location/Qualifiers |
| FT        | XX       | Misc-difference 358   |                     |
| FT        | XX       | /note= "Wild-type Gly is substituted with Asp"                            |                     |
| FN        | XX       | US2004043921-A1.  |                     |
| PD        | XX       | 04-MAR-2004.  |                     |
| PF        | XX       | 29-SEP-2003; 2003US-00671697.   |                     |
| PR        | XX       | 13-DEC-1996; 96GB-00025889.   |                     |
| PR        | XX       | 12-NOV-1997; 97US-00969125.   |                     |
| PR        | XX       | 06-APR-2000; 2000US-00545002.   |                     |
| PA        | XX       | (BONN/) BONNEFOY J.   |                     |
| PA        | XX       | (GAUC/) GAUCHAT J.  |                     |
| PI        | XX       | Bonnefoy J, Gauchat J;  |                     |
| DR        | XX       | WPI; 2004-225726/21.  |                     |
| XX        | XX       | Treating a disease in which interleukin (IL)-13 and IL-4 cause adverse    |                     |
| PT        | XX       | effects, e.g. atopy, atopic dermatitis, allergy, rhinitis, eczema, asthma |                     |
| PT        | XX       | or AIDS, comprises administering a polypeptide or soluble polypeptide.    |                     |
| PS        | XX       | Claim 14; Page; 27pp; English.  |                     |
| CC        | XX       | The invention relates to polypeptides capable of binding human            |                     |
| CC        | XX       | interleukin (IL)-13 and/or IL-4 in the presence of IL-4 Ralpha. The       |                     |
| CC        | XX       | invention also relates to a method of treatment of a disease in which     |                     |
| CC        | XX       | IL13 and IL4 cause adverse effects. The method is useful for treating a   |                     |
| CC        | XX       | disease in which IL-13 and IL-4 cause adverse effects, e.g. atopy, atopic |                     |
| CC        | XX       | dermatitis, allergy, rhinitis, eczema, asthma or AIDS. The polypeptides   |                     |
| CC        | XX       | of the invention are useful in raising antibodies. It is also useful in   |                     |
| CC        | XX       | gene therapy. The present sequence is human interleukin-13 receptor alpha |                     |
| CC        | XX       | (IL-13 Ralpha) mutant protein. Note: This sequence is not shown in the    |                     |
| CC        | XX       | specification, however it is constructed based on human IL-13 Ralpha      |                     |
| CC        | XX       | protein shown as SEQ ID NO:9 in the specification.                        |                     |

XX Sequence 427 AA;  
SQ  
Query Match 77.7%; Score 331; DB 8; Length 427;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLMYFSHFQDKODKKIADETRRI 85  
DB 27 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLMYFSHFQDKODKKIADETRRI 86  
QY 86 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLISYMKCSW 145  
DB 87 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLISYMKCSW 146  
QY 146 LPRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 205  
DB 147 LPRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 206  
QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLYVOMENPQNFISRCLFYEVVNN 265  
DB 207 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLYVOMENPQNFISRCLFYEVVNN 266  
QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 325  
DB 267 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 326  
QY 326 WSNWSQEMSIGKKRNSTLYITMLLIVPIVA 356  
DB 327 WSNWSQEMSIGKKRNSTLYITMLLIVPIVA 357  
RESULT 15  
AAE13745  
ID AAE13745 standard; protein: 322 AA.  
AC AAE13745;  
XX 26-FEB-2002 (first entry)  
DT 26-FEB-2002 (first entry)  
XX  
DE Human soluble cytokine IL-13 receptor alpha1 (IL-13RA1) protein.  
XX  
KW Human; Zalphal1; cytokine receptor; immunosuppressive; cyostatic;  
KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;  
KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;  
KW viral infection; IL-13 receptor alpha1; IL-13RA1.  
XX  
OS Homo sapiens.  
XX  
PN MO200177171-A2.  
PD 18-OCT-2001.  
XX  
PF 03-APR-2001; 2001WO-US010872.  
XX  
PR 05-APR-2000; 2000US-0194731P.  
XX 28-JUL-2000; 2000US-0222121P.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ,  
XX  
DR MPI: 2002-025998/03.  
XX N-PSDB; AAD22979.  
XX  
XX Novel soluble receptor polypeptides and polynucleotides used as cytokine  
PT antagonist for stimulating ligand activity-induced proliferation of  
PT hematopoietic cells and for suppressing immune response in a mammal.  
XX  
PS Claim 29; Page 236-237; 243pp; English.  
XX

CC The invention relates to an isolated soluble zalphal1 cytokine receptor  
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for  
CC inhibiting or antagonising the ligand activity-induced proliferation of  
CC haematopoietic cells and haematopoietic cell progenitors preferably  
CC lymphoid cells which are natural killer cells or cytotoxic T cells.  
CC Zalpha is useful for treating immune and inflammatory disorders, for  
CC reducing proliferation of neoplastic B or T cells, for suppressing an  
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is  
CC useful for treating diseases that require immune regulation including  
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,  
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;  
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,  
CC sepsis, viral infection (dengue virus infection) and cancer. The present  
CC sequence is human soluble cytokine IL-13 receptor alpha1 (IL-13RA1)  
CC protein related to the invention  
XX  
SQ Sequence 322 AA;  
Query Match 74.4%; Score 317; DB 5; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3.4e-306;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLMYFSHFQDKODKKIADETRRI 85  
DB 6 APTETQPPVTNLVSVENLCTVIWTWNPPEGASSNCSLMYFSHFQDKODKKIADETRRI 65  
QY 86 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLISYMKCSW 145  
DB 66 EVPLNERICQVGSQCSSTNESEKPSILVEKICISPEEDPESAVTELOCIMWNLISYMKCSW 125  
QY 146 LPRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 205  
DB 126 LPRGNTSPDNTNYTLTYWHRSLLEKIHOCENIFREGQYGCSEFDLTKVDSSEFGHSVOIMV 185  
QY 206 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLYVOMENPQNFISRCLFYEVVNN 265  
DB 186 KDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFHNDLYVOMENPQNFISRCLFYEVVNN 245  
QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 325  
DB 246 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDILNTVIRIKVTKNKLCEYEDKL 305  
QY 326 WSNWSQEMSIGKKRNST 342  
DB 306 WSNWSQEMSIGKKRNST 322

Search completed: July 8, 2006, 01:24:54  
Job time : 199 secs



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:25:13 ; Search time 41 Seconds

(without alignments)  
999,716 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 426  
Sequence: 1 MEMPARLCGMALLLCAGGG.....QTKETDSVVLIENTKRAQ 426

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 43    | 10.1        | 426    | 2 JC7773 | IL-13Ralpha 1 prot |
| 2          | 43    | 2.3         | 201    | 2 C40040 | alternative splici |
| 3          | 10    | 2.3         | 201    | 2 S26404 | alternative splici |
| 4          | 10    | 2.3         | 248    | 2 A40040 | alternative splici |
| 5          | 10    | 2.3         | 272    | 2 T02745 | nucleic acid bindi |
| 6          | 10    | 2.3         | 285    | 2 S69312 | probable membrane  |
| 7          | 10    | 2.3         | 292    | 2 B40040 | alternative splici |
| 8          | 10    | 2.3         | 331    | 2 A36358 | T-cell acute lymph |
| 9          | 10    | 2.3         | 405    | 2 T29167 | hypothetical prote |
| 10         | 10    | 2.3         | 465    | 2 G02738 | transcription fact |
| 11         | 10    | 2.3         | 479    | 1 A41753 | transcription fact |
| 12         | 10    | 2.3         | 864    | 2 A48266 | transcription fact |
| 13         | 10    | 2.3         | 888    | 2 I58378 | tyrosine kinase -  |
| 14         | 10    | 2.3         | 1433   | 2 A46053 | bullous pemphigoid |
| 15         | 10    | 2.3         | 1621   | 2 T30200 | hypothetical prote |
| 16         | 9     | 2.1         | 102    | 2 D71415 | hypothetical prote |
| 17         | 9     | 2.1         | 115    | 2 B84676 | 60S acidic ribosom |
| 18         | 9     | 2.1         | 151    | 2 S43296 | bone morphogenetic |
| 19         | 9     | 2.1         | 199    | 2 T49450 | hypothetical prote |
| 20         | 9     | 2.1         | 201    | 2 J01094 | hypothetical 20.2k |
| 21         | 9     | 2.1         | 206    | 2 I53066 | gene M-twist prote |
| 22         | 9     | 2.1         | 211    | 2 T04098 | CBP20 preproteol   |
| 23         | 9     | 2.1         | 212    | 2 T49559 | related to prolina |
| 24         | 9     | 2.1         | 212    | 2 A83680 | spore germination  |
| 25         | 9     | 2.1         | 221    | 2 T04592 | glycine-rich cell  |
| 26         | 9     | 2.1         | 238    | 2 T05344 | hypothetical prote |
| 27         | 9     | 2.1         | 253    | 2 A31444 | homeotic protein U |
| 28         | 9     | 2.1         | 255    | 2 B84777 | hypothetical prote |
| 29         | 9     | 2.1         | 256    | 2 T03571 | glycine-rich prote |

|    |   |     |     |          |                     |
|----|---|-----|-----|----------|---------------------|
| 30 | 9 | 2.1 | 257 | 2 B84346 | hypothetical prote  |
| 31 | 9 | 2.1 | 258 | 2 T13591 | tail fiber adhesin  |
| 32 | 9 | 2.1 | 260 | 2 S00276 | tail fiber protein  |
| 33 | 9 | 2.1 | 262 | 1 TLBPM1 | tail fiber protein  |
| 34 | 9 | 2.1 | 263 | 2 A34466 | calpain (EC 3.4.22  |
| 35 | 9 | 2.1 | 266 | 1 C1PGL  | calpain (EC 3.4.22  |
| 36 | 9 | 2.1 | 267 | 1 C1RBL  | calpain (EC 3.4.22  |
| 37 | 9 | 2.1 | 267 | 1 C1PGL  | calpain (EC 3.4.22  |
| 38 | 9 | 2.1 | 268 | 1 C1HUL  | corticosterone / 11 |
| 39 | 9 | 2.1 | 268 | 1 S09860 | calpain (EC 3.4.22  |
| 40 | 9 | 2.1 | 273 | 1 TVZMMB | hypothetical prote  |
| 41 | 9 | 2.1 | 291 | 1 S31415 | anthocyanin biosyn  |
| 42 | 9 | 2.1 | 301 | 2 B31219 | glycine-rich prote  |
| 43 | 9 | 2.1 | 307 | 2 T27609 | collagen 2 - Caeno  |
| 44 | 9 | 2.1 | 311 | 2 T02783 | hypothetical prote  |
| 45 | 9 | 2.1 | 315 | 2 T41868 | probable homeotic   |

#### ALIGNMENTS

##### RESULT 1

JC7773 IL-13Ralpha 1 protein - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004

C/Accession: JC7773

R/Proct: C.; Beniguel, L.; Begue, A.; Khalife, J.

Biochem. Biophys. Res. Commun. 287, 969-976, 2001.

A/Title: Expression of a functional IL-13Ralpha1 by rat B cells.

A/Reference number: JC7773; PMID:11573960

A/Accession: JC7773

A/Molecule type: mRNA

A/Residues: 1-426 <PIR>

A/Cross-references: UNIPROT:Q8VHC2; UNIPARC:UP1000017CC49; GB:AY044251

C/Comment: This protein is an functionally binding protein involved in B cell prolifera

C/Genetics:

A/Gene: il-13ralpha1

##### Query Match

Best Local Similarity 100.0%; Score 43; DB 2; Length 426;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 YLRKLTIIIPPIPDGKIFKEMFGQNDTLHKKYDIYEKQ 407  
DB 365 YLRKLTIIIPPIPDGKIFKEMFGQNDTLHKKYDIYEKQ 407

##### RESULT 2

C40040 alternative splicing factor ASF-3 - human

C/Species: Homo sapiens (man)

C/Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 05-Oct-2004

C/Accession: C40040

R/Ge: H.; Zuo, P.; Manley, J. L.

Cell 66, 373-382, 1991

A/Title: Primary structure of the human splicing factor ASF reveals similarities with D

A/Reference number: A40040; PMID:91309149; PMID:1855257

A/Accession: C40040

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-201 <GEA>

A/Cross-references: UNIPROT:Q07955; UNIPARC:UP1000017A383; GB:M72709

F;17-81/Domain: ribonucleoprotein repeat homology <RNM1>

F;122-182/Domain: ribonucleoprotein repeat homology <RNM2>

##### Query Match

Best Local Similarity 2.3%; Score 10; DB 2; Length 201;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27  
DB 99 GGGGGGGGAP 108



RESULT 3  
S26404  
alternative splicing factor ASF - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 25-Feb-1994 #sequence\_revision 26-May-1995 #text\_change 05-Oct-2004  
C:Accession: S26404  
R:Take, R.; Bored, A.; Goridis, C.  
Nucleic Acids Res. 20, 5482, 1992  
A:Title: ASF alternative transcripts are highly conserved between mouse and man.  
A:Reference number: S26404; PMID:93065226; PMID:1437571  
A:Accession: S26404  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-201 <TAC>  
A:Cross-references: UNIPROT:Q8BJV3; UNIPARC:UPI000008B65F; EMBL:X66091  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1992  
F:12-81/Domain: ribonucleoprotein repeat homology <RRM1>  
F:12-182/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 2.3%; Score 10; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.045;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27  
|||||  
DB 99 GGGGGGGGAP 108

RESULT 4  
A40040  
alternative splicing factor ASF-1 - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 31-Dec-2004  
C:Accession: A40040; B40041  
R:Ge, H.; Zuo, P.; Manley, J.L.  
Cell 66, 373-382, 1991  
A:Title: Primary structure of the human splicing factor ASF reveals similarities with D1  
A:Reference number: A40040; PMID:91309149; PMID:1855257  
A:Accession: A40040  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-248 <EBA>  
A:Cross-references: UNIPROT:Q07955; UNIPARC:UPI0000001220; GB:M72709; NID:g179073; PIDN:  
R:Kraener, A.R.; Mayeda, A.; Kozak, D.; Bins, G.  
Cell 66, 383-394, 1991  
A:Title: Functional expression of cloned human splicing factor SF2: homology to RNA-bind  
A:Reference number: A40041; PMID:91309150; PMID:1830244  
A:Accession: B40041  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-248 <KRA>  
A:Cross-references: UNIPARC:UPI0000001220; GB:M69040; NID:g338046; PIDN:AAA03476.1; PID:  
F:17-81/Domain: ribonucleoprotein repeat homology <RRM1>  
F:12-182/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 2.3%; Score 10; DB 2; Length 248;  
Best Local Similarity 100.0%; Pred. No. 0.054;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27  
|||||  
DB 99 GGGGGGGGAP 108

RESULT 5  
T02745  
nucleic acid binding protein - rice  
C:Species: Oryza sativa (rice)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 31-Dec-2004  
C:Accession: T02745; T02718  
R:Yoon, U.H.; Hahn, J.H.; Yun, C.H.; Eun, M.Y.

submitted to the EMBL Data Library, February 1998  
A:Description: The rice genome contains at least two different genes encoding nucleic a  
A:Reference number: Z14712  
A:Accession: T02745  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-272 <YOO>  
A:Cross-references: UNIPROT:Q49228; UNIPARC:UPI00000ABD51; EMBL:AF047428; NID:g4091116;  
A:Experimental source: strain Ilpoombyeo  
R:Yoon, U.H.; Hahn, J.H.; Yun, C.H.; Eun, M.Y.  
submitted to the EMBL Data Library, January 1998  
A:Description: Cloning and molecular characterization of nucleic acid binding protein g  
A:Reference number: Z14705  
A:Accession: T02718  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-181,183-272 <YOO>  
A:Cross-references: UNIPARC:UPI00000AB867; EMBL:AF045571; NID:g2854124; PID:g2854125  
A:Experimental source: strain Ilpoombyeo  
C:Superfamily: Putative PHD-type Nucleic acid binding protein

Query Match 2.3%; Score 10; DB 2; Length 272;  
Best Local Similarity 100.0%; Pred. No. 0.059;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27  
|||||  
DB 15 GGGGGGGGAP 24

RESULT 6  
S69312  
probable membrane protein YLR338w - Yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein L8300.13-a  
C:Species: Saccharomyces cerevisiae  
C:Date: 20-Jul-1996 #sequence\_revision 23-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: S69312  
R:Yu, Z.  
submitted to the EMBL Data Library, January 1994  
A:Description: The sequence of S. cerevisiae cosmid 8300.  
A:Reference number: S69312  
A:Accession: S69312  
A:Molecule type: DNA  
A:Residues: 1-288 <UZZ>  
A:Cross-references: UNIPROT:Q94084; UNIPARC:UPI000006ABEE; EMBL:U19028; NID:g609380; PII  
C:Genetics:  
A:Gene: SGD:KRE21; MIPS:YLR338w  
A:Cross-references: SGD:S0004330  
A:Map position: 12R  
C:Keywords: transmembrane protein  
F:142-158/Domain: transmembrane #status predicted <TM1>  
F:201-217/Domain: transmembrane #status predicted <TM2>

Query Match 2.3%; Score 10; DB 2; Length 285;  
Best Local Similarity 100.0%; Pred. No. 0.062;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGA 26  
|||||  
DB 240 AGGGGGGGA 249

RESULT 7  
B40040  
alternative splicing factor ASF-2 - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 31-Dec-2004  
C:Accession: B40040  
R:Ge, H.; Zuo, P.; Manley, J.L.  
Cell 66, 373-382, 1991  
A:Title: Primary structure of the human splicing factor ASF reveals similarities with Dr  
A:Reference number: A40040; PMID:91309149; PMID:1855257  
A:Accession: B40040

GenCore version 5.1.1.9  
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:21:52 ; Search time 299 Seconds  
(without alignments)  
1317.915 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 426

Sequence: 1 MEWPARLGLWALLCAGG.....QTKETDSVVLLENLKASQ 426

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Uniprot 7.2.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match | Length | DB | ID           | Description         |
|------------|-------|-------|--------|----|--------------|---------------------|
| 1          | 401   | 94.1  | 427    | 1  | I13R1_HUMAN  | P78552 homo sapien  |
| 2          | 401   | 94.1  | 427    | 2  | Q96BB4_HUMAN | Q96BB4 homo sapien  |
| 3          | 401   | 94.1  | 427    | 2  | Q5JSL4_HUMAN | Q5JSL4 homo sapien  |
| 4          | 300   | 70.4  | 426    | 2  | Q59EG2_HUMAN | Q59EG2 homo sapien  |
| 5          | 251   | 58.9  | 279    | 2  | Q9UDY5_HUMAN | Q9UDY5 homo sapien  |
| 6          | 144   | 33.8  | 409    | 2  | Q7YRV5_MACFA | Q7YRV5 macaca fasc  |
| 7          | 91    | 21.4  | 226    | 2  | Q6ZW70_HUMAN | Q6ZW70 homo sapien  |
| 8          | 65    | 15.3  | 401    | 2  | Q6UET1_SHEEP | Q6UET1 ovis aries   |
| 9          | 62    | 14.6  | 423    | 2  | Q86326_PIG   | Q86326 sus scrofa   |
| 10         | 43    | 10.1  | 252    | 2  | Q8VDP7_MOUSE | Q8VDP7 mus musculus |
| 11         | 43    | 10.1  | 424    | 1  | I13R1_MOUSE  | Q09030 mus musculus |
| 12         | 43    | 10.1  | 424    | 2  | Q8C1Z3_MOUSE | Q8C1Z3 mus musculus |
| 13         | 43    | 10.1  | 426    | 2  | Q561K3_RAT   | Q561K3 rattus norv  |
| 14         | 43    | 10.1  | 426    | 2  | Q8VHC2_RAT   | Q8VHC2 rattus norv  |
| 15         | 40    | 9.4   | 424    | 2  | Q8ENM4_MOUSE | Q8ENM4 mus musculus |
| 16         | 37    | 8.7   | 349    | 2  | Q97597_BOVIN | Q97597 bos taurus   |
| 17         | 37    | 8.7   | 405    | 2  | Q95LF1_CANFA | Q95LF1 canis famil  |
| 18         | 26    | 6.1   | 399    | 2  | Q3UPQ9_MOUSE | Q3UPQ9 mus musculus |
| 19         | 11    | 2.6   | 307    | 2  | Q3V913_9SPHN | Q3V913 sphingopyxi  |
| 20         | 11    | 2.6   | 444    | 2  | Q76472_MUSDO | Q76472 musca domes  |
| 21         | 11    | 2.6   | 457    | 2  | Q7G604_ORYSA | Q7G604 oryza sativ  |
| 22         | 11    | 2.6   | 1000   | 2  | Q5JKR1_ORYSA | Q5JKR1 oryza sativ  |
| 23         | 11    | 2.6   | 1226   | 1  | M1B_DROME    | Q9VUX2 drosophila   |
| 24         | 10    | 2.3   | 51     | 2  | Q5N8N0_ORYSA | Q5N8N0 oryza sativ  |
| 25         | 10    | 2.3   | 157    | 2  | Q7XNH1_ORYSA | Q7XNH1 oryza sativ  |
| 26         | 10    | 2.3   | 170    | 2  | Q6H5T9_ORYSA | Q6H5T9 oryza sativ  |
| 27         | 10    | 2.3   | 175    | 2  | Q6AVT7_ORYSA | Q6AVT7 oryza sativ  |
| 28         | 10    | 2.3   | 191    | 2  | Q5TQU2_ANOGA | Q5TQU2 anopheles g  |
| 29         | 10    | 2.3   | 224    | 2  | Q6Z541_ORYSA | Q6Z541 oryza sativ  |
| 30         | 10    | 2.3   | 233    | 2  | Q59FA2_HUMAN | Q59FA2 homo sapien  |
| 31         | 10    | 2.3   | 244    | 2  | Q7XUT6_ORYSA | Q7XUT6 oryza sativ  |

#### RESULT 1

| ID | I13R1_HUMAN   | STANDARD; | PRT; | 427 AA. |
|----|---|-----------|------|---------|
| AC | P78552; Q95646; Q99656;   |           |      |         |
| DT | 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.  |           |      |         |
| DT | 01-MAY-1997, sequence version 1.  |           |      |         |
| DT | 07-MAR-2006, entry version 50.  |           |      |         |
| DE | Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen).   |           |      |         |
| GN | Name=IL13RA1; Synonyms=IL13R, IL13RA;   |           |      |         |
| OS | Homo sapiens (Human).   |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |           |      |         |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  |           |      |         |
| OC | Homo.   |           |      |         |
| OX | NCBI_TaxID=9606;  |           |      |         |
| RN | [1]   |           |      |         |
| RP | NUCLEOTIDE SEQUENCE [MRNA].   |           |      |         |
| RC | TISSUE=Carcinoma;   |           |      |         |
| RX | MEDLINE=97165986; PubMed=9013879; DOI=10.1016/S0014-5793(96)01462-7;  |           |      |         |
| RA | Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N., Ferrara P.;   |           |      |         |
| RT | "Cloning of the human IL-13R alpha chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex.";  |           |      |         |
| RL | FEBS Lett. 401:163-166(1997).   |           |      |         |
| RN | [2]   |           |      |         |
| RP | NUCLEOTIDE SEQUENCE [MRNA].   |           |      |         |
| RC | TISSUE=B-cell;  |           |      |         |
| RA | Gauchat J.F.M., Schlagenhaut E., Feng N.P., Moser R., Yamage M., Jeannin P., Alouani S., Elson G., Notarangelo L.D., Wells T., Eugster H.P., Bonnefoy J.Y.;   |           |      |         |
| RA | Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.   |           |      |         |
| RL | [3]   |           |      |         |
| RP | NUCLEOTIDE SEQUENCE [MRNA].   |           |      |         |
| RC | TISSUE=T-cell;  |           |      |         |
| RX | MEDLINE=97067184; PubMed=8910586; DOI=10.1074/jbc.271.46.29265;   |           |      |         |
| RA | Anan M.J., Tayebi N., Obiri N.I., Puri R.K., Modi W.S., Leonard W.J.;   |           |      |         |
| RT | "CDNA cloning and characterization of the human interleukin 13 receptor alpha chain.";  |           |      |         |
| RL | J. Biol. Chem. 271:29265-29270(1996).   |           |      |         |
| RN | [4]   |           |      |         |
| RP | NUCLEOTIDE SEQUENCE [MRNA].   |           |      |         |
| RA | Wada M., Hisano T., Kuwano M.;  |           |      |         |
| RL | Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.   |           |      |         |
| RN | [5]   |           |      |         |
| RP | NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].   |           |      |         |
| RC | TISSUE=Pancreas;  |           |      |         |
| RX | MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603099;  |           |      |         |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., |           |      |         |

Q7exp4 brachydanio  
Q07955 homo sapien  
Q5pdm2 mus musculus  
Q5r7h2 pongo pygma  
Q3yla6 sus scrofa  
Q3uch2 mus musculus  
Q7krl2 drosophila  
Q3zml3 gallus gall  
Q6dl12 xenopus tro  
Q49216 oryza sativ  
Q49228 oryza sativ  
Q7f2z1 oryza sativ  
Q6h7a7 oryza sativ  
Q7sfql neurospora

#### ALIGNMENTS

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha  
CC can form a functional receptor for IL13. Also serves as an  
CC alternate accessory protein to the common cytokine receptor gamma  
CC chain for IL4 signaling, but cannot replace the function of gamma  
CC C in allowing enhanced IL2 binding activity.  
CC -!- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,  
CC and possibly other components.  
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
CC protein.  
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highest levels in heart, liver,  
CC skeletal muscle and ovary; lowest levels in brain, lung and  
CC kidney. Also found in B-cells, T-cells and endothelial cells.  
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
CC folding and thereby efficient intracellular transport and cell-  
CC surface receptor binding.  
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
CC activation.  
CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5  
CC subfamily.  
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CC Distributed under the Creative Commons Attribution-NoDerivs License  
CC  
CC -----  
CC EMBL: Y10659; CAA71669.1; -; mRNA.  
CC EMBL: Y09328; CAA70508.1; -; mRNA.  
CC EMBL: U62858; AAB37127.1; -; mRNA.  
CC EMBL: U81379; AAD00510.3; -; mRNA.  
CC EMBL: BC009960; AAH09960.1; -; mRNA.  
CC Ensembl: ENSG00000131724; Homo sapiens.  
CC H-InvDB: HIX0017008; -;  
CC HGNC: HGNC:5974; IL13RA1.  
CC MIM: 300119; gene.  
CC GO: GO:0005898; C:interleukin-13 receptor complex; TAS.  
CC GO: GO:0005886; C:plasma membrane; TAS.  
CC GO: GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.  
CC InterPro: IPR002996; Cytok rcpt B/G.  
CC InterPro: IPR003532; Hempt\_rcpt\_S\_F2.  
CC PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; 1.  
KW Glycoprotein; Membrane; Receptor; Signal; Transmembrane.  
FT SIGNAL 1 21  
FT CHAIN 22 427  
FT  
FT Interleukin-13 receptor alpha-1 chain.  
FT /FTID=PRO\_0000010939.  
FT  
FT TOPO\_DOM 22 343  
FT Extracellular (Potential).  
FT TRANSMEM 344 367  
FT TOPO\_DOM 368 427  
FT POTENTIAL  
FT MOTIF 327 331  
FT WSXWS motif.  
FT MOTIF 374 382  
FT Box 1 motif.  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 61 61  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 105 105  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 138 138  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 157 157  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 235 235  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 265 265  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 293 293  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 329 329  
FT N-linked (GlcNAc. .) (Potential).  
FT FT CARBOHYD 341 341  
FT N-linked (GlcNAc. .) (Potential).  
FT FT DISULFID 46 95  
FT By similarity.  
FT FT DISULFID 134 144  
FT By similarity.  
FT FT DISULFID 173 185

FT CONFLICT 130 130 T -> I (in Ref. 3).  
FT CONFLICT 358 358 G -> D (in Ref. 3).  
SQ SEQUENCE 427 AA; 48760 MW; 5983B3E8F554107B CRC64;  
  
Query Match 94.1%; Score 401; DB 1; Length 427;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 26 APTETQPTVNLVSVENLCTVIWTNPPEGASSCSLWYFHFQDKQDKIAPETRRSI 85  
Db 27 APTETQPTVNLVSVENLCTVIWTNPPEGASSCSLWYFHFQDKQDKIAPETRRSI 86  
  
QY 86 EVPLNERICLVGSGCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 145  
Db 87 EVPLNERICLVGSGCSTNESEKPSILVEKICISPEGDPESAVTELOCIWHNLSYMKCSW 146  
  
QY 146 LPGRNTSPDTNVTLYYHRSLEKIHQCENIPREGQYFGCSFDTLVKQSSPQHSVQIMV 205  
Db 147 LPGRNTSPDTNVTLYYHRSLEKIHQCENIPREGQYFGCSFDTLVKQSSPQHSVQIMV 206  
  
QY 206 KDNAGKIPSPNIVELTSRVKPDPPHINKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 265  
Db 207 KDNAGKIPSPNIVELTSRVKPDPPHINKNLSFHNDDLYVQWENPQNFISRCIFYEVEVNN 266  
  
QY 266 SOTETHNVFYVQEAACENPEPERNVENTSCFMPVGVLPDTLNTVIRVKTNLKCYEDDKL 325  
Db 267 SOTETHNVFYVQEAACENPEPERNVENTSCFMPVGVLPDTLNTVIRVKTNLKCYEDDKL 326  
  
QY 326 WSNWQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIDPDKIKPK 385  
Db 327 WSNWQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLLYLRLKLIIPPPIDPDKIKPK 386  
  
QY 386 EMFGQNDTTLHWKDYIEYKQTEEDTSVVLNIENLKASQ 426  
Db 387 EMFGQNDTTLHWKDYIEYKQTEEDTSVVLNIENLKASQ 427  
  
RESULT 2  
Q96BB4 HUMAN  
ID Q96BB4 HUMAN PRELIMINARY; PRT; 427 AA.  
AC Q96BB4; Q8WX08;  
DC 01-DEC-2001, integrated into UniProtKB/TrEMBL.  
DT 01-DEC-2001, sequence version 1.  
DT 21-FEB-2006, entry version 23.  
DE Interleukin 13 receptor, alpha 1, .  
GN Name=IL13RA1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Colon;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human

```
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -1- DOMAIN: The WSXS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
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CC -----
CC EMBL; BC015768; AA15768.1; -; mRNA.
CC Ensembl; ENSG00000131724; Homo sapiens.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC InterPro; IPR002996; Cytokn_rcpt_B/G.
CC InterPro; IPR003532; Hempt_rcpt_S_F2.
CC PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
CC Receptor; Transmembrane.
CC KW SEQUENCE 427 AA; 48677 MW; B6A42F7466A39A09 CRC64;
CC -----
Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTEPTPPVNLVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 85
DB 27 APTEPTPPVNLVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 86
QY 86 EYPLNERICLVGSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELCIWHNLSYMKCSW 145
DB 87 EYPLNERICLVGSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTVKYKDSFEGHSVQIMV 205
DB 147 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTVKYKDSFEGHSVQIMV 206
QY 206 KDNAGIKPSFNIPLTISRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCIFYEVEVNN 265
DB 207 KDNAGIKPSFNIPLTISRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCIFYEVEVNN 266
QY 266 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 325
DB 267 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 326
QY 326 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIPPPIDPGKIFK 385
DB 327 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIPPPIDPGKIFK 386
QY 386 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 426
DB 387 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 427
RESULT 3
Q5JSL4 HUMAN
ID Q5JSL4_HUMAN PRELIMINARY; PRT; 427 AA.
AC Q5JSL4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 21-FEB-2006, entry version 6.
DE Interleukin 13 receptor, alpha 1.
GN Name=IL13RA1; ORFNames=RP13-12804.2-001;
OS Homo sapiens (Human).
and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -1- DOMAIN: The WSXS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -1- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
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CC -----
CC EMBL; BC015768; AA15768.1; -; mRNA.
CC Ensembl; ENSG00000131724; Homo sapiens.
CC GO; GO:0016021; C:integral to membrane; IEA.
CC GO; GO:0016020; C:membrane; IEA.
CC GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
CC GO; GO:0004872; F:receptor activity; IEA.
CC InterPro; IPR002996; Cytokn_rcpt_B/G.
CC InterPro; IPR003532; Hempt_rcpt_S_F2.
CC PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
CC Receptor; Transmembrane.
CC KW SEQUENCE 427 AA; 48677 MW; B6A42F7466A39A09 CRC64;
CC -----
Query Match 94.1%; Score 401; DB 2; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTEPTPPVNLVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 85
DB 27 APTEPTPPVNLVSVENLCTVIWTWNPPEGASNCSLWYFSGDKQDKKIAPETRRSI 86
QY 86 EYPLNERICLVGSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELCIWHNLSYMKCSW 145
DB 87 EYPLNERICLVGSGQCSSTNESEKPSILVEKCIIPPEGDPESAVTELCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTVKYKDSFEGHSVQIMV 205
DB 147 LPRGNTSPDNTYLYYWHRSLEKIHQENIFREGQYFGCSFDLTVKYKDSFEGHSVQIMV 206
QY 206 KDNAGIKPSFNIPLTISRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCIFYEVEVNN 265
DB 207 KDNAGIKPSFNIPLTISRVKPDPPHINKLSFNHDDLIVQWENPQNFISRCIFYEVEVNN 266
QY 266 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 325
DB 267 SQTETHNVFYVQAEKCNPEFERNVENTSCFMVPGVLPDTLNTVIRVTKNLCYEDDKL 326
QY 326 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIPPPIDPGKIFK 385
DB 327 WSNWSQEMSIGKRNSTLYITMLLIYPVIVAGAIIVLLLYLKLKLIIPPPIDPGKIFK 386
QY 386 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 426
DB 387 EMFGDQNDTLLHWKYDYIEKQTKETSDSVLIENLKASQ 427
RESULT 4
Q5JSL4 HUMAN
ID Q5JSL4_HUMAN PRELIMINARY; PRT; 426 AA.
AC Q5JSL4;
DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
DT 26-APR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Interleukin 13 receptor, alpha 1 variant (Fragment).
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AB20849; BAD93086.1; -; mRNA.
DR Ensembl; ENSG00000131724; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn_rcpt_B/G.
DR InterPro; IPR003532; Hempt_rcpt_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 426 AA; 48555 MW; 342A3A6F7347261B CRC64;
Query Match 70.4%; Score 300; DB 2; Length 426;
Best Local Similarity 99.8%; Pred. No. 2.3e-291;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 26 APTETQPPVTNLVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 85
DB 26 APTETQPPVTNLVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 85
QY 86 EYPLNERICLVGSGQSCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 145
DB 86 EYPLNERICLVGSGQSCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 145
QY 146 LPGRNTSPDTNTLYYHRSLEKIHQECENIFREGQYFGCSFDLTVKVDSFQHSVQIMV 205
DB 146 LPGRNTSPDTNTLYYHRSLEKIHQECENIFREGQYFGCSFDLTVKVDSFQHSVQIMV 205
QY 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCFLFYEVVNN 265
DB 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCFLFYEVVNN 265
QY 266 SQTETHNVFYVQEAECENPEFERNVENTSCFVMPVGLPDTLNTVIRVTKNLCYEDDKL 325
DB 266 SQTETHNVFYVQEAECENPEFERNVENTSCFVMPVGLPDTLNTVIRVTKNLCYEDDKL 325
QY 326 WSNWSQEMSIGKRNSTLYITMLLIIVPVIAGAIIVLLIYLRKLIIPPPIDPGKIPK 385
DB 326 WSNWSQEMSIGKRNSTLYITMLLIIVPVIAGAIIVLLIYLRKLIIPPPIDPGKIPK 385
QY 386 EMFGQNDTTLHWKYDYIEKQKETSVDLSVLIENLKQASQ 426
DB 386 EMFGQNDTTLHWKYDYIEKQKETSVDLSVLIENLKQASQ 426
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RESULT 5
Q9UDY5 HUMAN
ID Q9UDY5_HUMAN PRELIMINARY; PRT; 279 AA.
AC Q9UDY5;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 21-FEB-2006, entry version 26.
DE Interleukin-13 receptor soluble form (Interleukin 13 receptor, alpha
DE 1).
GN Name=IL13R1; ORFNames=RP13-12804.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wada M., Hisano T., Kuwano M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or
CC activation (By similarity).
CC -----
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CC -----
CC EMBL; U81380; AAD00511.2; -; mRNA.
DR EMBL; AL391280; CA141409.1; -; Genomic DNA.
DR Ensembl; ENSG00000131724; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn_rcpt_B/G.
DR InterPro; IPR003532; Hempt_rcpt_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 279 AA; 31659 MW; E74141FE9F8E9EBB CRC64;
Query Match 58.9%; Score 251; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.1e-242;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTETQPPVTNLVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 85
DB 26 APTETQPPVTNLVSVENICTVIWTWNPPEGASSNCSLWYFSGDKQDKKIAPETRRSI 86
QY 86 EYPLNERICLVGSGQSCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 145
DB 86 EYPLNERICLVGSGQSCSTNESEKPSILVEKCISSPEGDPESAVTELQCIWHNLSYMKCSW 146
QY 146 LPGRNTSPDTNTLYYHRSLEKIHQECENIFREGQYFGCSFDLTVKVDSFQHSVQIMV 205
DB 146 LPGRNTSPDTNTLYYHRSLEKIHQECENIFREGQYFGCSFDLTVKVDSFQHSVQIMV 206
QY 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCFLFYEVVNN 265
DB 206 KDNAGIKPSFNIVPLTSRVKDPDPHINKLSFNHNDLYVQWENPQNFISRCFLFYEVVNN 266
QY 266 SQTETHNVFYV 276
DB 266 SQTETHNVFYV 277
RESULT 6
Q7YRV5 MACFA
ID Q7YRV5_MACFA PRELIMINARY; PRT; 409 AA.
AC Q7YRV5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Interleukin 13 receptor alpha 1 (Fragment).
GN Name=IL13R1;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
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RN  NUCLEOTIDE SEQUENCE.
RA  Maccarone P., Drinkwater C.C., Nash A.D.;
RT  "Cynomolgus monkey interleukin 13 receptor alpha 1.";
RL  Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC  -----
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CC  -----
DR  EMBL; AY312267; AAP78901.1; -; mRNA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  InterPro; IPR002996; Cytln rcpt B/G.
DR  InterPro; IPR003532; Hemot_rcpt_S_F2.
DR  PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW  Receptor.
FT  CHAIN  1 409  interleukin 13 receptor alpha 1.
FT  NON TER 1 1
SQ  SEQUENCE  409 AA; 46685 MW; 9B98A52671686AF4 CRC64;

Query Match      33.8%; Score 144; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 5.4e-135;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  283 NPSEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCYEDDKLWSNWSQEMSIGKKNST 342
DB  ||||| 266 NPSEFERNVENTSCFMVPGVLPDTLNTVIRVTKNKLCYEDDKLWSNWSQEMSIGKKNST 325
QY  343 LYITMLLIVPVIVAGAILVLLLYKRLIIFFPPDPGKIFKEMFGDQNDTTLHWKKYD 402
DB  ||||| 326 LYITMLLIVPVIVAGAILVLLLYKRLIIFFPPDPGKIFKEMFGDQNDTTLHWKKYD 385
QY  403 IYEQTKTEETSDSVLIENLKASQ 426
DB  ||||| 386 IYEQTKTEETSDSVLIENLKASQ 409

RESULT 7
ID  Q6ZV70 HUMAN PRELIMINARY; PRT; 226 AA.
AC  Q6ZV70;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  21-FEB-2006, entry version 7.
DE  CDNA FLJ41521 fis, clone BRTHA2012980, moderately similar to
DE  INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN (IL-13RA-1) (IL-13RA-1).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
[1]
RN  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Thalamus;
RA  Teshiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA  Fukuzumi Y., Fujimori Y., Koniyama M., Sugiyama T., Irie R.,
RA  Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA  Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA  Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA  Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA  Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA  Isogai T.;
RT  "NEDO human cDNA sequencing project.";
RL  Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AK123515; BAC85635.1; -; mRNA.
DR  GO; GO:0004872; F:receptor activity; IEA.
KW  Receptor.
SQ  SEQUENCE  226 AA; 24825 MW; 0CBB9208934F18DF CRC64;

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Query Match      21.4%; Score 91; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.2e-82;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  336 GKRNSTLYITMLLIVPVIVAGAILVLLLYKRLIIFFPPDPGKIFKEMFGDQNDT 395
DB  ||||| 136 GKRNSTLYITMLLIVPVIVAGAILVLLLYKRLIIFFPPDPGKIFKEMFGDQNDT 195
QY  396 LHWKKYDIYEQTKTEETSDSVLIENLKASQ 426
DB  ||||| 196 LHWKKYDIYEQTKTEETSDSVLIENLKASQ 226

RESULT 8
ID  Q6U6T1 SHEEP PRELIMINARY; PRT; 401 AA.
AC  Q6U6T1;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  07-FEB-2006, entry version 9.
DE  Interleukin 13 receptor alpha 1 (Fragment).
OS  Ovis aries (Sheep).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC  Pecora; Bovidae; Caprinae; Ovis.
OX  NCBI_TaxID=9940;
[1]
RN  NUCLEOTIDE SEQUENCE.
RA  Maccarone P., Drinkwater C.C., Nash A.D.;
RT  "Cloning of the sheep interleukin 13 receptor alpha 1 cDNA.";
RL  Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; AY377582; AA083584.1; -; mRNA.
DR  GO; GO:0016020; C:membrane; IEA.
DR  GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. .; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  InterPro; IPR002996; Cytln rcpt B/G.
DR  InterPro; IPR003532; Hemot_rcpt_S_F2.
DR  PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW  Receptor.
FT  CHAIN  <1 401  interleukin 13 receptor alpha 1.
FT  NON TER 1 1
SQ  SEQUENCE  401 AA; 45834 MW; 4E7AD6162BD42B25 CRC64;

Query Match      15.3%; Score 65; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.3e-56;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  360 IVLLLYKRLIIFFPPDPGKIFKEMFGDQNDTTLHWKKYDIYEQTKTEETSDSVLIE 419
DB  ||||| 335 IVLLLYKRLIIFFPPDPGKIFKEMFGDQNDTTLHWKKYDIYEQTKTEETSDSVLIE 394
QY  420 NLKKA 424
DB  ||||| 395 NLKKA 399

RESULT 9
ID  Q863Z6 PIG PRELIMINARY; PRT; 423 AA.
AC  Q863Z6;
DT  01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT  01-JUN-2003, sequence version 1.
DT  21-FEB-2006, entry version 14.
DE  Interleukin 13 receptor alpha 1.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC  Sus.

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OX NCBI_TaxID=9823;
RN NUCLEOTIDE SEQUENCE
RP PubMed=1530752; DOI=10.1016/j.vetimm.2004.05.003;
RX Zarlenga D.S., Dawson H., Kringel H., Solano-Aguilar G.,
RA Urban J.F. Jr.;
RT "Molecular cloning of the Swine IL-4 receptor alpha and IL-13 receptor
RT 1-chains: effects of experimental Toxoplasma gondii, Ascaris suum and
RT Trichuris suis infections on tissue mRNA levels.";
RL Vet. Immunol. Immunopathol. 101:223-234(2004).
CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane
CC protein (By similarity).
CC -!- DOMAIN: The WXXWS motif appears to be necessary for proper protein
CC folding and thereby efficient intracellular transport and cell-
CC surface receptor binding (By similarity).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AY266142; AAP23301.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .); IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; Cytkn rcpt B/G.
DR PROSITE; PS013532; Hempt_rcpt_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 423 AA; 47985 MW; EA636PB6BCA533D9 CRC64;

Query Match 14.6%; Score 62; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 8.8e-53;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 358 AIIIVLLYLKRLKIIIFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQTSVVL 417
Db |||||
355 AIIIVLLYLKRLKIIIFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQTSVVL 414

OY 418 IE 419
Db ||
415 IE 416

RESULT 10
Q8VDP7 MOUSE
ID Q8VDP7;
AC Q8VDP7; PRELIMINARY; PRT; 252 AA.
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE IL13ral protein (Fragment).
GN Name=Il13ral;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC021472; AAH21472.1; -; mRNA.
DR Ensembl; ENSMUSG0000017057; Mus musculus.
DR MGI; MGI:105052; Il13ral.
DR GO; GO:0005615; C:extracellular space; RCA.
DR GO; GO:0016021; C:integral to membrane; RCA.
FT NON_TER 1
SQ SEQUENCE 252 AA; 29044 MW; E303CF276C7A5E81 CRC64;

Query Match 10.1%; Score 43; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 6.1e-34;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 365 YLKRLLKIIIFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQ 407
Db |||||
191 YLKRLLKIIIFPPDPGKIFKEMFGDQNDTLHWKKYDIYEKQ 233

RESULT 11
I13R1 MOUSE
ID I13R1;
AC O09030; Q7TT27;
DT 01-NOV-1997, integrated into UniProtKB/Swiss-Prot.
DT 01-JUL-1997, sequence version 1.
DT 07-MAR-2006, entry version 52.
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
DE 13RA-1) (Interleukin-13-binding protein) (NR4) (CD213al antigen).
GN Name=Il13ral; Synonyms=Il13r, Il13ra,
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=96133964; PubMed=8552669; DOI=10.1073/pnas.93.1.497;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
RT "Cloning and characterization of a binding subunit of the interleukin
RT 13 receptor that is also a component of the interleukin 4 receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=FVB/N; TISSUE=Brain, and Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Binds IL13 with a low affinity. Together with IL4R-alpha  
 CC can form a functional receptor for IL13. Also serves as an  
 CC alternate accessory protein to the common cytokine receptor gamma  
 CC chain for IL4 signaling, but cannot replace the function of gamma  
 CC in allowing enhanced IL2 binding activity (By similarity).  
 CC -!- SUBUNIT: Interleukin 13 receptor is a complex of IL4R, IL13RA1,  
 CC and possibly other components (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Membrane; single-pass type I membrane  
 CC protein.  
 CC -!- TISSUE SPECIFICITY: Spleen, liver, thymus, heart, lung, kidney,  
 CC testis, stomach, brain, skin, and colon; but not skeletal muscle.  
 CC -!- DOMAIN: The WSXWS motif appears to be necessary for proper protein  
 CC folding and thereby efficient intracellular transport and cell-  
 CC surface receptor binding.  
 CC -!- DOMAIN: The box 1 motif is required for JAK interaction and/or  
 CC activation.  
 CC -!- SIMILARITY: Belongs to the type I cytokine receptor family. Type 5  
 CC subfamily.  
 CC  
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 CC  
 CC EMBL: S80963; AAB50695.1; -; mRNA.  
 CC EMBL: BC052425; AAH52425.2; -; mRNA.  
 CC EMBL: BC058939; AAH58939.1; -; mRNA.  
 CC Ensembl: ENSMUSG0000017057; Mus musculus.  
 CC MGI: MGI:105052; Il13ral.  
 CC GO: GO:0005615; C:extracellular space; TAS.  
 CC GO: GO:0016021; C:integral to membrane; TAS.  
 CC InterPro: IPR002986; Cytok\_rcpt\_B/G.  
 CC InterPro: IPR003532; Hempt\_rcpt\_S\_F2.  
 CC PROSITE: PS01356; HEMATOPO RECS\_F2; 1.  
 CC Glycoprotein; Membrane; Receptor; Signal; Transmembrane.  
 CC SIGNAL 1 25 Potential.  
 CC CHAIN 26 424 Interleukin-13 receptor alpha-1 chain.  
 CC  
 CC FT TOPO DOM 26 340 /FTID=PRO\_0000010940.  
 CC FT TRANSMEM 341 364 Extracellular (Potential).  
 CC FT TOPO DOM 365 424 Potential.  
 CC FT MOTIF 324 328 Cytoplasmic (Potential).  
 CC FT MOTIF 371 379 WSXWS motif.  
 CC FT CARBOHYD 35 35 Box 1 motif.  
 CC FT CARBOHYD 35 35 N-linked (GlcNAc...) (Potential).  
 CC FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).  
 CC FT CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).  
 CC FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).  
 CC FT CARBOHYD 262 262 N-linked (GlcNAc...) (Potential).  
 CC FT CARBOHYD 338 338 N-linked (GlcNAc...) (Potential).  
 CC FT DISULFID 44 93 Potential.  
 CC FT DISULFID 132 142 By similarity.  
 CC FT DISULFID 171 183 By similarity.  
 CC SEQUENCE 424 AA; 48402 MW; EB8330A0DC82C9F9 CRC64;  
 SQ  
 Query Match 10.1%; Score 43; DB 1; Length 424;  
 Best Local Similarity 100.0%; Pred. No. 9.8e-34;  
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 365 YLRLRLIIIFPIPPDGKIFKEMFGDNDTLHWKXYDIYEKQ 407  
 Db 363 YLRLRLIIIFPIPPDGKIFKEMFGDNDTLHWKXYDIYEKQ 405  
 RESULT 12  
 Q8C123 MOUSE PRELIMINARY; PRT; 424 AA.  
 ID Q8C123\_MOUSE  
 AC Q8C123;

DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 21-FEB-2006, entry version 22.  
 DE Colon RCB-0549 C1e-H3 cDNA, RIKEN full-length enriched library.  
 DE clone:G430044I06 product:interleukin 13 receptor, alpha 1, full insert  
 DE sequence.  
 GN Name=Il13ral; (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Nuroidea; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Colon;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning.";  
 RT Methods Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Colon;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RX Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bono H., Chalk A.M.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
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 RA Hill D., Huminecki L., Iacono M., Ikeno K., Iwama A., Ishikawa T.,  
 RA Takt M., Kanapin A., Katoh M., Kawasawa Y., Kelson J., Kitamura H.,  
 RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
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 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,  
 RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,  
 RA Tammaja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Grimmer S.M., Teasdale R.D., Liu E.T., Bruscia V., Quackenbush J.,  
 RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Inamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno K., Nakano K., Ninomiya N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.,  
 RT "The transcriptional landscape of the mammalian genome.";  
 RL Science 309:1559-1563(2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Colon;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Colon;



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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:31:52 ; Search time 21 seconds  
(without alignments)  
544.307 Million cell updates/sec

Title: US-09-051-843D-4

Perfect score: 426

Sequence: 1 MWPRLGLIALLCAGG.....QTKETDSVLIENLKASQ 426

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 112942 seqs, 26832045 residues

Word size: 1

Total number of hits satisfying chosen parameters: 112925

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Published Applications AA New.\*

- 1: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/ECT\_NEW\_PUB.pep.\*
- 6: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description         |
|------------|-------|-------------|--------|----|---------------------|
| 1          | 17    | 4.0         | 17     | 7  | US-11-134-871-727   |
| 2          | 10    | 2.3         | 25     | 7  | US-11-134-871-3230  |
| 3          | 10    | 2.3         | 175    | 6  | US-10-449-902-33914 |
| 4          | 10    | 2.3         | 176    | 6  | US-10-449-902-32626 |
| 5          | 10    | 2.3         | 274    | 6  | US-10-449-902-43265 |
| 6          | 10    | 2.3         | 285    | 6  | US-10-449-902-51966 |
| 7          | 10    | 2.3         | 538    | 6  | US-10-449-902-51820 |
| 8          | 10    | 2.3         | 623    | 6  | US-10-449-902-56221 |
| 9          | 10    | 2.3         | 1493   | 6  | US-10-511-814-18    |
| 10         | 9     | 2.1         | 29     | 7  | US-11-134-871-2683  |
| 11         | 9     | 2.1         | 35     | 6  | US-10-449-902-34876 |
| 12         | 9     | 2.1         | 96     | 6  | US-10-953-349-14842 |
| 13         | 9     | 2.1         | 98     | 6  | US-10-953-349-9576  |
| 14         | 9     | 2.1         | 99     | 6  | US-10-953-349-9575  |
| 15         | 9     | 2.1         | 100    | 6  | US-10-953-349-9574  |
| 16         | 9     | 2.1         | 101    | 6  | US-10-449-902-28815 |
| 17         | 9     | 2.1         | 125    | 6  | US-10-449-902-47247 |
| 18         | 9     | 2.1         | 139    | 6  | US-10-953-349-27506 |
| 19         | 9     | 2.1         | 139    | 6  | US-10-449-902-34201 |
| 20         | 9     | 2.1         | 146    | 6  | US-10-449-902-35115 |
| 21         | 9     | 2.1         | 159    | 6  | US-10-449-902-56503 |
| 22         | 9     | 2.1         | 170    | 6  | US-10-449-902-30189 |
| 23         | 9     | 2.1         | 173    | 6  | US-10-449-902-50881 |
| 24         | 9     | 2.1         | 183    | 6  | US-10-449-902-42575 |
| 25         | 9     | 2.1         | 185    | 6  | US-10-449-902-34633 |

26 9 2.1 186 6 US-10-449-902-42360 Sequence 42360, A  
27 9 2.1 189 6 US-10-449-902-42125 Sequence 42125, A  
28 9 2.1 191 6 US-10-449-902-43679 Sequence 43679, A  
29 9 2.1 196 6 US-10-449-902-34401 Sequence 34401, A  
30 9 2.1 204 6 US-10-449-902-49137 Sequence 49137, A  
31 9 2.1 208 6 US-10-449-902-40257 Sequence 40257, A  
32 9 2.1 222 6 US-10-449-902-32123 Sequence 32123, A  
33 9 2.1 227 6 US-10-449-902-28912 Sequence 28912, A  
34 9 2.1 230 6 US-10-449-902-56230 Sequence 56230, A  
35 9 2.1 241 6 US-10-449-902-48778 Sequence 48778, A  
36 9 2.1 246 6 US-10-449-902-42341 Sequence 42341, A  
37 9 2.1 246 6 US-10-449-902-54590 Sequence 54590, A  
38 9 2.1 248 6 US-10-449-902-49085 Sequence 49085, A  
39 9 2.1 257 6 US-10-953-349-38261 Sequence 38261, A  
40 9 2.1 265 6 US-10-449-902-37490 Sequence 37490, A  
41 9 2.1 269 7 US-11-234-731-617 Sequence 617, App  
42 9 2.1 271 6 US-10-953-349-38260 Sequence 38260, A  
43 9 2.1 271 6 US-10-449-902-32465 Sequence 32465, A  
44 9 2.1 273 6 US-10-449-902-30912 Sequence 30912, A  
45 9 2.1 273 6 US-10-449-902-50092 Sequence 50092, A

#### ALIGNMENTS

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US-11-134-871-727  
; Sequence 727, Application US/11134871  
; Publication No. US20060141528A1  
; GENERAL INFORMATION:  
; APPLICANT: Aebersold, Rudolf H.  
; APPLICANT: Zhang, Hui  
; TITLE OF INVENTION: Compositions and Methods for  
; TITLE OF INVENTION: Quatification of Serum Glycoproteins  
; FILE REFERENCE: 66661-116  
; CURRENT APPLICATION NUMBER: US/11/134,871  
; CURRENT FILING DATE: 2005-05-20  
; PRIOR APPLICATION NUMBER: 60/573,593  
; PRIOR FILING DATE: 2004-05-21  
; NUMBER OF SEQ ID NOS: 3602  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 727  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-134-871-727

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Best Local Similarity 100.0%; Pred. No. 7.5e-10;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 RNTSPDNTNTLYYWHRS 17

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US-11-134-871-3230  
; Sequence 3230, Application US/11134871  
; Publication No. US20060141528A1  
; GENERAL INFORMATION:  
; APPLICANT: Aebersold, Rudolf H.  
; APPLICANT: Zhang, Hui  
; TITLE OF INVENTION: Compositions and Methods for  
; TITLE OF INVENTION: Quatification of Serum Glycoproteins  
; FILE REFERENCE: 66661-116  
; CURRENT APPLICATION NUMBER: US/11/134,871  
; CURRENT FILING DATE: 2005-05-20  
; PRIOR APPLICATION NUMBER: 60/573,593  
; PRIOR FILING DATE: 2004-05-21  
; NUMBER OF SEQ ID NOS: 3602  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3230

; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-134-871-3230

Query Match 2.3%; Score 10; DB 7; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0063;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
US-10-449-902-33914  
; Sequence 33914, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33914  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-33914

Query Match 2.3%; Score 10; DB 6; Length 175;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGGA 26  
Db 19 AGGGGGGGGA 28  
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RESULT 4  
US-10-449-902-32626  
; Sequence 32626, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32626  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-32626

Query Match 2.3%; Score 10; DB 6; Length 176;  
Best Local Similarity 100.0%; Pred. No. 0.034;  
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QY 18 GGGGGGGGAP 27  
Db 56 GGGGGGGGAP 65  
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RESULT 5  
US-10-449-902-43265  
; Sequence 43265, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43265  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-43265

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Best Local Similarity 100.0%; Pred. No. 0.05;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 46 AGGGGGGGGA 55  
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RESULT 6  
US-10-449-902-51966  
; Sequence 51966, Application US/10449902  
; Publication No. US20060123505A1  
; GENERAL INFORMATION:  
; APPLICANT: National Institute of Agrobiological Sciences.  
; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
; APPLICANT: The Institute of Physical and Chemical Research.  
; APPLICANT: Foundation for Advancement of International Science.  
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
; FILE REFERENCE: MOA-A0205Y1-US  
; CURRENT APPLICATION NUMBER: US/10/449,902  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: JP 2002-203269  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2002-383870  
; PRIOR FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 56791  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 51966  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-449-902-51966

Query Match 2.3%; Score 10; DB 6; Length 285;  
Best Local Similarity 100.0%; Pred. No. 0.052;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AGGGGGGGGA 26

GenCore version 5.1.9  
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OM protein - protein search, using sw model

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Title: US-09-051-843D-4

Perfect score: 426  
Sequence: 1 MEMPARLCGIMALLCAGGCG.....QTKRETDVYLINLKASQ 426

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Gapop 60.0, Gapext 60.0

Searched: 650591 seqs, 87530628 residues

Word size: 1

Total number of hits satisfying chosen parameters: 649417

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
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| 1          | 426   | 100.0       | 426    | 2  | US-09-688-286D-4   |
| 2          | 401   | 94.1        | 427    | 2  | US-08-969-125-9    |
| 3          | 401   | 94.1        | 427    | 2  | US-09-545-002-9    |
| 4          | 401   | 94.1        | 427    | 2  | US-09-949-016-6094 |
| 5          | 317   | 74.4        | 322    | 2  | US-09-825-561A-82  |
| 6          | 317   | 74.4        | 784    | 2  | US-09-313-942-30   |
| 7          | 317   | 74.4        | 784    | 2  | US-10-282-162-30   |
| 8          | 317   | 74.4        | 793    | 2  | US-09-313-942-32   |
| 9          | 317   | 74.4        | 793    | 2  | US-10-282-162-32   |
| 10         | 231   | 54.2        | 233    | 2  | US-09-949-016-8550 |
| 11         | 43    | 10.1        | 424    | 2  | US-09-688-286D-2   |
| 12         | 37    | 8.7         | 405    | 2  | US-09-828-995B-50  |
| 13         | 22    | 5.2         | 22     | 2  | US-09-028-937-25   |
| 14         | 10    | 2.3         | 289    | 2  | US-09-949-016-8825 |
| 15         | 10    | 2.3         | 331    | 2  | US-09-949-016-6323 |
| 16         | 10    | 2.3         | 335    | 2  | US-09-949-016-7186 |
| 17         | 10    | 2.3         | 803    | 2  | US-09-949-002-340  |
| 18         | 10    | 2.3         | 1492   | 2  | US-09-697-898-5    |
| 19         | 10    | 2.3         | 1493   | 2  | US-09-423-890-8    |
| 20         | 10    | 2.3         | 1493   | 2  | US-10-000-864-8    |
| 21         | 10    | 2.3         | 1593   | 2  | US-08-628-829-4    |
| 22         | 10    | 2.3         | 1620   | 1  | US-08-542-163-2    |
| 23         | 10    | 2.3         | 1620   | 2  | US-09-100-089-2    |
| 24         | 10    | 2.3         | 1620   | 2  | US-09-670-827-2    |
| 25         | 10    | 2.3         | 1620   | 2  | US-09-827-949-2    |
| 26         | 9     | 2.1         | 25     | 2  | US-09-721-154-10   |

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| 27 | 9 | 2.1 | 29 | 2 | US-09-270-767-38456 | Sequence 38456, A |
| 28 | 9 | 2.1 | 29 | 2 | US-09-270-767-53673 | Sequence 53673, A |
| 29 | 9 | 2.1 | 30 | 1 | US-08-935-886-2     | Sequence 2, App1  |
| 30 | 9 | 2.1 | 36 | 2 | US-09-428-082B-14   | Sequence 14, App1 |
| 31 | 9 | 2.1 | 36 | 2 | US-09-428-082B-349  | Sequence 349, App |
| 32 | 9 | 2.1 | 36 | 2 | US-09-428-082B-354  | Sequence 354, App |
| 33 | 9 | 2.1 | 36 | 2 | US-09-428-082B-355  | Sequence 355, App |
| 34 | 9 | 2.1 | 36 | 2 | US-09-428-082B-356  | Sequence 356, App |
| 35 | 9 | 2.1 | 36 | 2 | US-09-422-838C-11   | Sequence 11, App1 |
| 36 | 9 | 2.1 | 36 | 2 | US-09-422-838C-12   | Sequence 12, App1 |
| 37 | 9 | 2.1 | 36 | 2 | US-09-422-838C-13   | Sequence 13, App1 |
| 38 | 9 | 2.1 | 36 | 2 | US-09-422-838C-21   | Sequence 21, App1 |
| 39 | 9 | 2.1 | 36 | 2 | US-09-422-838C-24   | Sequence 24, App1 |
| 40 | 9 | 2.1 | 36 | 2 | US-09-422-838C-26   | Sequence 26, App1 |
| 41 | 9 | 2.1 | 36 | 2 | US-09-422-838C-27   | Sequence 27, App1 |
| 42 | 9 | 2.1 | 36 | 2 | US-09-422-838C-28   | Sequence 28, App1 |
| 43 | 9 | 2.1 | 36 | 2 | US-09-422-838C-29   | Sequence 29, App1 |
| 44 | 9 | 2.1 | 37 | 2 | US-09-428-082B-350  | Sequence 350, App |
| 45 | 9 | 2.1 | 38 | 2 | US-09-428-082B-351  | Sequence 351, App |

#### ALIGNMENTS

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US-09-688-286D-4
; Sequence 4, Application US/09688286D
; Patent No. 6911530
; GENERAL INFORMATION:
; APPLICANT: Willson, Tracey
; APPLICANT: Nicols, Nicos
; APPLICANT: Hilton, Douglas
; APPLICANT: Metcalf, Donald
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding same
; FILE REFERENCE: 23199-215
; CURRENT APPLICATION NUMBER: US/09/688,286D
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: AU PM6135
; PRIOR FILING DATE: 1995-10-23
; PRIOR APPLICATION NUMBER: AU PM7276
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: AU PM2208
; PRIOR FILING DATE: 1996-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: human
US-09-688-286D-4

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 361 VLLLYLKRKLIIIFPPIPDGKIFKEMFGDNDTLHWKKYDIYEKQTEETDSVLIEN 420  
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QY 421 LKXASQ 426  
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RESULT 2  
US-08-969-125-9  
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; Patent No. 6143871  
; GENERAL INFORMATION:  
; APPLICANT: BONNEFOY, JEAN-YES  
; GAUCHAT, JEAN-FRANCOIS  
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/969,125B  
; FILING DATE: 12-No. 6143871-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9625899.1  
; FILING DATE: 13-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 1430-179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 427 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-08-969-125-9  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 27 APTEPOPVTNLSVSEVNICTVIWTNPPREGASSNSCLWYFSHFGDKODKKIAPETRRR 86  
QY 86 EYPLNRIQLQVSGQSTNESEKPSILVEKCIAPPREGDPESAATBELQCIWHNLSYMKCSW 145  
Db 87 EYPLNRIQLQVSGQSTNESEKPSILVEKCIAPPREGDPESAATBELQCIWHNLSYMKCSW 146  
QY 146 LFGRTSPDTNVTLYYWHRSLEKIHQECENIFREGQYFGCSFDLTXYKXDSSEFQHSVQIWM 205

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Db 147 LFGRTSPDTNVTLYYWHRSLEKIHQECENIFREGQYFGCSFDLTXYKXDSSEFQHSVQIWM 206  
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QY 266 SQTETHNVFYOQAKCENPEFERNVENTSCFVWPVGLPDTLNTVTRIRVKTNKLCEYDDKL 325  
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Db 327 WSNWSQEMSIGKRNSTLYITMLLIVPVIVAGAIIVLLYLKRKLIIIFPPIPDGKIFX 386  
QY 386 EMFGDNDTLHWKKYDIYEKQTEETDSVLIENLKXASQ 426  
Db 387 EMFGDNDTLHWKKYDIYEKQTEETDSVLIENLKXASQ 427  
RESULT 3  
US-09-545-002-9  
; Sequence 9, Application US/09545002  
; Patent No. 6743604  
; GENERAL INFORMATION:  
; APPLICANT: BONNEFOY, JEAN-YES  
; GAUCHAT, JEAN-FRANCOIS  
; TITLE OF INVENTION: SUBSTANCES AND THEIR USES  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: NIXON & VANDERHAYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/545,002  
; FILING DATE: 12-No. 6743604-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9625899.1  
; FILING DATE: 13-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 1430-179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 427 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-545-002-9  
Query Match 94.1%; Score 401; DB 2; Length 427;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 APTEPOPVTNLSVSEVNICTVIWTNPPREGASSNSCLWYFSHFGDKODKKIAPETRRR 85  
Db 27 APTEPOPVTNLSVSEVNICTVIWTNPPREGASSNSCLWYFSHFGDKODKKIAPETRRR 86

|    |     |   |     |
|----|-----|---|-----|
| QY | 86  | EVLPLNERICLOVQSGCSTHSEKSPSTLVKXCISPEPGDEPESATVLEQCIIMHNSYMKGM | 145 |
| Db | 87  | EVLPLNERICLOVQSGCSTHSEKSPSTLVKXCISPEPGDEPESATVLEQCIIMHNSYMKGM | 146 |
| QY | 146 | LPGRNTSPDNTVTLVYMHRSLEKIHOCENIIFREGQVFGCSFDLTUKYDSSFEOSHVOJMW | 205 |
| Db | 147 | LPGRNTSPDNTVTLVYMHRSLEKIHOCENIIFREGQVFGCSFDLTUKYDSSFEOSHVOJMW | 206 |
| QY | 206 | KDNACKIKPSENIIVPLTSRVKDPPIIKULSFINDLVYQWENPQNFISRCLEFYEVAVNN  | 265 |
| Db | 207 | KDNACKIKPSENIIVPLTSRVKDPPIIKULSFINDLVYQWENPQNFISRCLEFYEVAVNN  | 266 |
| QY | 266 | SQTEHNFVYVOEACENPEPERNAVNTSCFMPGCVLPDLTNAVIRVYTKNLCYEDDKL     | 325 |
| Db | 267 | SQTEHNFVYVOEACENPEPERNAVNTSCFMPGCVLPDLTNAVIRVYTKNLCYEDDKL     | 326 |
| QY | 326 | MSNMSOEMSIGKKRNSTLYITMLLYIPVIVAGIIVLLYLTKRKIIIFPPPIIDPEKIFK   | 385 |
| Db | 327 | MSNMSOEMSIGKKRNSTLYITMLLYIPVIVAGIIVLLYLTKRKIIIFPPPIIDPEKIFK   | 386 |
| QY | 386 | EMFGQNDDTLHMKKYDIYEKQTEETDSVLIENLKKAQO                        | 426 |
| Db | 387 | EMFGQNDDTLHMKKYDIYEKQTEETDSVLIENLKKAQO                        | 427 |

RESULT 4  
 US-09-949-016-6094  
 ; Sequence 6094, Application US/09949016  
 ; Patent No. 6612339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: C1001107  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 6094  
 ; LENGTH: 427  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-949-016-6094

```

Query Match      94.1%  Score 401;  DB 2;  length 427;
Best Local Similarity 100.0%  Pred. NO. 0;
Matches 401;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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|    |     |   |     |
|----|-----|---|-----|
| QY | 26  | APFTOPPVNTLSTSVENLCTVITMTWNPBEGASSNCSLMTWSHEDRDXDKKIAPETRST   | 85  |
| Db | 27  | APFTOPPVNTLSTSVENLCTVITMTWNPBEGASSNCSLMTWSHEDRDXDKKIAPETRST   | 86  |
| QY | 86  | EVPLANERLCLOVSGQCSNTSEKESILVEKCLSPREGDPESAATVLEOCLIMNLSYMKCSW | 145 |
| Db | 87  | EVPLANERLCLOVSGQCSNTSEKESILVEKCLSPREGDPESAATVLEOCLIMNLSYMKCSW | 146 |
| QY | 146 | LPGNTSPDNTYTLTYWMHRSLEKTHOCENIFREGQFCCSGEDLTVKVKSFEHOSVQIMV   | 205 |
| Db | 147 | LPGNTSPDNTYTLTYWMHRSLEKTHOCENIFREGQFCCSGEDLTVKVKSFEHOSVQIMV   | 206 |
| QY | 206 | KDNAGKIKPSFNIPVLTSRVKPDPPHINKLSFHNDDLTVQOMENPONTSRCLFPEVEVANN | 265 |
| Db | 207 | KDNAGKIKPSFNIPVLTSRVKPDPPHINKLSFHNDDLTVQOMENPONTSRCLFPEVEVANN | 266 |
| QY | 266 | SOETHNVVYVOEAKCENPFEFRVENVSCMVGVLPDLNTAARIRKTKNLCYEDDKL       | 325 |

|     | Qy  | Db   |
|-----|---|------|
| 267 | SECRETINPVYQAEKCEPDEFEERNVENTSCMGVGLPDTLNTVRIRVKTNKCLYEDDKL | 3366 |
| Qy  | MSMSQEMSGISGKKRSTLYITMLLVPIYVAGAIIVLLLYIKRKIIIFPIPDGKIFK    | 385  |
| Db  | MSMSQEMSGISGKKRSTLYITMLLVPIYVAGAIIVLLLYIKRKIIIFPIPDGKIFK    | 386  |
| Qy  | EMFGQNDPDLFMKKYDIYEKOTKEETSIVLIENLKQASQ                     | 426  |
| Db  | EMFGQNDPDLFMKKYDIYEKOTKEETSIVLIENLKQASQ                     | 427  |

```

RESULT 5
US-09-825-561A-82
: Sequence 82, Application US/09825561A
Patient No. 6777539
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: No. 6777539ak, Julia E.
APPLICANT: West, James W.
APPLICANT: Pressnell, Scott R.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
FILE REFERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/222,121
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 86
SOFTWARE: SeqSed for Windows Version 3.0
: SEQ ID NO 82
: LENGTH: 322
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-825-561A-82

```

|                           |        |                     |           |             |
|---------------------------|--------|---------------------|-----------|-------------|
| Query Match               | 74.4%  | Score 317;          | DB 2;     | Length 322; |
| Best Local Similarity     | 100.0% | Pred. No. 5.4e-310; |           |             |
| Matches 317; Conservative | 0;     | Mismatches 0;       | Indels 0; | Gaps 0.     |

|    |     |  |     |
|----|-----|--|-----|
| Qy | 26  | AATELEOPPTNLSVSEVNLCTVIMTNPPEASANSGLWTFESHGDKODKKIAPETRRS1     | 85  |
| Db | 6   | AATELEOPPTNLSVSEVNLCTVIMTNPPEASANSGLWTFESHGDKODKKIAPETRRS1     | 65  |
| Qy | 86  | EYPLNERICLOVGSQCSSTNESEKPSILVEKCISPEEGDPESAATVETLOCIMHNLSYKCSW | 145 |
| Db | 66  | EYPLNERICLOVGSQCSSTNESEKPSILVEKCISPEEGDPESAATVETLOCIMHNLSYKCSW | 125 |
| Qy | 146 | LEGRNTSPDNTYTLTYMHRSLKTHOCENIFREOQYGCSPDLTKYKDSFEGHSVOINW      | 205 |
| Db | 126 | LEGRNTSPDNTYTLTYMHRSLKTHOCENIFREOQYGCSPDLTKYKDSFEGHSVOINW      | 185 |
| Qy | 206 | KONACKIKPSFNIVPLTSRVKDPDPHINKLSFHHDDLTYOMENPONEFSRCLFEYEVANN   | 265 |
| Db | 186 | KONACKIKPSFNIVPLTSRVKDPDPHINKLSFHHDDLTYOMENPONEFSRCLFEYEVANN   | 245 |
| Qy | 266 | SOTETIHNFYVOALACENPEFERVENTSCPMYGVLPDLTNVVRIRVKTKNKLCTYEDDKL   | 325 |
| Db | 246 | SOTETIHNFYVOALACENPEFERVENTSCPMYGVLPDLTNVVRIRVKTKNKLCTYEDDKL   | 305 |
| Qy | 326 | WSNMSQEMSIGKQNST   | 342 |
| Db | 306 | WSNMSQEMSIGKQNST   | 322 |

RESULT 6  
US-09-313-942-30  
; Sequence 30, Application US/09313942  
; Patent No. 6472179  
; GENERAL INFORMATION  
; APPLICANT: REGENERON PHARMACEUTICALS, INC



```

; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-30
```

```

Query Match      74.4%; Score 317; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 26 APTETQPPVTNLSVSEVNICTVIWMTNPPREGASSNCSLMYFSGHGDKODKXIAPETRRSI 85
    |||
Db 239 APTETQPPVTNLSVSEVNICTVIWMTNPPREGASSNCSLMYFSGHGDKODKXIAPETRRSI 298

QY 86 EYPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDPEASVTELOCIWHNLSYMKCSW 145
    |||
Db 299 EYPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDPEASVTELOCIWHNLSYMKCSW 358

QY 146 LPERNTSPDTNLTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVOIMV 205
    |||
Db 359 LPERNTSPDTNLTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVOIMV 418

QY 206 KDNAGKIKPSFNIIVPLTSRVKDPPEPHIKNLSFHNDLTYQWENPQNFISRCLEFEVEVNN 265
    |||
Db 419 KDNAGKIKPSFNIIVPLTSRVKDPPEPHIKNLSFHNDLTYQWENPQNFISRCLEFEVEVNN 478

QY 266 SOTETHNVFYQAKCENPEFERENVNTSCFMVPGVLPDLTNTVRIKVTNKLCYEDDKL 325
    |||
Db 479 SOTETHNVFYQAKCENPEFERENVNTSCFMVPGVLPDLTNTVRIKVTNKLCYEDDKL 538

QY 326 WSNWSQEMSIGKKRNST 342
    |||
Db 539 WSNWSQEMSIGKKRNST 555
```

```

RESULT 7
US-10-282-162-30
; Sequence 30, Application US/10282162
; Patent No. 6927044
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-B-US
; CURRENT APPLICATION NUMBER: US/10/282,162
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/787,835
; PRIOR FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-162-30
```

```

Query Match      74.4%; Score 317; DB 2; Length 784;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 26 APTETQPPVTNLSVSEVNICTVIWMTNPPREGASSNCSLMYFSGHGDKODKXIAPETRRSI 85
    |||
Db 239 APTETQPPVTNLSVSEVNICTVIWMTNPPREGASSNCSLMYFSGHGDKODKXIAPETRRSI 298

QY 86 EYPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDPEASVTELOCIWHNLSYMKCSW 145
    |||
Db 299 EYPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDPEASVTELOCIWHNLSYMKCSW 358

QY 146 LPERNTSPDTNLTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVOIMV 205
    |||
Db 359 LPERNTSPDTNLTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVOIMV 418

QY 206 KDNAGKIKPSFNIIVPLTSRVKDPPEPHIKNLSFHNDLTYQWENPQNFISRCLEFEVEVNN 265
    |||
Db 419 KDNAGKIKPSFNIIVPLTSRVKDPPEPHIKNLSFHNDLTYQWENPQNFISRCLEFEVEVNN 478

QY 266 SOTETHNVFYQAKCENPEFERENVNTSCFMVPGVLPDLTNTVRIKVTNKLCYEDDKL 325
    |||
Db 479 SOTETHNVFYQAKCENPEFERENVNTSCFMVPGVLPDLTNTVRIKVTNKLCYEDDKL 538

QY 326 WSNWSQEMSIGKKRNST 342
    |||
Db 539 WSNWSQEMSIGKKRNST 555
```

```

RESULT 8
US-09-313-942-32
; Sequence 32, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 793
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-32
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```

Query Match      74.4%; Score 317; DB 2; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 26 APTETQPPVTNLSVSEVNICTVIWMTNPPREGASSNCSLMYFSGHGDKODKXIAPETRRSI 85
    |||
Db 27 APTETQPPVTNLSVSEVNICTVIWMTNPPREGASSNCSLMYFSGHGDKODKXIAPETRRSI 86

QY 86 EYPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDPEASVTELOCIWHNLSYMKCSW 145
    |||
Db 87 EYPLNERICLQVSGQSTNESEKPSILVEKCISSPEGDPEASVTELOCIWHNLSYMKCSW 146

QY 146 LPERNTSPDTNLTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVOIMV 205
    |||
Db 147 LPERNTSPDTNLTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTXYKXDSFEQHSVOIMV 206

QY 206 KDNAGKIKPSFNIIVPLTSRVKDPPEPHIKNLSFHNDLTYQWENPQNFISRCLEFEVEVNN 265
    |||
Db 207 KDNAGKIKPSFNIIVPLTSRVKDPPEPHIKNLSFHNDLTYQWENPQNFISRCLEFEVEVNN 266

QY 266 SOTETHNVFYQAKCENPEFERENVNTSCFMVPGVLPDLTNTVRIKVTNKLCYEDDKL 325
    |||
Db 267 SOTETHNVFYQAKCENPEFERENVNTSCFMVPGVLPDLTNTVRIKVTNKLCYEDDKL 326

QY 326 WSNWSQEMSIGKKRNST 342
    |||
```

Db 327 WSNWSQEMSIGKKNST 343

RESULT 9  
US-10-282-162-32

; Sequence 32, Application US/10282162  
; Patent No. 6927044  
; GENERAL INFORMATION:  
; APPLICANT: REGENERON PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
; FILE REFERENCE: REG 203-B-US  
; CURRENT APPLICATION NUMBER: US/10/282,162  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: 09/787,835  
; PRIOR FILING DATE: 1999-09-22  
; PRIOR APPLICATION NUMBER: PCT/US99/22045  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 793  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-282-162-32

Query Match 74.4%; Score 317; DB 2; Length 793;  
Best Local Similarity 100.0%; Pred. No. 1.3e-309;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPTNLISVSVENLCTVITWNPPEGASNSCLMTFHSFGDKODKKIAPETRSI 85  
DB 27 APETOPPTNLISVSVENLCTVITWNPPEGASNSCLMTFHSFGDKODKKIAPETRSI 86  
QY 86 EVDPLNERICLVQVSGQSTNSEKPSILVEKICISPEGDPSAVTELQCIWHNLSYMKCSW 145  
DB 87 EVDPLNERICLVQVSGQSTNSEKPSILVEKICISPEGDPSAVTELQCIWHNLSYMKCSW 146  
QY 146 LPRNTPSPDNTNLTLYWHRSLKTHOCENIFREGQYFGCSFDLTLYVQWENPQNFISR 205  
DB 147 LPRNTPSPDNTNLTLYWHRSLKTHOCENIFREGQYFGCSFDLTLYVQWENPQNFISR 206  
QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLFEYEVVNN 265  
DB 207 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISRCLFEYEVVNN 266  
QY 266 SQTETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTNKLCYEDDKL 325  
DB 267 SQTETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTNKLCYEDDKL 326  
QY 326 WSNWSQEMSIGKKNST 342  
DB 327 WSNWSQEMSIGKKNST 343

RESULT 10  
US-09-949-016-8550

; Sequence 8550, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO: 8550  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8550

Query Match 54.2%; Score 231; DB 2; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1e-223;

Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 KIAPETRSIEVPLNERICLVQVSGQSTNSEKPSILVEKICISPEGDPSAVTELQCIW 135  
DB 1 KIAPETRSIEVPLNERICLVQVSGQSTNSEKPSILVEKICISPEGDPSAVTELQCIW 60  
QY 136 HNLSYMKCSWLPGNTPSDNTNLTLYWHRSLKTHOCENIFREGQYFGCSFDLTLYVQW 195  
DB 61 HNLSYMKCSWLPGNTPSDNTNLTLYWHRSLKTHOCENIFREGQYFGCSFDLTLYVQW 120  
QY 196 FEQHSVOIMWKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISR 255  
DB 121 FEQHSVOIMWKDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDDLYVQWENPQNFISR 180  
QY 256 CLFEYEVVNNSTQETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTL 306  
DB 181 CLFEYEVVNNSTQETHNVFYVQAKCENPEFERVENTSCFMVPGVLPDTL 231

RESULT 11  
US-09-688-286D-2

; Sequence 2, Application US/09688286D  
; Patent No. 6911530  
; GENERAL INFORMATION:  
; APPLICANT: Willison, Tracey  
; APPLICANT: Nicola, Nicos  
; APPLICANT: Hilton, Douglas  
; APPLICANT: Metcalf, Donald  
; APPLICANT: Zhang, Jian  
; TITLE OF INVENTION: A novel haemopoietin receptor and genetic sequences encoding sam  
; FILE REFERENCE: 23199-215  
; CURRENT APPLICATION NUMBER: US/09/688,286D  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: AU PN6135  
; PRIOR FILING DATE: 1995-10-23  
; PRIOR APPLICATION NUMBER: AU PN7276  
; PRIOR FILING DATE: 1995-12-22  
; PRIOR APPLICATION NUMBER: AU PP2208  
; PRIOR FILING DATE: 1996-09-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-688-286D-2

Query Match 10.1%; Score 43; DB 2; Length 424;  
Best Local Similarity 100.0%; Pred. No. 1.4e-34;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 YLRLKILIFPPIDPKIKFKEMFGQNDTTLWKKYDIYEKO 407  
DB 363 YLRLKILIFPPIDPKIKFKEMFGQNDTTLWKKYDIYEKO 405

RESULT 12

US-09-828-995B-50  
; Sequence 50, Application US/09828995B  
; Patent No. 6703360  
; GENERAL INFORMATION:  
; APPLICANT: Heska Corporation  
; APPLICANT: McCall, Catherine A.

APPLICANT: Tang, Liang A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IGG AND CANINE IL-13 R  
FILE REFERENCE: AL-7  
CURRENT APPLICATION NUMBER: US/09/828,995B  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 60/195,874  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/195,659  
PRIOR FILING DATE: 2000-04-07  
NUMBER OF SEQ ID NOS: 104  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 50  
LENGTH: 405  
TYPE: PRT  
ORGANISM: Canis familiaris  
US-09-828-995B-50

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 LLLYKRLKIIIPPIPPDKIFKEMFGDONDDTLHM 398  
Db 341 LLLYKRLKIIIPPIPPDKIFKEMFGDONDDTLHM 377

RESULT 13  
US-09-028-937-25  
Sequence 25, Application US/09028937  
Patent No. 6333031  
GENERAL INFORMATION:  
APPLICANT: Oleson, Lemart  
TITLE OF INVENTION: Receptor Derived Peptides As Modulators  
TITLE OF INVENTION: Of Receptor Activity  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fleht, Hohbach, Test, Albritton & Herbert  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/028,937  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/788,820  
FILING DATE: 23-JAN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/701,382  
FILING DATE: 22-AUG-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/612,999  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Silva, Robin M.  
REGISTRATION NUMBER: 38,304  
REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 949-8711  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown

TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-028-937-25

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.1e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 KODKIAPEPTRRSIEVPLNERI 93  
Db 1 KODKIAPEPTRRSIEVPLNERI 22

RESULT 14  
US-09-949-016-8825  
Sequence 8825, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6323  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6323

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GGGGGGGGAP 27  
Db 140 GGGGGGGGAP 149

RESULT 15  
US-09-949-016-6323  
Sequence 6323, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
PRIOR FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6323  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6323

Query Match  
Best Local Similarity 100.0%; Pred. No. 0.14;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 8, 2006, 01:30:58 ; Search time 188 Seconds  
(Without alignments)  
1049.625 Million cell updates/sec

Title: US-09-051-843d-4

Perfect score: 426

Sequence: 1 MEMPARLCGLMALLCAGGG.....QTKERTDVLLENLKASQ 426

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications\_AA\_Main:\*

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- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10B\_PUBCOMB.pep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                | Description        |
|------------|-------|-------------|--------|----|-------------------|--------------------|
| 1          | 401   | 94.1        | 427    | 4  | US-10-671-697-9   | Sequence 9, Appl1  |
| 2          | 401   | 94.1        | 427    | 6  | US-11-067-251-3   | Sequence 3, Appl1  |
| 3          | 401   | 94.1        | 427    | 6  | US-11-185-230-4   | Sequence 4, Appl1  |
| 4          | 401   | 94.1        | 427    | 6  | US-11-182-384-4   | Sequence 4, Appl1  |
| 5          | 401   | 94.1        | 427    | 6  | US-11-183-699A-4  | Sequence 4, Appl1  |
| 6          | 401   | 94.1        | 427    | 6  | US-11-149-309-37  | Sequence 3, Appl1  |
| 7          | 331   | 77.7        | 427    | 5  | US-10-850-270-4   | Sequence 8, Appl1  |
| 8          | 317   | 74.4        | 322    | 3  | US-09-825-561A-82 | Sequence 8, Appl1  |
| 9          | 317   | 74.4        | 322    | 5  | US-10-872-087-82  | Sequence 8, Appl1  |
| 10         | 317   | 74.4        | 664    | 5  | US-10-850-270-10  | Sequence 10, Appl1 |
| 11         | 317   | 74.4        | 776    | 3  | US-09-935-868-36  | Sequence 36, Appl1 |
| 12         | 317   | 74.4        | 780    | 3  | US-09-935-868-34  | Sequence 3, Appl1  |
| 13         | 317   | 74.4        | 784    | 3  | US-09-313-942-30  | Sequence 30, Appl1 |
| 14         | 317   | 74.4        | 784    | 3  | US-09-935-868-30  | Sequence 30, Appl1 |
| 15         | 317   | 74.4        | 784    | 4  | US-10-287-035-30  | Sequence 30, Appl1 |
| 16         | 317   | 74.4        | 784    | 4  | US-10-282-162-30  | Sequence 30, Appl1 |
| 17         | 317   | 74.4        | 784    | 6  | US-11-134-114-30  | Sequence 30, Appl1 |
| 18         | 317   | 74.4        | 783    | 3  | US-09-313-942-32  | Sequence 32, Appl1 |
| 19         | 317   | 74.4        | 783    | 3  | US-09-935-868-32  | Sequence 32, Appl1 |
| 20         | 317   | 74.4        | 783    | 4  | US-10-287-035-32  | Sequence 32, Appl1 |
| 21         | 317   | 74.4        | 783    | 4  | US-10-282-162-32  | Sequence 32, Appl1 |
| 22         | 317   | 74.4        | 783    | 6  | US-11-134-114-32  | Sequence 32, Appl1 |
| 23         | 313   | 73.5        | 776    | 4  | US-10-287-035-40  | Sequence 40, Appl1 |
| 24         | 311   | 73.0        | 776    | 4  | US-10-287-035-34  | Sequence 34, Appl1 |
| 25         | 297   | 69.7        | 776    | 3  | US-09-935-868-40  | Sequence 40, Appl1 |
| 26         | 297   | 69.7        | 776    | 3  | US-09-935-868-44  | Sequence 44, Appl1 |
| 27         | 297   | 69.7        | 776    | 6  | US-11-067-251-8   | Sequence 8, Appl1  |

|    |     |      |     |   |                  |                    |
|----|-----|------|-----|---|------------------|--------------------|
| 28 | 297 | 69.7 | 776 | 6 | US-11-067-251-10 | Sequence 10, Appl1 |
| 29 | 297 | 69.7 | 776 | 6 | US-11-067-251-12 | Sequence 12, Appl1 |
| 30 | 297 | 69.7 | 776 | 6 | US-11-067-251-14 | Sequence 14, Appl1 |
| 31 | 297 | 69.7 | 776 | 6 | US-11-067-251-16 | Sequence 16, Appl1 |
| 32 | 297 | 69.7 | 778 | 3 | US-09-935-868-16 | Sequence 46, Appl1 |
| 33 | 297 | 69.7 | 778 | 3 | US-09-935-868-50 | Sequence 50, Appl1 |
| 34 | 297 | 69.7 | 778 | 4 | US-10-287-035-46 | Sequence 46, Appl1 |
| 35 | 297 | 69.7 | 778 | 4 | US-10-287-035-50 | Sequence 50, Appl1 |
| 36 | 297 | 69.7 | 778 | 4 | US-10-287-035-56 | Sequence 56, Appl1 |
| 37 | 297 | 69.7 | 778 | 4 | US-10-287-035-56 | Sequence 60, Appl1 |
| 38 | 297 | 69.7 | 780 | 3 | US-09-935-868-38 | Sequence 38, Appl1 |
| 39 | 297 | 69.7 | 780 | 3 | US-09-935-868-42 | Sequence 42, Appl1 |
| 40 | 297 | 69.7 | 782 | 3 | US-09-935-868-48 | Sequence 48, Appl1 |
| 41 | 297 | 69.7 | 782 | 3 | US-09-935-868-52 | Sequence 48, Appl1 |
| 42 | 293 | 68.8 | 776 | 4 | US-10-287-035-36 | Sequence 52, Appl1 |
| 43 | 293 | 68.8 | 776 | 4 | US-10-287-035-44 | Sequence 36, Appl1 |
| 44 | 291 | 68.3 | 780 | 4 | US-10-287-035-38 | Sequence 44, Appl1 |
| 45 | 291 | 68.3 | 780 | 4 | US-10-287-035-38 | Sequence 38, Appl1 |

#### ALIGNMENTS

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RESULT 1
US-10-671-697-9
; Sequence 9, Application US/10671697
; Publication No. US20040043921A1
GENERAL INFORMATION:
APPLICANT: BONNEFOY, JEAN-YVES
GAUCHAT, JEAN-FRANCOIS
TITLE OF INVENTION: SUBSTANCES AND THEIR USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/671,697
FILING DATE: 29-Sep-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/545,002
FILING DATE: 06-APR-2000
APPLICATION NUMBER: US 08/969,125
FILING DATE: 12-NOV-1997
APPLICATION NUMBER: GB 9625899.1
FILING DATE: 13-DEC-1996
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-671-697-9
Query Match 94.1%; Score 401; DB 4; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 APTETOPVNLIVSVENLCTVITWNPFGASNGSLWYFSHRGDKDKKIAPEFRSI 85
DB 27 APTETOPVNLIVSVENLCTVITWNPFGASNGSLWYFSHRGDKDKKIAPEFRSI 86
QY 86 EVPLNERICLVQVSGSTNESEKPSILVERKISPFGDPESAVTELOCIMHNLVSYMKSW 145
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Db      87 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 146
      146 LRGRTNSPDTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTQKXDSFEQHSVQIYW 205
      147 LRGRTNSPDTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTQKXDSFEQHSVQIYW 206
Qy      206 KUNAGKIKPSFNIIVPLTSRVKPDPPHIKNLSFHNDLLYQWENPQNFISRCLEFYEEVANN 265
      207 KUNAGKIKPSFNIIVPLTSRVKPDPPHIKNLSFHNDLLYQWENPQNFISRCLEFYEEVANN 266
Qy      266 SOTETHNIVFYVOAKCENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 325
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Db      326 WSNWSQEMSIGKKRNSTLYITMLLIVPVIAGAILVLLYLKRLKIIIPPIPDGKIFK 385
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Qy      386 EMFGQNDPDTLHMKKYDIYEKQTEKETSVDVLIENLKKASQ 426
      387 EMFGQNDPDTLHMKKYDIYEKQTEKETSVDVLIENLKKASQ 427
Db
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RESULT 2
US-11-067-251-3
; Sequence 3, Application US/11067251
; Publication No. US20050191730A1
; GENERAL INFORMATION:
; APPLICANT: Karow, Margaret
; APPLICANT: Fairhurst, Jeanette
; TITLE OF INVENTION: IL-4/IL-13 Specific Polypeptides and Therapeutic Uses Thereof
; FILE REFERENCE: 2020A
; CURRENT APPLICATION NUMBER: US/11/067,251
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: 60/548,541
; PRIOR FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: 60/602,139
; PRIOR FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 60/628,343
; PRIOR FILING DATE: 2004-11-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastaSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-067-251-3
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Query Match      94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      86 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 145
      87 EVPLNRIQLQVGSQOSTNESEKPSILVEKCIISPREDPESAVTELOCIWHNLSYMKCSW 146
Qy      146 LRGRTNSPDTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTQKXDSFEQHSVQIYW 205
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Db      206 KUNAGKIKPSFNIIVPLTSRVKPDPPHIKNLSFHNDLLYQWENPQNFISRCLEFYEEVANN 265
      207 KUNAGKIKPSFNIIVPLTSRVKPDPPHIKNLSFHNDLLYQWENPQNFISRCLEFYEEVANN 266
Qy      266 SOTETHNIVFYVOAKCENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 325
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Db
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Qy      326 WSNWSQEMSIGKKRNSTLYITMLLIVPVIAGAILVLLYLKRLKIIIPPIPDGKIFK 385
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RESULT 3
US-11-185-230-4
; Sequence 4, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vito, Natalio
; TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
; FILE REFERENCE: IVD924 US CNT 1
; CURRENT APPLICATION NUMBER: US/11/185,230
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 427
; TYPE: PRT 3
; ORGANISM: Homo sapiens
; FEATURE:
US-11-185-230-4
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      146 LRGRTNSPDTNLTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTQKXDSFEQHSVQIYW 205
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Db      206 KUNAGKIKPSFNIIVPLTSRVKPDPPHIKNLSFHNDLLYQWENPQNFISRCLEFYEEVANN 265
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Qy      266 SOTETHNIVFYVOAKCENPEFERNVENTSCEFWPGVLPDTLNTVRIRVKTNKLCEYDDXL 325
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Db      326 WSNWSQEMSIGKKRNSTLYITMLLIVPVIAGAILVLLYLKRLKIIIPPIPDGKIFK 385
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RESULT 4
US-11-182-384A-4
; Sequence 4, Application US/11182384A
; Publication No. US20060035855A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
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APPLICANT: Laurent, Patrick
APPLICANT: Vltá, Natallio
TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
FILE REFERENCE: IVD924 US Div 2
CURRENT APPLICATION NUMBER: US/11/182,384A
CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: 09/077,817
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/FR96/01756
PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 4
LENGTH: 427
TYPE: PRT
ORGANISM: Homo sapiens
US-11-182-384A-4

Query Match      94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 87 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEDPSAVTELQCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTNLTLYYHRSLEKIHQENIFREGQYGCSPDLTKVDSSEFGHSVQIMV 205
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DB 207 KDNAGKIKPSFNIVPLTSRKPDPPRIKNTSFHNDLIYVQWENPQNTISRCLFYEVEVNN 266
QY 266 SQTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 325
DB 267 SQTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 326
QY 326 WSNWSQEMSGIKRNSLTLYTMLLIYVYVAGAIIVLLLYKRLKIIIFPIPDGKIFK 385
DB 327 WSNWSQEMSGIKRNSLTLYTMLLIYVYVAGAIIVLLLYKRLKIIIFPIPDGKIFK 386
QY 386 EMFGDNDDTLHMKKYDIYEKQTEETDSVLLIENLKKAQ 426
DB 387 EMFGDNDDTLHMKKYDIYEKQTEETDSVLLIENLKKAQ 427

RESULT 5
US-11-183-599A-4
Sequence 4, Application US/11183599A
Publication No. US20060035856A1
GENERAL INFORMATION:
APPLICANT: Caput, Daniel
APPLICANT: Ferrara, Pasqual
APPLICANT: Laurent, Patrick
APPLICANT: Vltá, Natallio
TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
FILE REFERENCE: IVD924 US Div 1
CURRENT APPLICATION NUMBER: US/11/183,599A
CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: 09/077,817
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: PCT/FR96/01756
PRIOR FILING DATE: 1996-11-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.3
SEQ ID NO 4
LENGTH: 427
TYPE: PRT
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ORGANISM: Homo sapiens
US-11-183-599A-4

Query Match      94.1%; Score 401; DB 6; Length 427;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 87 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEDPSAVTELQCIWHNLSYMKCSW 146
QY 146 LPRGNTSPDNTNLTLYYHRSLEKIHQENIFREGQYGCSPDLTKVDSSEFGHSVQIMV 205
DB 147 LPRGNTSPDNTNLTLYYHRSLEKIHQENIFREGQYGCSPDLTKVDSSEFGHSVQIMV 206
QY 206 KDNAGKIKPSFNIVPLTSRKPDPPRIKNTSFHNDLIYVQWENPQNTISRCLFYEVEVNN 265
DB 207 KDNAGKIKPSFNIVPLTSRKPDPPRIKNTSFHNDLIYVQWENPQNTISRCLFYEVEVNN 266
QY 266 SQTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 325
DB 267 SQTETHNVFVVOEAKCENPEFERNVENTSCFMVPGVLPDLNTVRIKVTNKLCEYEDKL 326
QY 326 WSNWSQEMSGIKRNSLTLYTMLLIYVYVAGAIIVLLLYKRLKIIIFPIPDGKIFK 385
DB 327 WSNWSQEMSGIKRNSLTLYTMLLIYVYVAGAIIVLLLYKRLKIIIFPIPDGKIFK 386
QY 386 EMFGDNDDTLHMKKYDIYEKQTEETDSVLLIENLKKAQ 426
DB 387 EMFGDNDDTLHMKKYDIYEKQTEETDSVLLIENLKKAQ 427

RESULT 6
US-11-149-309-37
Sequence 37, Application US/11149309
Publication No. US20060063228A1
GENERAL INFORMATION:
APPLICANT: Kasaiian, Marion T.
APPLICANT: Tchistiakova, Lioudmila
APPLICANT: Veldman, Geertuida M.
APPLICANT: Marquette, Kimberly Ann
APPLICANT: Tan, Xiang-Yang
APPLICANT: Donaldson, Debra D.
APPLICANT: Lin, Laura Long
APPLICANT: Shane, Tania
APPLICANT: Tam, Amy Szepui
APPLICANT: Feyfaut, Eric
APPLICANT: Wood, Nancy L.
APPLICANT: Fitz, Lori J.
APPLICANT: Widom, Angela M.
APPLICANT: Parris, Kevin D.
APPLICANT: Goldman, Samuel J.
TITLE OF INVENTION: Antibodies against Human Interleukin-13 and Uses Therefor
FILE REFERENCE: 16158-048001 / AM101493
CURRENT APPLICATION NUMBER: US/11/149,309
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: US 60/578,473
PRIOR FILING DATE: 2004-06-09
PRIOR APPLICATION NUMBER: US 60/581,375
PRIOR FILING DATE: 2004-06-22
PRIOR APPLICATION NUMBER: US 60/578,736
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.3
SEQ ID NO 37
LENGTH: 427
TYPE: PRT
ORGANISM: Homo sapiens
US-11-149-309-37
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Query Match 94.1%; Score 401; DB 6; Length 427;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETOPPYTNLSVSVENICTVIWNNPPEGASSNCSLMYFSHFGDKODKKAIPETRRS1 85  
DB 27 APTETOPPYTNLSVSVENICTVIWNNPPEGASSNCSLMYFSHFGDKODKKAIPETRRS1 86  
QY 86 EYPLNERICLQVGSQOSTNESEKPSILVEKCI SPPEGDPESATELOCIWHNLSYMKCSW 145  
DB 87 EYPLNERICLQVGSQOSTNESEKPSILVEKCI SPPEGDPESATELOCIWHNLSYMKCSW 146  
QY 146 LPEGNTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 205  
DB 147 LPEGNTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 206  
QY 206 KDNAGKIKPSFNI VPLTSRKVPDPPHIKNLSFHNDDL YQWENPQNFISRCLEFEVEVNN 265  
DB 207 KDNAGKIKPSFNI VPLTSRKVPDPPHIKNLSFHNDDL YQWENPQNFISRCLEFEVEVNN 266  
QY 266 SOTETHNVFVVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL CYEDDKL 325  
DB 267 SOTETHNVFVVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL CYEDDKL 326  
QY 326 WSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAII VLLLYLKRKLIIPPIPDGKIFK 385  
DB 327 WSNWSQEMSIGKKRNSTLYITMLLIVPVI VAGAII VLLLYLKRKLIIPPIPDGKIFK 386  
QY 386 EMFGDNDDTLHMKKYDIYKQTKETDSVLLIENLKKASQ 426  
DB 387 EMFGDNDDTLHMKKYDIYKQTKETDSVLLIENLKKASQ 427

## RESULT 7

US-10-850-270-4  
; Sequence 4, Application US/10850270  
; Publication No. US20050058645A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)  
; APPLICANT: Dunlop, Felicity (US only)  
; APPLICANT: Baca, Manuel (US only)  
; APPLICANT: Nash, Andrew (US only)  
; APPLICANT: Fabri, Louis (US only)  
; TITLE OF INVENTION: Novel peptides  
; FILE REFERENCE: 12175890/ECH  
; CURRENT APPLICATION NUMBER: US/10/850,270  
; CURRENT FILING DATE: 2004-05-20  
; PRIOR APPLICATION NUMBER: AU PS1301  
; PRIOR FILING DATE: 2002-03-22  
; PRIOR APPLICATION NUMBER: AU 2003900437  
; PRIOR FILING DATE: 2003-02-03  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 4  
; LENGTH: 427  
; TYPE: PRT  
; ORGANISM: human  
US-10-850-270-4

Query Match 77.7%; Score 331; DB 5; Length 427;  
Best Local Similarity 100.0%; Pred. No. 36-302;  
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETOPPYTNLSVSVENICTVIWNNPPEGASSNCSLMYFSHFGDKODKKAIPETRRS1 85  
DB 27 APTETOPPYTNLSVSVENICTVIWNNPPEGASSNCSLMYFSHFGDKODKKAIPETRRS1 86  
QY 86 EYPLNERICLQVGSQOSTNESEKPSILVEKCI SPPEGDPESATELOCIWHNLSYMKCSW 145  
DB 87 EYPLNERICLQVGSQOSTNESEKPSILVEKCI SPPEGDPESATELOCIWHNLSYMKCSW 146  
QY 146 LPEGNTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 205

DB 147 LPEGNTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 206  
QY 206 KDNAGKIKPSFNI VPLTSRKVPDPPHIKNLSFHNDDL YQWENPQNFISRCLEFEVEVNN 265  
DB 207 KDNAGKIKPSFNI VPLTSRKVPDPPHIKNLSFHNDDL YQWENPQNFISRCLEFEVEVNN 266  
QY 266 SOTETHNVFVVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL CYEDDKL 325  
DB 267 SOTETHNVFVVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL CYEDDKL 326  
QY 326 WSNWSQEMSIGKKRNSTLYITMLLIVPVI V 356  
DB 327 WSNWSQEMSIGKKRNSTLYITMLLIVPVI V 357

## RESULT 8

US-09-825-561A-82  
; Sequence 82, Application US/09825561A  
; Patent No. US20020137677A1  
; GENERAL INFORMATION:  
; APPLICANT: Sprecher, Cindy A.  
; APPLICANT: No. US20020137677A1ak, Julia E.  
; APPLICANT: West, James W.  
; APPLICANT: Presnell, Scott R.  
; APPLICANT: Holly, Richard D.  
; APPLICANT: Nelson, Andrew J.  
; TITLE OF INVENTION: SOLUBLE ZALPHAL1 CYTOKINE RECEPTORS  
; FILE REFERENCE: 00-22  
; CURRENT APPLICATION NUMBER: US/09/825,561A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/194,731  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/222,121  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 82  
; LENGTH: 322  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-561A-82

Query Match 74.4%; Score 317; DB 3; Length 322;  
Best Local Similarity 100.0%; Pred. No. 3-5e-289;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETOPPYTNLSVSVENICTVIWNNPPEGASSNCSLMYFSHFGDKODKKAIPETRRS1 85  
DB 6 APTETOPPYTNLSVSVENICTVIWNNPPEGASSNCSLMYFSHFGDKODKKAIPETRRS1 65  
QY 86 EYPLNERICLQVGSQOSTNESEKPSILVEKCI SPPEGDPESATELOCIWHNLSYMKCSW 145  
DB 66 EYPLNERICLQVGSQOSTNESEKPSILVEKCI SPPEGDPESATELOCIWHNLSYMKCSW 125  
QY 146 LPEGNTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 205  
DB 126 LPEGNTSPDTNNTLYYWHRSLEKIHOCENIFREGQYFGCSFDLTXYKXSSFEQHSVOIMV 185  
QY 206 KDNAGKIKPSFNI VPLTSRKVPDPPHIKNLSFHNDDL YQWENPQNFISRCLEFEVEVNN 265  
DB 207 KDNAGKIKPSFNI VPLTSRKVPDPPHIKNLSFHNDDL YQWENPQNFISRCLEFEVEVNN 266  
QY 266 SOTETHNVFVVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL CYEDDKL 325  
DB 246 SOTETHNVFVVOAKCENEFERNVENTSCFMVPGVLPDTLNTVRIRVKTNKL CYEDDKL 305  
QY 326 WSNWSQEMSIGKKRNST 342  
DB 306 WSNWSQEMSIGKKRNST 322

## RESULT 9



```
US-10-872-087-82
; Sequence 82, Application US/10872087
; Publication No. US20040235743A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Novak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22D1
; CURRENT APPLICATION NUMBER: US/10/872,087
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US 60/194,731
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 09/825,561
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-087-82

Query Match          74.4%; Score 317; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 3,5e-289;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPVNTNLSVSENLCTVIWTWNPPEGASSNCSLMYFSHFGDKODKXIAPETRST 85
DB 6 APETOPPVNTNLSVSENLCTVIWTWNPPEGASSNCSLMYFSHFGDKODKXIAPETRST 65
QY 86 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEEDPESAVTELOCIWHNLSYMKCSW 145
DB 66 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEEDPESAVTELOCIWHNLSYMKCSW 125
QY 146 LPRGNTSPDTNNTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 205
DB 126 LPRGNTSPDTNNTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 185
QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYOWENPQNFISRCLFYEVAVNN 265
DB 186 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYOWENPQNFISRCLFYEVAVNN 245
QY 266 SQETHNHVFYVOAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRIRVKTNKLCEYEDDKL 325
DB 246 SQETHNHVFYVOAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRIRVKTNKLCEYEDDKL 305
QY 326 WSNWSQEMSIGKKRNT 342
DB 306 WSNWSQEMSIGKKRNT 322

RESULT 10
US-10-850-270-10
; Sequence 10, Application US/10850270
; Publication No. US20050058645A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd (for all States except the US)
; APPLICANT: Dunlop, Felicity (US only)
; APPLICANT: Baca, Manuel (US only)
; APPLICANT: Nash, Andrew (US only)
; APPLICANT: Rabi, Louis (US only)
; TITLE OF INVENTION: Novel peptides
; FILE REFERENCE: 1215890/EJH
; CURRENT APPLICATION NUMBER: US/10/850,270
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: AU PS1301
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: AU 2003900437
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; PRIOR FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 664
; TYPE: PRT
; ORGANISM: human
US-10-850-270-10

Query Match          74.4%; Score 317; DB 5; Length 664;
Best Local Similarity 100.0%; Pred. No. 6,5e-289;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPVNTNLSVSENLCTVIWTWNPPEGASSNCSLMYFSHFGDKODKXIAPETRST 85
DB 45 APETOPPVNTNLSVSENLCTVIWTWNPPEGASSNCSLMYFSHFGDKODKXIAPETRST 104
QY 86 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEEDPESAVTELOCIWHNLSYMKCSW 145
DB 105 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEEDPESAVTELOCIWHNLSYMKCSW 164
QY 146 LPRGNTSPDTNNTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 205
DB 165 LPRGNTSPDTNNTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 224
QY 206 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYOWENPQNFISRCLFYEVAVNN 265
DB 225 KDNAGKIKPSFNIVPLTSRVKPPPHIKNLSFHNDLLYOWENPQNFISRCLFYEVAVNN 284
QY 266 SQETHNHVFYVOAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRIRVKTNKLCEYEDDKL 325
DB 285 SQETHNHVFYVOAKCENPEFERNVENTSCFMVPGVLPDTLNTVIRIRVKTNKLCEYEDDKL 344
QY 326 WSNWSQEMSIGKKRNT 342
DB 345 WSNWSQEMSIGKKRNT 361

RESULT 11
US-09-935-868-36
; Sequence 36, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneration Pharmaceuticals, Inc
; APPLICANT: Regeneration Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-36

Query Match          74.4%; Score 317; DB 3; Length 776;
Best Local Similarity 100.0%; Pred. No. 7,5e-289;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APETOPPVNTNLSVSENLCTVIWTWNPPEGASSNCSLMYFSHFGDKODKXIAPETRST 85
DB 232 APETOPPVNTNLSVSENLCTVIWTWNPPEGASSNCSLMYFSHFGDKODKXIAPETRST 291
QY 86 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEEDPESAVTELOCIWHNLSYMKCSW 145
DB 292 EVPLNERICLOVGSQCSSTNESEKPSILVEKCISSPEEDPESAVTELOCIWHNLSYMKCSW 351
QY 146 LPRGNTSPDTNNTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 205
DB 352 LPRGNTSPDTNNTLYWHRSLSEKIHOCENIFREGQYFGCSFDLTWKVDSFEQHSVOIMV 411
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QY 146 LPRNTSPDTNYTLTYWHRSLKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 205  
 Db 359 LPRNTSPDTNYTLTYWHRSLKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 418  
 QY 206 KDNAGKIKPSFNIVPLTSRYKPDPPHINKLSFHNDLTYQWENPQNFISRLCFYEVEVNN 265  
 Db 419 KDNAGKIKPSFNIVPLTSRYKPDPPHINKLSFHNDLTYQWENPQNFISRLCFYEVEVNN 478  
 QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 325  
 Db 479 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 538  
 QY 326 WSNWSQEMSIGKKRNST 342  
 Db 539 WSNWSQEMSIGKKRNST 555

Db 539 WSNWSQEMSIGKKRNST 555  
 Search completed: July 8, 2006, 01:34:51  
 Job time : 189 secs

RESULT 15  
 US-10-287-035-30  
 ; Sequence 30, Application US/10287035  
 ; Publication No. US20030104567A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neil Stahl and George D. Yancopoulos  
 ; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING  
 ; FILE REFERENCE: REG 203DA  
 ; CURRENT APPLICATION NUMBER: US/10/287,035  
 ; PRIOR FILING DATE: 2002-11-01  
 ; PRIOR APPLICATION NUMBER: USSN 09/935,868  
 ; PRIOR FILING DATE: 2001-08-23  
 ; PRIOR APPLICATION NUMBER: USSN 09/787,835  
 ; PRIOR FILING DATE: 2001-03-22  
 ; PRIOR APPLICATION NUMBER: USSN 09/313,942  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: 09/313,942  
 ; PRIOR FILING DATE: 1999-05-19  
 ; PRIOR APPLICATION NUMBER: 60/101,858  
 ; PRIOR FILING DATE: 1998-09-25  
 ; NUMBER OF SEQ ID NOS: 60  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 30  
 ; LENGTH: 784  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-287-035-30

Query Match 74.4%; Score 317; DB 4; Length 784;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-289;  
 Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 APTETQPPVTNLVSVENICTVITWTNMPREGASSNCSLWYFSHFGDKODKKIAPETRAST 85  
 Db 239 APTETQPPVTNLVSVENICTVITWTNMPREGASSNCSLWYFSHFGDKODKKIAPETRAST 298  
 QY 86 EYPLNERICLOVSSQCSSTNESEKPSILVEKISPPREGDPESAVTELOCIMHNLSTYMKCSW 145  
 Db 299 EYPLNERICLOVSSQCSSTNESEKPSILVEKISPPREGDPESAVTELOCIMHNLSTYMKCSW 358  
 QY 146 LPRNTSPDTNYTLTYWHRSLKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 205  
 Db 359 LPRNTSPDTNYTLTYWHRSLKIHOCENIFREGQYFGCSFDLTKVDSSEFQHSVQIMV 418  
 QY 206 KDNAGKIKPSFNIVPLTSRYKPDPPHINKLSFHNDLTYQWENPQNFISRLCFYEVEVNN 265  
 Db 419 KDNAGKIKPSFNIVPLTSRYKPDPPHINKLSFHNDLTYQWENPQNFISRLCFYEVEVNN 478  
 QY 266 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 325  
 Db 479 SOTETHNVFYVOEAKCENPEFERVENTSCFMVPGVLPDTLNTVIRIKTKNKLCEBDDKL 538  
 QY 326 WSNWSQEMSIGKKRNST 342

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